STIC-Biotech/Ch mLib

Fr m: Sent:

Chan, Christina

To:

Subject:

Tuesday, January 07, 2003 10:25 AM
Duffy, Patricia; STIC-Biotech/ChemLib
RE: PLEASE RUSH SEQUENCE SEARCH--- Amendment due this Biweek

importance:

High

Please rush: Thanks Chris

Chris Chan TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From: Duffy, Patricia
Sent: Monday, January 06, 2003 10:43 AM
To: Chan, Christina

Subject:

PLEASE RUSH SEQUENCE SEARCH--- Amendment due this Biweek

Importance: High

In re: 09/438,185

Please search SEQ ID NO:1047.

Please search na residues 1200675-1199590 of SEQ ID NO:1.

Please include an interference search.

Please print out top 50 hits in each category.

Thank you.



AU 1645

703-305-7555

POINT OF CONTACT: PAUL SCHULWITZ TECHNICAL INFO. SPECIALIST CM1 6B06 TEL. (703) 305-1954

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CURRENT FILING DATE: 1998-12-03
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EARLIER PLILAGATION NUMBER: 08/88,534
EARLIER APPLICATION NUMBER: 08/88,534
EARLIER PILING DATE: 1997-07-07
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FactSEQ for Windows Version 4.0
LENGTH: 1642
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US-10-007-693-117
US-09-864-761-16616
US-09-842-552-90
              0 US-09-770-791-78

0 US-09-770-791-78

0 US-09-86-801A-60

0 US-09-98-842A-4005

0 US-09-76-864-1726

0 US-09-76-864-1726

0 US-09-76-891-39-235

US-09-78-897

US-10-046-935-897

US-09-878-170-446-89

0 US-09-878-170-446-89

0 US-09-881-576-490

0 US-09-881-576-490

0 US-09-881-576-548
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US-09-795-686-1
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RESULT 2

1. Sequence 314, Application US/09205658

1. Patent No. US20010029617A1

1. GENERAL INFORMATION:

1. APPLICANT: NUVENN. GAY

2. APPLICANT: OGY. SCOCT

2. TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

3. TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS

3. TITLE OF INVENTION: UMPAIRED GLUCOSE TOLERANCE CONDITIONS

5. TILLE REFERENCE: 00786/331004

5. CURRENT APPLICATION NUMBER: US/09/205,658

5. CURRENT FILING DATE: 1998-12-03
                                                                                                                                                 933 ATATCTT 927
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APPLICANT: Ruvkun, Gary
APPLICANT: Ogg, Scott
TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR
TITLE OF INVENTION: IMPAIRED GLUCOSE TOLERANCE CONDITIONS
FILE REFERENCE: 00786/351004

Sequence 312, Application US/09205658 Patent No. US20010029617A1 GENERAL INFORMATION:

09-205-658-312/c

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LENGTH: 640681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 cGAACGTATTGAGTGCAGAAGAAGACACGATATGCAAGACCTGCCAAGAATCACGAGCT 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 ATAAGTCCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 CCATTITCITITACIGGAG-AAICGGCAGCGICATCAGACGAGAGCGAAAITCAAIGGA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 AGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400 AAAGAAGTAGAGGTTGCAAGCTTCTTCAAA-----TCTTCCTCTGATGCTCCAAGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                         579 TCAACAACACGATCCGGATCAAAACGAATAATGGTTGCACTACCCTCAACGGCATGTTGC 520
                                                                                                                                                                                                                                                                                                                                                                          113 TCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                639 TCTTCAAAATTTCTAGTATAGAAATACGCTGGAAAGTAGTAATGAGACATTCTTGC 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HESULT 3
US-09-790-988-1
Sequence 1, Application US/09790988
Factent No. US20020127687A1
SEQUENCE 1, NFORMATION:
APPLICANT: WATANABE, HIDEMI
APPLICANT: MATANABE, HORSEN
CURRENT FILME DATE: 2001-00-23
CURRENT FILME DATE: 2001-00-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 1
                                                                                                                                                                                                                                                                                        Score 41.4; DB 10; Length 817;
Pred. No. 0.28;
0; Mismatches 281; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        593 GCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 08/857,076
EARLIER FILING DATE: 1997-05-15
EARLIER PLING DATE: 1997-05-15
EARLIER PLING DATE: 1997-07-07
EARLIER PLILAGE DATE: 1997-07-07
EARLIER APPLICATION NUMBER: US98/10080
EARLIER FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 328
SEQ_ID NO 314
                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-205-658-314
                                                                                                                                                                                                                                                                                                  Query Match 3.8%;
Best Local Similarity 45.2%;
Matches 239; Conservative (
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Xu, Tian TITLE OF INVENTED KUZ: A NO. US20020127621A1el Family of Metalloproteases NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 190362 CATCTAAATTATTAAATAAACACTCTTTAAATACTTTAGTAATAGTTTCTTTTAGTCGT 190421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 190302 ACTAATTTAGTACAAAAAAAAATCATATCATAGAAGAAATAATCATATTCGATACGCAT 190361
                                                                                                                                                                                                                                                                                                                                                                                                                            Db 190242 AATCGAAACATCGTAACAACACGTGTAATAGATCTTTTTAATTTTTAAATATACAACAT 190301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             479 AAAAGGICAIGGAIGAGAICAGGAGITAAGGAGAAAITAICIITAATCGAGAGIICGCAII 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 CTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCT 478
                                                                                                                                                                                                                                                                                                                                                                                 299 CCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGTAGGGTT 358
                                                                                                                                                                                                                                                                                 179 ATCTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCC 238
                                                                                                                                                                               119 AAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATA 178
                                                                                                                                    0; Gaps
                                                                                Query Match 3.7%; Score 40.6; DB 10; Length 640681; Best Local Similarity 43.4%; Pred. No. 7.3; Matches 187; Conservative 0; Mismatches 244; Indels 0; C
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APPLICATION NUMBER: US/09/871,388
FILING DATE: 31-May-2001
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION NUMBER: 08/937,931
FILING DATE: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09871388
Patent No. US20020127621A1
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan, Duojia
Rooke, Jenny
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yavari, Reza
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TYPE: DNA
CORGANISM: Buchnera Sp.
US-09-790-988-1
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APPLICANT: Harper, Jeff
APPLICANT: Harper, Jeff
APPLICANT: Areps, Joel
APPLICANT: Areps, Joel
APPLICANT: Harper, Joel
APPLICANT: Hang, Xuol
APPLICANT: Alu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
CURRENT PELLOATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/224,647
PRIOR PLILNG DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
LENGTH: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 1789 TAGGTGTTGATGTTTACAAGTGAATTCTAGTGTTTTCTCTTTGAGATCTGTGAAGTTTGA 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 TATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTTAGTGAAGAGTCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 TATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTTAGTGAAGAGTCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
3.4%; Score 36.4; DB 9; Length 2000;
Best Local Similarity 59.8%; Pred. No. 7.4%
Matches 61; Conservative 0; Mismatches 41; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 256, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM: Arabidopsis thaliana US-09-938-842A-3348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Arabidopsis thallana US-09-887-576-256
  Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Budworth, P.
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US-09-887-576-256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Flacker, Karen
APPLICANT: Flacker, Karen
APPLICANT: Flacker, Stanislaw
APPLICANT: Flacker, Jack
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION (0.20020144304Alel Plant Expression Constructs
FILE REFERENCE: 38-21(51499)B
CURRENT APPLICATION UNDER: US/09/737,626A
CURRENT FILING DATE: 2002-02-25
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.0
LENGTH: 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: promoter (1). (1241)
OTHER INFORMATION: n- a or g or c or t/u
OTHER INFORMATION: Act7 promoter polynucleotide sequence and intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Best Local Similarity 65.1%; Pred. No. 7;
Matches 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 3.4%; Score 36.4; DB 10; Length 1241; Best Local Similarity 59.8%; Pred. No. 6.3; Matches 61; Conservative 0; Mismatches 41; Indels 0;
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                                                         REFERENCE/DOCKET NUMBER: 897-081
TELECONMUNICATION INFORMATION:
TELEFAX: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                TOPOLOGY: Ilnear

MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-871-388-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-938-842A-3348
: Sequence 3348, Application US/09938842A
                       NAME: OSMAN, RICHARD A REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 25, Application US/09737626A
; Patent No. US20020144304A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1076 AGGCTACTGAAATATTATTAT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      876 AAAATTCTAAAATAGAAATGCAT 898
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-737-626A-25
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APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
TITLE OF INVENTION: Inhibition of Specific Histone Deacetylase Isoforms
FILE REFERENCE: 106101.145
CURRENT APPLICATION NUMBER: US/09/817,913
CURRENT FILING DATE: 2000-03-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGING 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799 AACAGCCATATCAGIGGAGCAACCTTCCCTTIGATTCTTTGATAATGACAGAAGAIGAAC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            859 AAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGGTAAAGCTTG 918
                                                                                                               799 AACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAAC 858
                                                                                                                                                                                                                                                                                                                                          Sequence 111 Application US/10033528;
Sequence 111 Application US/10033528;
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Scrist, Heather;
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER;
FILE DE INVENTION: AND DIAGNOSIS OF COLON CANCER;
FILE REPERENCE: 2001-15-4701
CURRENT APPLICATION WUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEQ ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 111
LENGTH: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.3%; Score 36.2; DB 12; Length 580; Best Local Similarity 53.1%; Pred. No. 5.2; Matches 77; Conservative 0; Mismatches 68; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        919 CTTCTCTTTATTTCCTTTTGTAGA 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 TTCATCTCCACTGTCTTCATGAACA 527
                                                                                                                                                                                            919 CTTCTCTTTATTTTCCTTTTGTAGA 943
                                                                                                                                                                                                                                  503 Trcarcrccacrcrcrcrcardadca 527
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US-09-817-913-4/c
; Sequence 4, Application US/09817913
; Patent No. US20020061860A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-033-528-111
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GENERAL INCRMATION
GENERAL INCRMATION
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOOLOO
CURRENT APPLICATION NUMBER: US/09/731,231A
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASASEQ for Windows Version 4.0
SEQ ID NO 3.6
SOFTWARE: PASASEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 42622 AGATGACAATAAAATCAAGATACAAATTGAGTTTTAAGAAGCAACAAAAGCTGA 42563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            815 GAGCAACCITCCCITICATTCTTIGATAAIGACAGAAGAIGAACAAAGAGIAAGITITIG 874
1789 IAGGIGITGAIGITIACAAGTGAAITCTAGIGITITCTCTITGAGAICTGIGAAGTTIGA 1848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.4%; Score 36.4; DB 10; Length 326014; Best Local Similarity 52.7%; Pred. No. 65; Astches 79; Conservative 0; Mismatches 71; Indels 0; Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
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Sequence 111, Application US/09920300A

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangfulun
APPLICANT: Secrist, Heather
ITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 2.10.12.1.547
CURRENT APPLICATION UNMBER: US/09/920,300A

CURRENT FILING DATE: 2.001-07-31

NUMBER OF SEQ ID NOS: 1789

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                            421 TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 42502 TIAAATTATAATCTAGGCAAGAAGTTGTT 42473
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                                                                                                                                                                              RESULT 8
US-09-731-231A-3/c
Sequence 3, Application US/09731231A
; Patent No. US20020082189A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
COCATION: (1)...(326014)
OTHER INFORMATION: n = A,T,C or G
US-09-731-231A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
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US-09-920-300A-111
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SOFTWARE: FASTS
SEQ ID NO 111
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Db 18667 GCAGGGTTTATGACGGGCATAGAAGAGACTGACTTTTTATTAGACTTTTCGTTATTTGC 18726
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DD 18727 TTTTAACTAGAAATTAAAATTTAAAAATTACCAAAAAAGCAATGTAATT 18779
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US-09-764 869-1955
Sequence 1955, Application US/09764869
Sequence 1955, Application US/09764869
Sequence 1955, Application US/09764869
Sequence 1955, Application US/09764869
TITLE OF INVENTION:
TITLE OF INVENTION:
SETTE REFERENCE: PC007
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 2442
SEQ ID NO 1955
SEQ ID NO 1955
LENGTH: 32191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 31920 TTTTAACTAGAGAAAATTAAGTTTTTAAAAATTACCAAAAAAGGAATGTAATT 31972
                                                                                                                                                                                                                               Length 18998;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Indels
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Best Local Similarity 57.5%; Pred. No. 23;
Matches 65; Conservative 0; Mismatches
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Best Local Similarity 57.5%; Pred. No. 28;
Matches 65; Conservative 0; Mismatches
                                                                                                  ; LOCATION: (1690)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-869-1952
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US-09-815-242-4614
US-09-815-242-4614
Sequence 4614, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Obligen, Rari L.
  LENGTH: 18998
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-764-869-1955
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APPLICANT: Li, Zuomei
APPLICANT: Li, Zuomei
APPLICANT: Li, Zuomei
APPLICANT: Bonfils, Claire
APPLICANT: Besterman, Jeffrey
TITLE OF INVENTION: Antisense Oligonucleotide Inhibition of Specific Histone
TITLE OF INVENTION: Deacetylase Isoforms
TITLE OF INVENTION: Deacetylase Isoforms
TITLE OF INVENTION: Deacetylase Isoforms
CURRENT FILING DATE: 2001-03-26
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin version 3.1
SEQ ID NO 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          799 AACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAAC 858
                                                                                                        Gaps
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                                                  Length 1985;
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Fatent No. US20020061521A1
GENERAL INFORMATION:
TITLE OF INFORMATION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: FC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
FILE REFERENCE: FOR IN SECULO ACID ACID ACID ACID ACID ACID ACID NO. SECULO ACID NO. SECULO ACID NO. SECULO ACID NO. 1952
SECULO 1952
                                                3.3%; Score 36.2; DB 10; Length 53.1%; Pred. No. 8.7; tive 0; Mismatches 68; Indels
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; Patent No. US20020137162A1
; GENERAL INFORMATION:
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Best Local Similarity 53.19
                                                  Query Match 3.39
Best Local Similarity 53.19
Matches 77; Conservative
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; ORGANISM: Human
US-09-817-538-4
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US-09-764-869-1952
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US-09-817-538-4/c
US-09-817-913-4
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ORGANISM: Staphylococcus aureus
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ORGANISM: Homo sapiens
                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)...(1134)
US-09-815-242-8602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 17
US-10-044-090-455
LENGTH: 1134
TYPE: DNA
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APPLICANT: Haseleck, NOJELL
APPLICANT: 2yskind, Judith W. -
APPLICANT: 2yskind, Judith W. -
APPLICANT: 3yskind, Judith W. -
APPLICANT: All, Daniel Daniel
APPLICANT: Will, Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURREWY APPLICATION NUMBER: 06/201,078
PRIOR APPLICATION NUMBER: 60/101,078
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-216
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-216
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-216
PRIOR APPLICATION NUMBER: 60/259,308
PRIOR PILING DATE: 2000-10-216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90; Indels
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      PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-00-37
PRIOR PPLICATION NUMBER: 60/253,625
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,939
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLILING DATE: 2001-12-22
PRIOR PLILING DATE: 2001-10-16
SUPPRARE: ESSO, ID NOS: 14110
SSDO, ID NO 4614
LILING APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ. ID NOS: 14110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Staphylococcus aureus
US-09-815-242-4614
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90;
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Sequence 455, Application US/10044090
Sequence 455, Application US/10044090
Patent No. US/20020137081A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION UNMABER: US/10/044,090
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGRAM
SEQ ID NO 455
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                                                                                                                                                                                                                                                                                                  792 TGCTTACAACAGCGATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAA 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                 35 TCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTAATTTT 94
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Query Match 3.3%; Score 36; DB 10; Length 1134; Best Local Similarity 50.0%; Pred. No. 7.7; Matches 90; Conservative 0; Mismatches 90; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 18
US-09-764-877-2599/c
US-09-764-877-2599, Application US/09764877
; Sequence 2599, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INCRMATION:
    APPLICANT: Rosen et al.
    TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 347926.5
; OTHER INFORMATION: Incyte ID No. US20020137081A1 347926.5
; LOCATION: 5438, 5455, 5470, 5482, 5495, 5512, 5559
; OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-455
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Gaps

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34 CTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTAATTT 93
                                                                                                                         Ouery Match
Best Local Similarity 49.7%; Pred. No. 11;
Matches 90; Conservative 0; Mismatches 91; Indels 0;
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Publication No. US20030005491A1
GENERAL INFORMATION:
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
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; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1653
                    ; LOCATION: (1)...(1134)
US-09-815-242-8628
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FILE REFERENCE: PCO05
CURRENT APLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2599
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3.3%; Score 35.4; DB 10; Length 9
Best Local Similarity 47.9%; Pred. No. 10;
Matches 102; Conservative 0; Mismatches 111; Indels
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; Patent No. US20020061569A1
; GENERAL INFORMATION:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawakck, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
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; ORGANISM: Homo sapiens
US-09-764-877-2599
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US-09-815-242-8628
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834 CTCTTTATTAGCGCGTGAAGGTGGTAATAACGTTATTAAATTAAGTACAGGTGATGACGT 893
                                             94 TGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAAGTCTTTGTGGAGT 153
                                                                                                                                        799 AACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAAC 858
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                                                                                                                                                                                                                                                                                                                                                              MESOUL 777-564-1653/C
US-09-777-564-1653/C
Sequence 1653, Application US/09777564
Patent No. US2000202591A1
GENERAL INFORMATION:
APPLICAMY: Algate, Paul A.
APPLICAMY: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 21012.49
CURRENT APPLICATION UNDER: US/09/777,564
CURRENT FILING DATE: 2001-205
NUMBER OF SEQ ID NOS: 1730
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Db 199945 ATTTTAGAATGTAAAAATTGGTGTGTCTATATCATTACTAACTTCAATTAAGGAAAAG 200004
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                                                                                                                                                         634 TAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACGAAAGC 693
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                                                   574 AGACAAGTATTGATGGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTC 633
0; Gaps
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0; Mismatches 162; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 66 Application US/09925301; Sequence 66 Application US/09925301; Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins.
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PLILOGATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PLEGATION NUMBER: 60/124,270
RIOR PRIOR FILING DATE: 1999-03-12
SEQ ID NO 66
SEQ ID NO 66: 1094
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OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
         Conservative
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            Matches 132;
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Best Local Si
Matches 61;
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APPLICANT: Hauge, Brian M.
APPLICANT: Parrell, Laurence D.
APPLICANT: Parrell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Noteic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
NUMBER OF SEO ID NOS: 1119
      APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION WINBER: US 60/174,880
NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
; LCGATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAA 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34.8; DB 9; Length 335913;
Pred. No. 1.6e+02;
0; Mismatches 162; Indels 0;
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; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09754853A publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.2%;
Best Local Similarity 44.9%;
Matches 132; Conservative
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ORGANISM: Glycine max
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Glycine max
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US-09-754-853A-3
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GENERAL INFORMATION:
APPLICANT: SOppet, Daniel
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-75
                                                                                                                                                                                                                                                                                        1944 TITITITITITITITITITITITAAGAIGGAGITITIACCCGTIGICCAGCCIGGAGIGCAAT 2003
                                                                                                                                                                                                           1884 GAAAAGAACAAAGATTTCTATCATTTAGATTTGGGGTAAAAGTTTGTTGTGGTTTTTTTG 1943
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                                                                                                          Gaps
                                                  3.2%; Score 34.4; DB 10; Length 10195; 50.0%; Pred. No. 50; tive 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                                                                                              994 GCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCTTC 1045
                                                                                                                                                                                                                                                                                                                                                                                                  2004 GCTGCGATCTCAGCTCCACCTCTGCTTCCCGGGTTCAGGGATTCTC 2055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2928 CCCATTTTTAATGAACTGAAGTAGCAAAATCATCTTTTCATTCTTTAGGA 2978
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APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIG
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 2000-03-08
PRIOR PILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1999-03-12
SOFTWARE: PALENTIN VOS: 12.0
SEQ ID NO 478
TEMPORTILIA OF 18
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LOCATION: (4077)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 478, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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                                                  Query Match
Best Local Similarity 50.00
Matches 86; Conservative
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ORGANISM: Homo sapiens
  US-09-764-864-1600
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US-09-925-301-478
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3027 TTTTTTAATTCAATAACATGTAGATTTATTTTAAGTCAGTTTGGTACATGATACAGATT 2968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 TATTTCTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCT 88
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Sequence 1600, Application US/09764864

Patent No. US20020132733A1

GENERAL INFORMATION:

APPLICANT: RESERVE et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PTZ23

CURRENT FILING NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1792

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.2%; Score 34.6; DB 10; Length 3092; 50.9%; Pred. No. 27; tive 0; Mismatches 79; Indels 0;
                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT APPLICATION NUMBER: US/09/925,302
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1099-03-12
PRIOR FILING DATE: 1999-03-12
                                                  688 GAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCC 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2907 GCAACAATATCTGTAAGGTAAATAAGGTATTTGATAGAA 2867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEX: misc feature
LOCATION: (28)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEX: misc feature
LOCATION: (3086)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (3089)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: n equals a,t,g, or c
                                                                                                                                                                                                                                ; Sequence 310, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
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Best Local Similarity 50.9%
Matches 82; Conservative
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ORGANISM: Homo sapiens
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US-09-925-302-310
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Sequence 6, Application US/10003806; Patent No. US20020119929A1; GENERAL INFORMATION:
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US-10-003-806-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Human
US-10-003-806-6
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                                                                     10-003-806-6
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                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 6
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; Sequence 2225, Application US/09880107
; Patent No. US20020112981A1
GENERAL INFORMATION:
APPLICANT: Uptorie, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFREENCE: 44921-5028-WO
CURRENT PLIING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
SEQ ID NOS: 3950
NUMBER OF SEQ ID NOS: 3950
SEQ ID NO 2225
LENGTH: 35641
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US-09-880-107-2225
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                                                                                                                                                                                                                                                                                                                      Score 34; DB 10; Length 35641;
Pred. No. 1.1e+02;
0; Mismatches 65; Indels 0.
CURRENT APPLICATION NUMBER: US/09/962,436
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,082
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/234,924
PRIOR PILING DATE: 2000-09-26
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 306
                                                                                                                                                                                                                                                                                                                            Query Match 3.1%;
Best Local Similarity 52.9%;
Matches 73; Conservative (
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                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens US-09-962-436-306
                                                                                                                                                                                                                 35641
                                                                                                                                                                                                                                         TYPE: DNA
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US-10-003-806-9
Sequence 9, Application US/10003806
Factor No. US20020119929A1
Sequence 9, Application US/10003806
Factor No. US20020119929A1
SPLICANT: Bishop, Colin E.
FAPLICANT: Application: CAN I AND ITS ROLE
FILE REFERENCE: P0206GUS1/10024824
CURRENT APLICATION: CAN I AND ITS ROLE IN MAMMALIAN INFERTILITY
FILE REFERENCE: P0206GUS1/10024824
CURRENT FILING DATE: 2001-11-02
FRIOR FILING DATE: 2001-11-03
FRIOR FILING DATE: 2001-11-03
SOFTWARE: PALENT VERSION NUMBER: 60/245,872
FRIOR FILING DATE: 2001-11-03
SOFTWARE: PALENT VERSION 3.1
FENOMEN: 0.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.1%; Score 33.8; DB 12; Length 180557; 53.4%; Pred. No. 2.3e+02; trive 0; Mismatches 62; Indels 0;
APPLICANT: Bishop, Colin E.
APPLICANT: Bishop, Colin E.
APPLICANT: Agoulnik, Alexander I.
APPLICANT: Agoulnik, Alexander I.
APPLICANT: Zhu, Qiche I.
APPLICANT: Aboultik, Alexander I.
APPLICANT: Zhu, Qiche I.
AITHE OF INVENTION: CAN I AND ITS ROLE IN MAMMALIAN INFERILITY
FILE REFERENCE: PO2066651/10024824
CURRENT APPLICATION NUMBER: US/10/003,806
PRIOR APPLICATION NUMBER: 60/245,872
PRIOR APPLICATION NUMBER: 60/245,872
PRIOR PILING DATE: 2000-11-03
NUMBER OF SEQ ID NOS: 14
SOFTMARE: PATENTIN VERSION 3.1
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180 TCTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCT 239
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Best Local Similarity 52:5%; Pred. no. 52;
Matches 73; Conservative 0; Mismatches 66; Indels 0;
                                                                                                                                          Query Match
3.1%; Score 33.4; DB 10; Length 2679;
Best Local Similarity 52.5%; Pred. No. 52;
Matches 73; Conservative 0; Mismatches 66; Indels 0;
                                                                         ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 L47726
US-09-880-107-2219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFICANT: Hearing, Patrick
APPLICANT: Hearing, Patrick
APPLICANT: Babhou, Wadie
APPLICANT: Sandalon, Ziv
APPLICANT: Sandalon, Ziv
TITLE OF INVENTION: Adenoviral Vectors
FILE REFERENCE: STONYB-04370
CURRENT APPLICATION NUMBER: 05/09/782,378A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/237,747
PRIOR FILING DATE: 2000-10.02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Version 3.0
LENGTH: 2680
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; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  300 CGCTTTCAACAGTAAACCA 318
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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-782-378A-20
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US-09-782-378A-20/c
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Patent No. US20020045166A1

REPERTOR NO. US20020045166A1

APPLICANT: CHANDRAMOULISARAN, Ishwar et al

APPLICANT: CHANDRAMOULISARAN, ISHWAR TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEROF

TITLE OF INVENTION: AND USES THEROF

CURRENT APPLICATION NUMBER: US/09/742,312

CURRENT FILING DATE: 2000-12-22

NUMBER OF SED ID NOS: 4

SOFUL NO 3

SOFUL NO 3

SED ID NOS: 4

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     Db 26358 TACTTTCAAAAGTGTAGTATACATGGTTGTACTTATCTGCAGTGGAAAAAAGATTAAAAC 26417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAAAGATGAACAAAGAGTAAGTTTTT 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        694 TTCTAAGTAATCAAGAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 3.1%; Score 33.6; DB 10; Length 147309; Local Similarity 48.0%; Pred. No. 2.4e+02; nes 96; Conservative 0; Mismatches 104; Indels 0; C
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Sequence 2219, Application US/09880107
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Wockley, Joseph G.
APPLICANT: Gene Expression Profiles in Liver Cancer:
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 4421-5028 WO
CURRENT FILICATION NUMBER: US/09/880,107
CURRENT FILICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-44
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VOR: 2.1
SEQ ID NO 2129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: misc_feature
; LOCATION: (1)...(147309)
; OTHER INFORMATION: n = A,T,C or G
US-09-742-312-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 35314 CCAATAGCTGAAAAATGAA 35333
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                                                                                               Db 26418 ACAAGAAGTTTTT 26430
                                                   861 AGAGTAAGTTTTT 873
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US-09-880-107-2219/c
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 147309
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889 AGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGAT 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             924 CITTATTITCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTT 983
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tive 0; Mismatches 58; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: 19723
CURRENT FILING DATE: 2001-01-17
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1784
LENGTH: 1738
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                                                                                                                                                                                                    OTHER INFORMATION: MAP TO AC009266.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTR, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTR, SIGNAL = 2.1
US-09-864-761-9781
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 9781
LENGHH: 568
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US-09-764 864-1784/c
US-09-764 864-1784, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 54.0%
Matches 68; Conservative
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; ORGANISM: Homo sapiens
US-09-764-864-1784
                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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Matches 80; Conserv
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APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hancal. David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE PERESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-27
PRIOR PRILICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-00-3
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 35096 GAATAAAATCAGAATTGAAAAAGGAGAAGGTACAACAGATATAACAG 35142
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        CURRENT APPLICATION NUMBER: US/10/109,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PARENTIN VOE: 2.1
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FILING DATE: 2001-01-30
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9781, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              61; Conservative
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                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Bos taurus
US-10-109-551-1
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US-09-864-761-9781
                                                                                                                                                        SEQ ID NO 1
LENGTH: 78056
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Conservative
Matches
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        EXECUT: APPLICATION US/09938842A

SEQUENCE 4741. APPLICATION US/09938842A

PETENT OF US2020160378A1

GENERAL INFORMATION:
APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: US AME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, APPLICANTON NUMBER: US 60/227,866

PRIOR PLICATION NUMBER: US 60/227,866

PRIOR PLICATION NUMBER: US 60/227,866

PRIOR APPLICATION NUMBER: US 60/300,111

PRIOR PLING DATE: 2001-01-16

PRIOR PLING DATE: 2001-01-16

NUMBER OF SED ID NOS: 5379

SEQ ID NO 4141

LENGTH: 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEMTURE:
. OTHER INFORMATION: Genbank Accession No. US20020142981A1 x87344
US-09-880-107-3814
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APPLICANT CANTHON VOCKLEY, Joseph G.
APPLICANT SCHET, USEPH G.
APPLICANT SCHET, USEPH G.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REPERBNCE: 4921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14 APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14 APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PRECENTIN VET: 2.1
SEQ ID NO 3814
LENGTH: 198285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
3.1%; Score 33.2; DB 9; Length 2000;
Best Local Similarity 49.4%; Pred. No. 51;
Matches 86; Conservative 0; Mismatches 88; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3814, Application US/09880107; Patent No. US20020142981A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4741
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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WESULA 19709/C
'Sequence 3709,Application US/09878574
'Sequence 3709,Application US/09878574
'Sequence 3709,Application US/09878574
'Sequence 3709,Application US/09878574
'GENERAL INFORMATION:
APPLICAMT: La Rosa, Thomas J.
APPLICAMT: La Rosa, Thomas J.
APPLICAMT: Thompson, Michael D.
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(15401)B
'CURRENT APPLICATION NUMBER: US/09/878,574
'CURRENT APPLICATION NUMBER: US/09/878,574
'CURRENT FILING DATE: 2001-12-21
'RIOR FILING DATE: 1999-06-14
'NUMBER OF SEC ID NOS: 15775
'SEC ID NO 3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Byrun, Joseph R.
APPLICANT: Byrun, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants ACID CONTRIBUTION: Plants CORRENT PLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR PILICATION NUMBER: 1999-06-14
PRIOR FILING DATE: 1999-06-14
MINIMARY OF FILING DATE: 1999-06-14
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                                                                                                Db 149985 ATTCAAATAAACACAATTAGGAATGACAAAGGGGGGTATTACCACTGACCCCACAGAAATA 149944
                                                            698 AAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGG 757
                                                                                                                                                                                      758 AGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAG 817
                                                                                                                                                                                                                                                                                                             Qy 818 CAACCTTCCCTTTGATTCTTTGATAATGACAAGATGAACAAAGAGTAAAGTTTTTGAAA 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 TIGATAATCTCTGAAGTTGAACTGATGCACGGTTTTGAGATGGCTTTCTAATAGAGCTAC 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                837 TTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATGC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
3.0%; Score 32.8; DB 10; Length 328;
Best Local Similarity 58.0%; Pred. NO. 30;
Matches 58; Conservative 0; Mismatches 42; Indels 0;
0; Mismatches 98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      897 ATTIGICGAGCIAAAGCIIGCIICTCIIIATITICCII 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 ACTITIGICGTAATACAGITGATGCCCTGCATTCTTCTT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA

CORGANISM: Glycine max

OTHER INFORMATION: Clone ID: LIB3028-047-Q1-B1-A3

US-09-878-574-733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-878-574-733; Application US/09878574; Sequence 733, Application US/09878574; Patent No. US20020110548A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 733
LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy 878 AATTCTAAAA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3709
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APPLICANT: Black, Michael
Burnham, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 GTGGA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 GATGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 TITGAGATITGIGITCTITAGITCTIACTIGITAGITGTTACACATITITGTAAGAACCTT 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          410 GIGAAGAGICTICCCAFGTTTAFGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                470 ACGIGCCCTAAAAGGICAIGGAIGAGAICAGGAGAGTTAAGGAGAAAITAICITIAICGAGA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 CTIGTACTGAACAATACGTCGATGTATAATGTGTATTTAGACAGGTCTTTTTCTCC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 GAGAAGTAGCATCAGTTTCTGATTAACGCGAGAAGATTATAAAATTTGGGCCCCAAAAG 70
                                                                                                                                                                                               517 ATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGA 576
                                                                                                                                                                                                                          577 CAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTTTAA 636
                                                                                                                                                                                                                                                                                                                                                                          637 ITCGAAGAATITAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTC 696
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                         ;
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                                                                                                         ch 3.0%; Score 32.8; DB 10; Length 406; 1 Similarity 48.0%; Pred. No. 33; 94; Conservative 0; Mismatches 102; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 32.8; DB 10; Length E
48.9%; Pred. No. 38;
tive 0; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 41

US-09-924-035A-396/C
US-09-924-035A, Application US/09924035A
Patent No. US20020142319A1
GENERAL INFORMATION:
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2011US
CURRENT APPLICATION NUMBER: US/09/924,035A
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,784
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 900
SOFTWARE: FRASLED FOR Windows Version 3.0
SEQ ID NO 396
ENGTH: 548
          ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-006-Q1-B1-H7
US-09-R38-574-3709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAMESKEY: misc_feature
LOCATION: (1)...(548)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 42
US-09-939-980-6
; Sequence 6, Application US/0993980
; Patent No. US20020082334A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
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les 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             697 TAAGTAATCAAGAAAA 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 AAACAAATCAAGAAGA 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-924-035A-396
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                                                                                                                   Query Match
Best Local 8
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                                  190 GAGACCCCTAATCATACTGAAGGACTGATTCATATATCAGAAATTATGGATGACTACGTT 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
Jos, Score 32.8; DB 10; Length 8
Local Similarity 53.68; Pred. No. 44;
Sonservative 0; Mismatches 58; Indels
es 67; Conservative 0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OFFATUR SYSTEM: DOS
SOFFWARE: FRASESEO for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/939,980
FFILING DATE: 27-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
RAPLICATION DATA:
RAPLICATION DATA:
FILING DATE: «Unknown»
ATTORNEY, AGET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLGGY: linear
MOLECULE TYPE: Genomic DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-980-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 43
US-10-109-551-3/c
Sequence 3, Application US/10109551
Publication No. US20020194635A1
GENERAL INFORMATION:
              Knowles, David
Lonetto, Michael
Nicholas, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 806 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
                                                                                                                                                                                                                                            King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO:
    Hodgson,
                                                                                                                                                                                                                                                              STATE: PA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 CATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 ATCAAAATAAAGTAGAATAAAAAGGCACACTCGAAAAATTTGAGCGCAGAAAGGACA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 CTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATT 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     702 AATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTC 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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APPLICANT: PIEDRAHITA, JORGE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: TRANSGENIC ANIMALS RESISTANT TO TRANSMISSIBLE
TITLE OF INVENTION: PRONGIFORM ENCEPHALOPATHIES
FILE REFERENCE: TAMK: 2070S
CURRENT APPLICATION NUMBER: US,10/10/9,551
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATEMENT INFORMATION:

APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
TAPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION UNMBER: US/09/854,133
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FestSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.0%; Score 32.8; DB 9; Length 31412; Best Local Similarity 58.0%; Pred. No. 2.1e+02; Matches 58; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.0%; Score 32.6; DB 9; Length 601;
Best Local Similarity 46.1%; Pred. No. 44.
Matches 107; Conservative 0; Mismatches 125; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 25496 AGTGTTTCAATCATTTCAGTAGAAAACTGCATGCGCAAA 25457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 AGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 294, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: (1)...(601)
; OTHER INFORMATION: n = A,T,C or G
US-09-854-133-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Ovis aries US-10-109-551-3
                                                                                                                                                                                                                                                                                                                                            LENGTH: 31412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 44
US-09-854-133-294
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Sequence 3797, Application US/09938842A
| Patent No. US20070160778A1
| Patent No. US20070160778A1
| APPLICANT: Harper, Jeff | APPLICANT: Kreps, Joel | APPLICANT: The Patent No. Transpar No. Same, AND METHODS OF USE | TITLE OF INVENTION: SAME, AND METHODS OF USE | TITLE REPERENCE: SCRIPIJAN NO. SCRIPIJAN 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GITCITITGITTGITTCIAATGICGGAAGAAAAAGAAAGAAGATATATAAAATCATIG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       762 GATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAAC 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  702 AATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTC 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mohamath, Race...
APPLICANT: Algate, Paul A.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Carol Yoseph
APPLICANT: Elliot, Mark
APPLICANT: Hanion, Darin R.
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Mannion, Anchael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: USAPPLICANT: AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
TITLE OF INVENTION: USAPPLICANT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
188 TITICAAGTGAAGGTTTCTGTCAGTTGAAGTAGTTAGCAATGGCTTCTTTTC 239
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3.0%; Score 32.6; DB 10; Length 601;
Best Local Similarity 46.1%; Pred. NO. 44;
Matches 107; Conservative 0; Mismatches 125; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 294, Application US/09738973; Patent No. US20020110563A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature; LOCATION: (1)...(601); OTHER INFORMATION: n = A,T,C or G US-09-738-973-294
                                                                                                                                                                                                                                                                                                                                                                                            Reed, Steven G.
Henderson, Robert A.
Lodes, Michael J.
Fling, Steven P.
Mohamath, Raodoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-938-842A-3797
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                                        QQ
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919 GTCATTGAAGGTGGGGAGGAAAAAAAACTACAAAATTTAAGAACATTTCAGAACAGGTA 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1039 AAAATGAAGCTAAAAGCTTCTCCCTACAGAAGAACAGACATGCACCAAACTTGTTAGTATG 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  979 GACAGTTGTGTGTGAGAAGGAGGAGGAGGAAAACCTATGGATAATAAATTAGAA 920
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APPLICANT: Mathway, Helena
APPLICANT: Mathway, Helena
APPLICANT: Magnor, Holena
APPLICANT: Magnor, Mency J.
TITLE OF INVENTION: TRAIT-ASSOCIATED GENE IDENTIFICATION
TITLE OF INVENTION: METHOD
FILE REFERENCE: 4257-0018.30
CURRENT PAPLICATION NUMBER: US/09/522,334
CURRENT FILING DATE: 2000-03-09
PRIOR FILING DATE: 1999-03-12
NUMBER OF SQL ID NOS: 28
SGCTWARE: FastSEQ for Windows Version 4.0
LENGTH: 4436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 3.0%; Score 32.4; DB 10; Length 1 Local Similarity 46.8%; Pred: No. 76; To Indels nes 102; Conservative 0; Mismatches 116; Indels
                                                                                                                                                                                                                           GENERAL INCOGRATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PALO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  858 CAAAGAGTAAGTTTTGAAAATTCTAAAATAGAAATG 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               859 AAACAATTGTGTATTAAAAATAGGGATAATAAAGTG 822
                                               157 TGTATTGAAGGGAAGACGAATAATCTGATCCAA 189
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                                                                                                                                                                                      ; Sequence 228, Application US/09925302
; Patent No. US20020044941A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 896
SOFTWARRE: PatentIn Ver. 2.0
SEQ ID NO 228
LENGTH: 1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
GORGANISM: Homo sapiens
US-09-925-302-228
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US-09-522-334-26
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Matches
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Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-70
CURRENT APPLICATION NUMBER: US/09/237,606
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR APPLICATION NUMBER: US/60/237,425
PRIOR PRILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 ATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 AGAACTGATAAGAACGGCTCCATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCT 303
                                                                                                                                                                                                                                                                                                                                                                                                               124 TCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTG 183
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                                                                                                                                                                                                                                                                                                               Query Match 3.0%; Score 32.6; DB 9; Length 2000; Best Local Similarity 47.0%; Pred. No. 73; Matches 101; Conservative 0; Mismatches 114; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 TTCAACAGTAAACCAAAAGCAGCGTACAATAGCGA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FLILING DAFE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : NAME/KEY: misc_feature
; OTHER INFORMATION: n=a,t,g or c
US-09-969-708-291
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PatentIn version 3.0
                                                                                                                                                                                                                              ; TYPE: DNA; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3797
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Best Local Similarity
Matches 75; Conserve
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US-09-969-708-291
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SOFTWARE:
SEQ ID NO 2
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Gaps

us-09-438-185a-1_1199590_1200675.rnpb

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APPLICANT: Hauge, Brian M.
APPLICANT: Hauge, Brian M.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parnell, Laurence D.
APPLICANT: Wang, Ming Li.
APPLICANT: Wang, Ming Li.
APPLICANT: Wang, Ming Li.
APPLICANT: Wang Ming Li.
APPLICANTON: Wordelc Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION WUMBER: US/09/754,883A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
NUMBER OF SOG ID NOS: 1119
SEQ ID NO 4
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                                                                                                                                                                                                                      3669 CCACCAAACCAAACAAAATCCATTCTTGTTCAAAAACATGATCTTTTGAGG 3728
                                                                                                                                                                                                                                                                                                                                               3729 TAAAATAAACAAGAAACAAGAAGAAGAGGGTACCTGAGTAATTCAGTTTCATTAGATGA 3788
                                                                                                                                                                                                                                                                                    662 TGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGA 721
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                                                                                                                                                                       602 CCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGA 661
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                                                                                                                      Gaps
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                                                    3.0%; Score 32.4; DB 9; Length 4436;
49.4%; Pred. No. 1.2e+02;
Live 0; Mismatches 86; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                            722 CANTAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (111805)..(113968),(114684)..(115204)
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LOCATION: (1)..(513509)

OTHER INFORMATION: unsure at all n locations

OTHER INFORMATION: Clone ID: 318013_region_A3

US-09-754-863A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09754853A; Publication No. US20030005491A1; GENERAL INFORMATION:
                                                                                                               84; Conservative
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ORGANISM: Glycine max
                                                           Query Match
Best Local Similarity
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US-09-522-334-26
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US-09-754-853A-4
                                                                                                                   Matches
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15, 3, 111, 111, 112, 3,	Sequence 1, Appli Sequence 51, Appl Sequence 51, Appl Sequence 2, Appli Sequence 6, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	17, App 17, App 1809, A 42, App 15, App	Sequence 22, Appl. Sequence 22, Appl. Sequence 16, Appl. Sequence 105, Appl. Sequence 105, Appl. Sequence 1598, Appl. Sequence 8, Appl. Sequence 8, Appl. Sequence 8, Appl. Sequence 8, Appl. Sequence 17,	equence 27 aguence 27 aguence 27 aguence 1, aguence 1, aguence 1, aguence 10 aguence 10 aguence 10 aguence 17	Sequence 21, Appl. Sequence 21, Appl. Sequence 16, Appl. Sequence 16, Appl. Sequence 16, Appl. Sequence 17, Appl. Sequence 21, Appl. Sequence 21, Appl. Sequence 21, Appl. Sequence 1, Appl. Sequence 17, Appl. Sequence 1, Appl.
US-08-930-285-16 US-08-484-438-3 US-08-965-762-15 US-09-134-0012-2094 US-08-568-459A-11 US-08-568-459A-11 US-08-487-8268-11 US-08-487-8268-13 US-08-356-925-12	US-07-667-276A-1 US-08-642-274D-51 US-08-952-014C-51 US-08-858-052-2 US-09-2000-884-2 US-09-486-9708-60 US-09-426-290-1 US-09-426-290-1 US-09-428-348-1	US-09-007-005-17 US-09-007-005-17 US-09-244-796-17 US-09-134-001C-1809 US-09-018-635-42	US-09-288-143-52 US-09-018-635-22 US-08-911-527-76 US-08-413-118-105 US-08-413-118-105 US-08-915-527-175 US-08-915-527-175 US-08-9134-001C-1598 5 543639-3 US-08-28-3-17-8	2 US-08 431-080-27 1 US-08 431-080-27 2 US-08 938-234-27 2 US-08 45-294-77 2 US-08 947-823-1 3 US-08 325-625-10 2 US-08 346-961A-10 4 US-09-134-001C-1741	1 US-08-484-105-21 1 US-08-484-106-21 3 US-08-627-9078-3 2 US-08-322-625-16 2 US-08-322-625-16 2 US-08-465-193B-18 4 US-09-134-001C-248 4 US-09-134-001C-248 4 US-09-134-001C-248 4 US-09-134-001C-248 4 US-09-134-001C-248 4 US-09-134-001C-248 4 US-09-134-001C-248 4 US-09-270-751-3 4 US-09-270-751-3 4 US-09-144-001C-1070 2 US-08-134-001C-1070 2 US-08-144-001C-1070 2 US-08-144-001C-2809 1 US-08-144-001C-2809 1 US-09-144-001C-2809 1 US-08-146-15 2 US-09-146-1
638 5555 3800 70000 70000 8220 8220 8220 19124 43676	1584 679 679 1734 1734 13977 168575	7521 289 289 999 591 882	979 1641 10011 162450 2951 2951 4597 1440 1529 2085	2 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	1676 16476 1
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. nucleic search, using sw model January 9, 2003, 06:43:27; Search time 39 Seconds (without alignments) (8539.768 Million cell updates/sec	S-09-438-185A-1_COPY_1199590_12000 086 ttggcaaagtacctcaaaacgt DENTITY_NUC apop 10.0 , Gapext 1.0		Maximum Match 0% Maximum Match 100% Listing first 150 summaries Issued_patents_NA: 1 Sen2 6/ptodata/1/ina/5A_COMB.seq:* 2 /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 4 /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 5 /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 6 /cgn2_6/ptodata/1/ina/6A_COMB.seq:* 7 /cgn2_6/ptodata/1/ina/fortorus_Comb.seq:* 6 /cgn2_6/ptodata/1/ina/fortorus_Comb.seq:* 7 /cgn2_6/ptodata/1/ina/fortorus_Comb.seq:* 7 /cgn2_6/ptodata/1/ina/fortorus_Comb.seq:* 7 /cgn2_6/ptodata/1/ina/fortorus_Comb.seq:* 7 /cgn2_6/ptodata/1/ina/fortorus_Comb.seq:*	is the number of results predicted by chance to arrived by analysis of the total score distribution summaries SUMMARIES Ouerv	Match Length DB ID 6.7 7218 1 US-08-232-453-14 6.7 7218 1 US-08-313-453-14 6.8 2098 4 US-09-813-138A-3 6.9 4 US-09-813-138A-5 6.9 4 US-09-16-502-5 6.9 4 US-09-16-502-5 6.9 4 US-09-16-18-55 6.9 4 US-09-16-18-55 6.9 4 US-09-16-18-55 6.9 4 US-09-18-55 6.9 4 US-09-18-55 6.9 6877 1 US-08-62-208A-1 6.0 6877 1 US-08-62-208A-1 6.0 6877 1 US-08-62-18-11 6.0 687 1 US-08-62-18-11 6.0 68 1 US-09-78-11 6.0 13149 1 US-09-78-11 6.0 68 1 US-09-78-1
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532 TCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGG 591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          712 AAATCTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 ATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTG 831
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                                                                                                                                                                                                                                                                                                                                     / Match 6.7%; Score 72.4; DB 1; Length 7218; Local Similarity 16.0%; Pred. No. 1.4e-10; les 97; Conservative 234; Mismatches 275; Indels 0
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION WHERE: US/07/935,313
                                                                                                                                                                             30472/114 IMMU
                                                                                                                      APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTONEY/AGENT INFORMATION: .

RAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 304
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
                                                                                                                                                                                                                                                   LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                             TELEX: 899149
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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APPLICANT: SCHEFFLINGER, F.
APPLICANT: SCHEFFLINGER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: AARANDAIA
                           US-08-181-271A-36
US-08-444-03.36
US-08-444-03.36
US-08-449-03.36
US-08-455-265A-36
US-08-455-416-36
US-08-455-416-36
US-08-455-416-36
US-08-455-741-36
US-08-456-758-36
US-08-456-758-36
US-08-456-758-36
US-08-456-758-36
US-08-456-758-36
US-08-456-758-36
US-08-458-37
US-09-218-207-17
US-09-218-207-17
US-09-218-207-179
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US-09-134-001C-1861
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US-08-461-592B-11
US-08-181-271A-1
US-08-449-315-1
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                              RESULT 1
US-08-232-463-14/C
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Gaps

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COUNTRY: USA ZIP: 22313-0299 COMPUTER READABLE FORM:

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NS-09-285-502-5/C

Sequence 5, Application US/09285502

Sequence 5, Application US/09285502

Patent No. 6190876

GENERAL INFORMATION:

APPLICANT: Rubin, Gerald M.

APPLICANT: Rocke, Jenny

APPLICANT: Ravari, Resa

APPLICANT: Wavari, Resa

TITLE OF INVENTION:

CORRESSONDENCES: 10

CORRESSONDENCES: 10

STATE: CALEPORNIA

STATE: CALIFORNIA

CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                            3.4%; Score 36.6; DB 2; Length 2098; 65.1%; Pred. No. 0.87; ative 0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,502
APPLICATION NUMBER: US/08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      CLASSIFICATION: 800
CLASSIFICATION: 800
NATORNEY/AGENT INFORMATION:
NAME: OSMAW, RICHARD A
REGISTRATION UNBER: 36,627
REFERENCE/COCKET NUMBER: 897-081
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1076 AGGCTACTGAAATATTATTAT 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               876 AAAATTCTAAAATAGAAATGCAT 898
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TELEPRICE (415) 343-4341
TELEPRICE (415) 343-4342
INFORMATION FOR SEC ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2098 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36,627
                                                                                                                                                                   TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
LENGTH: 2098 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RICHARD A
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les 54; Conserv
                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: 11:
; MOLECULE TYPE:
US-08-937-931-5
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APPLICANT: GAN, Weinlu et al
APPLICANT: GAN, Weinlu et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
AND
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
CURRENT APPLICATION NUMBER: US/09/813,133A
CURRENT FILING DATE: 2001-06-06
SOFTWARE: FASTERO FOR Windows Version 4.0
SEO ID NOS: 4
SOFTWARE: FASTERO FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29872 TGCAAGCTATCCAGCCAACAGGGACTTAATAACCAGAATATAAAGGAACGCAAACAATT 29813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29992 TCTCAAAAGCACAGTCAACAGAAGCAAAATAGATAAAGGGGATTACATCAAACTGAAAA 29933
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Patent No. 5935792
GENERAL INFORMATION
APPLICANT: Rubin, Gerald M.
APPLICANT: Pan, Duojia
APPLICANT: Pan, Duojia
APPLICANT: Roke, Jenny
APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ: A No. 5935792e1 Family of Metalloproteases
NUMBER OF SEQUENCES: US
     908 TAAAACTAACTGCTGTGTGTATGAAATGCTTTAAGGAGGCTTCCTTTTCTAAACGATTGG 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      702 AATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.7%; Score 39.8; DB 4; Length 55827; 48.1%; Pred. No. 0.46; tive 0; Mismatches 122; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: STREET: 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                    Sequence 3, Application US/09813133A Patent No. 6455294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 48.1
Matches 113; Conservative
                                                     1012 GGAAAG 1017
                                                                                                 848 GTGAGG 843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA; ORGANISM: Human US-09-813-133A-3
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US-08-937-931-5/c
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LENGTH: 55827
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1136 AGCCACAAAAGCTTTGAAGGTTTGATATTCAGAGAAGATGACCAAAGAGTTCTTTTATTT 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1076 AGGCTACTGAAATATTATTTAT 1054
                                                                     1076 AGGCTACTGAAATATTATTAT 1054
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TYPE: nucleic acid
STRANDEDNESS: double
                                           876 AAAATTCTAAAATAGAAATGCAT 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    876 AAAATTCTAAAATAGAAATGCAT 898
                                                                                                                                                                                                                                                                  APPLICANT: Rubin, Gerald M.
Pan, Duojia
Rooke, Jenny
Yavari, Reza
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Xu, Tian
FINVENTION: KUZ: A No. 6319704el Family of Metalloproteases
OF SEQUENCES: 10
                                                                                                                                                                                                                                                   816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTGA 875
                                                                                                                                                                                                                      816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                              Query Match
3.4%; Score 36.6; DB 4; Length 2098;
Best Local Similarity 65.1%; Pred. No. 0.87;
Matches 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.4%; Score 36.6; DB 4; Length 2098; Best Local Similarity 65.1%; Pred. No. 0.87; Matches 54; Conservative 0; Mismatches 29; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUW 194104
COMPUTER READABLE FORM:
MEDIUW FEE FLOOPPY disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NOWER: US/09/709,126
FILING DAYE: 08-No. 6319704-2000
CLASSIFICATION AND CURROWN>
PRIOR APPLICATION AND CURROWN>
PRIOR APPLICATION NAMBER: 09/285,502
FILING DATE: -CURROWN>
FILING DATE: -CURROWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 BUSH STREET, SUITE 3200 CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORILLS CALLE CALLE CALLE CALL AND A TORILL CALL AND A RECLETRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: 897-081

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-709-126-5
                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09709126
Patent No. 6319700:
GENERAL INFORMATION:
APPLICANT: Rubin, Gerald M.
Pan, Duojia
Rooke, Jenny
Yavari, Reza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2098 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: KUNNUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ropology: linear
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                         TOPOLOGY: linear

MOLECULE TYPE: CDNA
US-09-285-502-5
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US-09-709-126-5/c
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Xu, Tian
TITLE OF INVENTION: KUZ: A No. 6399350el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
3.4%; Score 36.6; DB 4; Length 2098;
Best Local Similarity 65.1%; Pred. No. 0.87;
Matches 54; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                        COMPUTER RADABLE FORM:

MEDIUM TYPE: FLORPLY disk
COMPUTER: IBM PC COMPALIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURREWN APPLICATION DATA:
APPLICATION NUMBER: US/09/871,385A
FILING DATE: 31 May-2001
CLASSIFICATION AND AND AND APPLICATION NUMBER: US/09/709,126
FILING DATE: 08-NO. 6399350-2000
APPLICATION NUMBER: US/09/709,126
FILING DATE: CUNKNOWN:
APPLICATION NUMBER: 09/285,502
FILING DATE: CUNKNOWN:
ATTORNEY/AGENT INFORMATION:
                                                                       CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B97-081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

$1.02-09-871-385A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHANE: (415) 343-4341
TELEPAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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121 GATATATAGTAGGCATTTGAAAGTTGAAAGATGAATTTCACACTAAACTCAGATAAGATG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              772 ATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTG 831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              832 ATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGA 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                         652 GACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 712 AAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAA 771
                                                                                                                                                                                                                                                                                                                                                              592 AGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAT 651
                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                   Query Match 3.2%; Score 34.8; DB 1; Length 6877; Best Local Similarity 44.5%; Pred. No. 4.6; Matches 138; Conservative 0; Mismatches 172; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Obestein, Fodstad
APPLICANT: Bodstain, Elvind
APPLICANT: Bright Elvind
APPLICANT: Bright Elvind
APPLICANT: Bright Elvind
APPLICANT: Bright Elvind
APPLICANT: Marlandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
AITLE OF INVENTION: CREL SPECIFIC OLIGONUCLEOTIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
OPERATING SYSTEM: PC -DOS/MS-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBER: US/08/602,036A
16-FEB-1996
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US-08-602-036A-1
Sequence 1, Application US/08602036A
Sequence 1, SP0924B
Fatent No. 570924B
GENERAL INFORMATION:
APPLICANT: Oeystein, Fodstad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Kerner, Ann-Louise
REGISTRATION NUMBER: 33,523
                                                                                                                             TOPOLGGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: ORGANISM: Nicotiana tabacum US-08-347-340-1
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6877 base pairs
                                                                LENGTH: 6877 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
FILING DATE: 16-FEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 TAATCACGIG 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 TATGCGTTGTTTTTACTAGGAAGACCTTGTACTTTTCTATGACTTTAGTGAAGAGTCT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: promoter; LOCATION: (1)..(1241); OTHER INFORMATION: n= a or g or c or t/u oTHER INFORMATION: Act7 promoter polynucleotide sequence and intron US-09-737-698B-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08347340
Patent No. 563439
GENERAL INFORMATION:
APPLICANT: WALTER, MICHAEL H
ATTILE OF INVENTION:
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.4%; Score 36.4; DB 4; Length 1241; 59.8%; Pred. No. 0.79; tive 0; Mismatches 41; Indels 0.
     Patent No. 6462258

GENERAL INFORMATION:
APPLICANT: Fincher, Karen
APPLICANT: Fincher, Karen
APPLICANT: Wilkinson, Jack
TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
FILE REPERENCE: 38-21(51499)C
CURRENT APPLICATION NUMBER: US/09/737,698B
PRIOR APPLICATION NUMBER: US 60/171,173
PRIOR FILING DATE: 1999-12-16
NUMBER OF SEQ. ID NOS: 30
SOFTWARE: PATENTIN VORSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1090 ACCTAGTTTTCTCAATAATCAACATATGAAGCGATGTTTGAG 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/347,340
FILING DATE: 06-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9320/212448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: CUSHMAN, DARBY & CUSHMAN : 1100 NEW YORK AVENUE, N.W. WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/GB93/01098
FILING DATE: 27-MAY-1993
PRIOR APPLICATION DATE: 37-MAY-1993
APPLICATION NUMBER: GB 9211416.4
FILING DATE: 29-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: KOKULIS, POLL N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 932
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/861-3000
TELEPAX: 202/822-0944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16773
                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 3.49
Best Local Similarity 59.89
Matches 61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 06-DEC-1
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                              1241
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                                                                                                                                                                                                                                                                                      SEQ ID NO 25
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7700 GTGGAGGGAGCCCGCTGTTTGCAGCAGGATATAGGCATTCTCGAATCCACCGT 7759
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                                                                                                            3.2%; Score 34.6; DB 2; Length 10952; 55.4%; Pred. No. 6.5; tive 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
3.2%; Score 34.6; DB 2; Length 10952;
Best Local Similarity 5.4%; Pred. NO. 6.5;
Matches 67; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1. Application US/08642407A
Patent No. 587308
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOVIG, Elivind
APPLICANT: Hovig, Elivind
APPLICANT: Maelandsmo, Gunhild H.
APPLICANT: Agrawal, Sudhir
TITLE OF INVENTION: CAPL SPECIFIC OLIGONUCLEGIDES AND
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION UNBER: US/08/642,407A
FILING DATE: 03-May-1996
CLASSIFICATION: 514
ATTORNEY APPLICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY AGENT INFORMATION:
NAME: Refrex, Ann-Louise
REGISTRATION NUMBER: 33,523
REFERENCE/DOCKET NUMBER: HYZ-O
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
      TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic DNA
                                                                                                              Query Match 3.2
Best Local Similarity 55.4
Matches 67; Conservative
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                                                              ; ANTI-SENSE:
US-08-502-374A-1
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                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.4%; Pred. No. 6.5;
Matches 67; Conservative 0; Mismatches 54; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08502374A
Patent No. 5872007
Patent No. 5872007
CENERAL INPORMATION:
APPLICANT: Engelraaten, Olav
APPLICANT: Maraten, Olav
APPLICANT: Agrawal, Sudhil
APPLICANT: Agrawal, Sudhil
TITLE OF INVENTION: METHODS OF INHIBITING METASTATIC CANCER
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: HYZ-039CIP
TELECOMMUNICATION INCORMATION:
TELEPHONE: (617) 526-6000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10952 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Hale and Dorr LLP
60 State Street
                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                       ; ANTI-SENSE: NO
US-08-602-036A-1
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STRANDEDNESS:
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US-08-502-374A-1
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FITLE OF INVENTION: USES THEREOF
FITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0968
CURRENT APPLICATION NUMBER: US/09/741,150
NUMBER OF SEO ID NOS: 4
SOFTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                Sequence 3, Application US/09784316

Patent No. 6461843

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC
TITLE OF INVENTION: THEREOF
FILLE REPREMENCE: CLOI139

CURRENT APPLICATION NUMBER: US/09/784,316

CURRENT FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PRASEEQ for Windows Version 4.0

SEQ ID NO 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1510 CITTRCARANARDATNGCCCARTGNARCATNCCDATNGTNSWNARYTTNARNARNACNG 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 AGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTGATCCAATTCTAAAGG 198
                                          1570 INGCRCANCKNGTNGGNARNGCNARNSWNGCNGGNARRTANCKNACDATYTGNARDATNC 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 CATCCATICIAATTITGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAA 138
                                                                             728 CITITCCAIAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAG 787
668 AAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAG 727
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0
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3.1%; Score 33.8; DB 4; Length 65042;
Best Local Similarity 52.5%; Pred. No. 23;
Matches 74; Conservative 0; Mismatches 67; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature
; LCGATION: (1)...(55042)
; CTHER INNORMATION: n = A,T,C or G
US-09-784-316-3
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US-09-741-150-3/c
; Sequence 3, Application US/09741150
; Patent No. 6436689
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                                                                                                                                                                  788 GGAGTGCTTA 797
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ORGANISM: Human
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                                                          548 ATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGGGGCTACAAATCCTGAA 607
                                                                                                            470 ACGIGCCCTAAAAGGICATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTTATCGAGA 529
                                410 GIGAAGAGICTICCCATGITIAIGAAAATICAGAAAAIGAGGAIGIAGAAGCCAAGGC 469
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holloway, James
APPLICANT: Jelinek, Laaura
APPLICANT: Durnam, Diane
APPLICANT: Blumberg, Hal
TITLE OF INVENTION: PPPR4
TITLE OF INVENTION: ZPPR4
WUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Mismatches 143;
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FILING DATE: CIASCET
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NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/09106194
Partent No. 626234
GENERAL INFORMATION:
APPLICANT: HOLLOway, James
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TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2067 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 206-442-6674
TELEFAX: 206-442-6678
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Matches 74; Conservative
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REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskett
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US-09-106-194-11/c
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US-09-106-194-11
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895 TATGTTTATGTTTTTTAATATATTCTAAAAGTTTTTTGTTTATCTATAAAGGTACCTTCAC 836
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                                                                                                                                                                                                                  265 ATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCA 324
                                                                                                                  Query Match
3.1%; Score 33.8; DB 4; Length 112132;
Best Local Similarity 51.0%; Pred. NO. 29;
Matches 80; Conservative 0; Mismatches 77; Indels 0; Gaps
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49.2%; Pred. No. 5;
tive 0; Mismatches 91; Indels 0.
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4000 Bell Atlantic Tower, 1717 Arch Stre
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Fosberry, Andrew P.
APPLICANT: Lavlor, Elizabeth J.
APPLICANT: Na'nolas, Richard O.
TITLE OF INVENTION: No. 6004556el rsbU-1
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P505!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
; NAME/KEY: misc_feature
; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
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Patent No. 6004555
GENERAL INFORMATION:
APPLICANT: FOSDERTY, Andrew P.
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SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 215-994-2222
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
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STREET: 4000 Bell A
CITY: Philadelphia
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US-08-938-546-1
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US-08-938-546-1/c
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835 TATTICTAGCTICAGICACACCATCCGTTAAAATGATAATTAAATCATCAAGGTATATAG 776
925 TITATTTTCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTG 984
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                                                                                                                                                                                                                                                                                   775 GAATITCITGITGATATCGIGITTGIGAACIGATICCIAACACTCTACCTTAACT 717
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3.1%; Score 33.4; DB 3; Length 1002;
Best Local Similarity 49.2%; Pred. NO. 5;
Matches 88; Conservative 0; Mismatches 91; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CTTY: Philadelphia
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APPLICATION NUMBER: US/09/340,812
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APPLICANT: LawLor, Elizabeth J.
APPLICANT: LawLor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTION: No. 6111078el rsbU-1
CORRESPONDENCES: 5
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,546
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09340812; Patent No. 6111078; GENERAL INFORMATION:
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NAME: Dicktison, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: PSC
TELECOMMUNICATION INFORMATION:
TELECHONONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Philadelphia STATE: PA COUNTR: US ZIP: 19103 CONPURR READABLE FORM: MEDIUM TYPE: IBM COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE COMPUTER: IBM COMPATIBLE COMPATI
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SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TELEFAX: 215-994-2222
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865 TAAGTITITGAAAAATICTAAAATAGAAATGCATTIGTGTCGAGCTAAAAGCTIGCTICTC 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           985 GAGTGATTGCCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCT 1043
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49.2%; Pred. No. 5;
tive 0; Mismatches 91; Indels
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APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTION: No. 6004556el rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
CARRESPONDENCE ADDRESS:
ADDRESSEE: A000 Bell Atlantic Tower, 1717 Arch Stre
ADDRESSEE: Dechert Price & Rhoads
STRRET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
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FastSEQ for Windows Version 2.0
                                                                                                                                                                      SOFTWARE: PASTEM: DOS CURRENT APPLICATION DAIA:
                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/340,812
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                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/938,546
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ATTORNEY/AGBET INFORMATION:
NAME: Dickinson, Todd 0
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      : Diskette
IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
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Matches 88; Conservative
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EDNESS: double
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-938-546-5/c
                                                                                            COUNTRY: U
ZIP: 19103
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TOPOLOGY:
US-09-340-812-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           913 TAIGITTATGITTITTAATATATTCTAAAAGITTTTIGITTATCTATAAAGGTACCTTCAC 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      925 ITTATITICCTITIGIAGAAIGATICGIAGIAGGAATATGGGGTCGAGIATGCACGTIG 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   985 GAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCT 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.1%; Score 33.4; DB 3; Length 1020;
49.2%; Pred. No. 5;
tive 0; Mismatches 91; Indels 0;
                                                                                                                                                                                                                                              ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
STRY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09340812
Patent No. G111078
GENERAL INFORMATION:
APPLICANT: Fosberry, Andrew P.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Molchlas, Richard O.
TITLE OF INVENTION: No. 6111078e1 rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                  APPLICANT: Fosberry, Andrew P.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTION: No. 6004556el rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                         Sequence 3, Application US/08938546 Patent No. 6004556 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dickinson, Todd O
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P55
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 215-994-2252
TELEPHONE: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1020 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.1'
Best Local Similarity 49.2
Matches 88; Conservative
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CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-09-340-812-3/C
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                                               US-08-938-546-3/c
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                       RESULT 17
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NESO14 21 727-1/C
Sequence 1, Application US/09149727
Sequence 1, Application US/09149727
Sequence 1, Application US/09149727
Setent No. 6391347
GENERAL INFORMATION:
APPLICANT: Keese, Paul Konrad
APPLICANT: Keese, Paul Konrad
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: MICROBIAL BETA-GLUCURONIDASE GENES, GENE PRODUCTS AND
TITLE OF INVENTION: UNGEST THEREOF;
FILLE REFERENCE: 190106-405
CURRENT APPLICATION NUMBER: US 60/058, 263
EARLIER APPLICATION NUMBER: US 60/058, 263
SEALIER FILLING DATE: 1997-09-09
NUMBER OF SEQ ID NOS: 71
SEQUENCE: DATE: 1997-09-09
SEQ ID NO ID NO ID NOS: 71
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                                                                                                                                                                                                                                                                                                                                                                                                                   1012 TATGTTTATGTTTTTAATATATTCTAAAAGTTTTTGTTTATCTATAAAGGTACCTTCAC 953
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                                                                                                                                                                                                                                                                                                            Query Match

3.1%; Score 33.4; DB 3; Length 3360;
Best Local Similarity 49.2%; Pred. No. 8.4;
Matches 88; Conservative 0; Mismatches 91; Indels 0.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                            TELEX:
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Bacillus sp.
                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-09-340-812-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1012 TATGTTTATGTTTTTAATATATTCTAAAAGTTTTTTGTTTATCTATAAAGGTACCTTCAC 953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      925 TTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTG 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.1%; Score 33.4; DB 3; Length 3360; 49.2%; Pred. No. 8.4; tive 0; Mismatches 91; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        мыркеssee: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FSSESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fosberry, Andrew P.
APPLICANT: Lawlor, Elizabeth J.
APPLICANT: Nicholas, Richard O.
TITLE OF INVENTON: No. 6111078e1 rsbU-1
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717
  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/340,812
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ATORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/938,546
                                                                                                                                                                                               NAME: DICKINSON, TOGG O
REGISTRATION NUMBER: 28,354
REFERENCE/POCKET NUMBER: P505;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09340812; Patent No. 6111078; GENERAL INFORMATION:
                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTONNEY/AGENT INFORMATION:
NAME: DICKINSON, TOOR O
                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3360 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 3.19
Best Local Similarity 49,29
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-938-546-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7239 CAACATCCATTTGGATTGTGTTGTGTGCAACTGGAGATACAACAACAACAGTGGTGAAG 7298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7299 AATTATTAAAGTGATCAGTTGTGATAAGCTTGTGAATCT--CTTTCCACAAATCCCATG 7356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           818 CAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAA 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   878 AATICIAAAAIAGAAAIGCAIITIGIGICGAGCIAAAGCIIGCIICTITIAIIIICCIII 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         938 IGIAGAAIGAIICGGIAGIAGGAAIAIGGGGICGAGIAIGCACGIIGGAGIGAIIGGCIG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Gaps
GENERAL INFORMATION:
APPLICANT: Michelmore, Richard W.
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
APPLICANT: Shen, Kathy
APPLICANT: Blake
TITLE OF INVENTION: Conferring Pest Resistance in Plants
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREET: Las FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: OF STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CARSIFICATION NUMBER: US/09/004,838
FILING DATE: 09-JAN 1998
CLASSIFICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 33; DB 4; Length 10815; 48.6%; Pred. No. 18; tive 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANAME: Elhhorn, Gregory P.
REGISTRATION NUMEER: 38,40
REFERENCE/DOCKET NUMEER: 023070-078810US
REFERENCE/DOCKET NUMEER: 023070-078810US
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LEWING: 10915 base pairs
TYDE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: - COATION: 1..10815
COATION: 1..10815
US-09-004-838-21
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APPLICATION NUMBER: US 08/781,734
FILING DATE: 10-7AN-1997
ATTORNEY, AGENT INFORMATION:
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Matches 120; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RESULT 23 US-09-004-838-87

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7238 TCTATACTGCATCATCTTGAAGAGCTTGAAGTCGAGAATTGTGGTTCCATTGAATCGTTA 7297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7180 AATTATTAAAGTGATCAGTTGTGATAAGCTTGTGAATCT--CTTTCCACAATCCCATG 7237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              938 TGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTG 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            818 CAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAA 877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%; Score 33; DB 4; Length 13149;
48.6%; Pred. No. 20;
tive 0; Mismatches 125; Indels 2
                                                              APPLICANT: Michelmore, Richard W.
APPLICANT: Mayers: Shen, Kathy
APPLICANT: Meyers: Blake
APPLICANT: Meyers: Blake
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCE ADDRESS:
ADDRESSE: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STREE: California
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USAA

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PE-DOS/MS-DOS
SOFTWARE: PE-DOS/MS-DOS
SOFTWARE: PE-DOS/MS-DOS
SOFTWARE: PE-DOS/MS-DOS
SOFTWARE: PE-DOS/MS-DOS
SOFTWARE: PE-DOS/MS-DOS
SOFTWARE: PS-DOS/MS-DOS
FILING DATE: 09-JAN-1998
CLASSIFICATION NUMBER: US/09/N81,734
FILING DATE: 10-JAN-1997
ATTORNEY/AGENT INFORMATION:
RECISTRATION NUMBER: 38,440
TELECHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 1..13149
; OTHER INFORMATION: /note= "RG2A"
US-09-004-838-87
Sequence 87, Application US/09004838 Patent No. 6350933 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
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NAME/KEY: - 1.13149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                 HSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Sim
Matches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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APPLICANT: AGODS, Kenneth
APPLICANT: MCCOY, John
APPLICANT: MCCOY, John
APPLICANT: Racie, Lisa
APPLICANT: Merberg, Lavid
APPLICANT: Merberg, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA: US/08/702,080
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              589 GGGAGCTACAAATCCTGAAACGGGATA 615
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Sequence 7, Application US/08702080 Patent No. 5654173 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: BLOWN, SCOLT A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.0%
Query Match
Best Local Similarity 60.9%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: CDNA
US-08-702-080-7
                                                                                                                                                                                                                                                                                                                                               STREET: 87 Camparty: Cambridge
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-858-830-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 CTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTTT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.0%; Score 32.8; DB 4; Length 806; Best Local Similarity 53.6%; Pred. No. 6.7; Matches 67; Conservative 0; Mismatches 58; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 GATATTTCTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATT 86
                                                                                                   APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Burnham, Martin
APPLICANT: Hodgeon, John
APPLICANT: Hodgeon, John
APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Reichard, Richard
APPLICANT: Resonberg, Martin
APPLICANT: Resonberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Novypeptides and Their Uses
NUMBER OF SEQUENCES: 334
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: 1709 Swedeland Road CITY: Road of Prussia STATE: PA COUNTY: USA COUNTY: USA COUNTY: USA COUNTY: USA COMPUTER READABLE FORM: MEDIUM TYPE: Diskettle COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: TESTSEE (FOR WINDOWS VERSION 2.0 CURRENT APPLICATION UMBRE: US/08/936,165A FITING DATE: 24-5FD-1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimml. Edwarf REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P50549
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                             Sequence 6, Application US/08936165A
Patent No. 6348582
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 806 base pairs TYPE: notelet acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-936-165A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 610-270-5090
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RESULT 24
US-08-936-165A-6
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                                                                                                               529 AGTICGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATG 588
                                                                                                                                               202 AGGCTGCATGACAGAGACCATAGGAAATCCTTGTTGCTGCATCGGCATCAGGCTTGAGG 143
                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08858830
Fatent No. 5965693
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Racie, Lisa
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Bency David
APPLICANT: Bency David
APPLICANT: Bency David
APPLICANT: Bency Bency
APPLICANT: BENCOTING THEM
TITLE OF INVENTION: ENCODING THEM
UNMARR OF SEQUENCES: IL
3.0%; Score 32.6; DB 1; Length 448; 60.9%; Pred. No. 5.9; tive 0; Mismatches 34; Indels (
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qq ò RESULT 25 US-08-702-080-7/c

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APPLICANT: Regents of the University of Minnesota, et al.
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING ACETYL COA CARBOXYLASE GE
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.0%; Score 32.6; DB 2; Length 448; 60.9%; Pred. No. 5.9; tive 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A. STREET: P. O. Box 2938
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04625
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
COMBUTER: IBM COMPALIBLE
COMPRATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,285
FILLING DATE: 13.APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         589 GGGAGCTACAAATCCTGAAACGGGATA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 GGGTCTTATCCCACCTGCAACAGGAAA 116
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/858,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application US/08930285; Patent No. 6222099; GENERAL INFORMATION:
                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/702,080
                                                                                                                                                                                     NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Embretson, Janet E. REGISWRATION NUMBER: 39,665 REFERENCE/DOCKET WUMBER: 600 TELECOMMUNICATION INFORMATION: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 638 base pairs
                                                                                                                                                                                                                                                                                                                                                   LENGTH: 448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 60.99
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MN COUNTRY: USA ZIP: 55402 COMPUTER READABLE FORM: MEDIUM IYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-858-834-7
                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13 CLASSIFICATION:
                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
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US-08-930-285-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 AGTICGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGAACAAGTATTGATG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/0885834;
Sequence 7, Application US/0885834;
Patent No. 598122
GENERAL INCPORATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: LaValie, Edward
APPLICANT: Recher, Lisa
APPLICANT: Recher, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Musuice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
CIRY: CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%; Score 32.6; DB 2; Length 448; 60.9%; Pred. No. 5.9; tive 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DoS/MS-DOS
OFFRATM: Pc-bos/Ms-DOS
OFFRATMARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
                ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 GGGTCTTATCCCACCTGCAACAGGAAA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           589 GGGAGCTACAAATCCTGAAACGGGATA 615
                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, V
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,830
FILING DATE:
                                                                                                                                                                                                                                                                                                                                FILING TAREST PROGRAMMENT AND THE APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/702,080
FILING DATE: APPORREY AGENT INFORMATION:
NAME: Brown, Scott A.
FELECOMMUNICATION INFORMATION:
TELEPRATION INFORMATION:
TELEPRATIC (617) 498-824
INFORMATION FOR SEQ. ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: A48 DASE PAIRS
TYPE: DUCIDIC COUNTY.
                                                                                                                                                  COMPUTER READABLE FORM and WEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 60.9
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 87 Cambridge
CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                 Massachusetts: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear; MOLECULE TYPE: CDNAUS-08-858-830-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A.
                                                           Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: U
ZIP: 02140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-858-834-7/c
                                                              CITY: Car
STATE: Ma
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 27
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Sequence 3, Application US/09851896
Patent No. 6410325
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Susan M. Freier
APPLICANT: Andrew T. Watt
APPLICANT: Andrew T. Watt
APPLICANT: Andrew T. Watt
ANTISENSE WODULATION OF PHOSPHOLIPASE A2, GROUP VI (CA2+-INDEP)
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5423 GTTGGTGGTAAATAACGTGCTAAAGGGAACATCTTAAAAGTGAATTTTGATCAAATAT 5482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       645 ATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAAT 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              856 AACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 GATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
3.0%; Score 32.4; DB 1; Length 5555;
Best Local Similarity 53.1%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 61; Indels 0;
Matches 69; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
3.0%, Score 32.2; DB 4; Length 3800;
Best Local Similarity 61.2%, Pred. No. 19.
Matches 52; Conservative 0; Mismatches 33; Indels 0.
Matches 52; Conservative 0; Mismatches 33; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-05-762-15
US-08-05-762-15
Sequence 15, Application US/08965762
Patent No. 6280963
GENERAL INFORMATION:
APPLICAMY: Rollin, Yigal
APPLICAMY: Rollin, Yigal
APPLICAMY: Rollin, Yigal
TITLE OF INVENTION: ESSENTIAL FUNGAL GENES AND THEIR USE
FILE REFERENCE: 07334/062001
CURRENT APPLICATION NUMBER: US/08/965,762
CURRENT FILING DATE: 1997-11-07
NUMBER OF SEC ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               916 TIGCTICTTIATITICCTITIGT 940
TELEFAX: (212) 869-8864/9741
FIELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5555 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-08-965-762-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ATAGTTCTCCTTATTGTTCTTTTT 87
                                                                                                                                                                                     TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                     ss: single
unknown
                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 34..3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5543 AAAAAAAAA 5552
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                                                                                                                                                                                                                                                                                                             US-08-484-438-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/0848438

Patent No. 5811098

APPLICANT: Plowman, Gregory D.

APPLICANT: Culouscou, Jean-Aichel

APPLICANT: Siegall, Clay B.

APPLICANT: Siegall, Clay B.

APPLICANT: Hellstr m, Ingegerd

APPLICANT: Hellstr m, Ingegerd

APPLICANT: Hellstr m, Ingegerd

APPLICANT: Hellstr m, Marl E.

TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE

CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

CORRESPONDENCE NAMES.
                                                                                                                                                                                                                                                   Query Match 3.0%; Score 32.6; DB 4; Length 638; Best Local Similarity 52.6%; Pred. No. 6.9; Matches 71; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/484,438
FILIGN DATE: 07-JUN-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-0CT-1994
APPLICATION NUMBER: 05 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 18,872
REGISTRATION NUMBER: 5524-230
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennie & Edmonds
1155 Avenue of the Americas
                                                                               Genomic DNA
  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 AGGAATATGGGGTCG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GTCAATTTACAGTCG 324
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MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: New York STATE: New York COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                  FRAGMENT TYPE:

ORIGINAL SOURCE:

US-08-930-285-16
                                                                                                                                ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-484-438-3
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APPLICANT: Sin, Kim L.
APPLICANT: Sin, Kim L.
APPLICANT: Chitais, Chetan
APPLICANT: Miler, Louis H.
APPLICANT: Miler, Louis H.
APPLICANT: Wellens, Phomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: 02
COUNTRY: US
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: AND PLASMODIUM ENTHHROCYTE BINDING PROTEINS
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERTHHROCYTE BINDING PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.9%; Score 32; DB 2; Length 822C illarity 56.7%; Pred. No. 31; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2849 TACAAAAACGTCTTTTTACCTCCCCGACGAGAACACATGTGTAC 2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 TCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAAC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION ADMER: US/08/568,459A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH121.001CP1
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Patent No. 5993827

GENERAL INFORMATION:

APPLICANT: Sim, Kim L.

APPLICANT: Chitnis, Chetan

APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Plasmodium falciparum
US-08-568-459A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSILLICATION: 43.30
ATTORNEY/AGENT INRORMATION:
NAME: ISTACLED.
REGISTRATION NUMBER: 20,655
REFERENCE/DOCKET NUMBER: NIH12
TELECOMMUTICATION INFORMATION:
TELEPHONE: (619) 235-8850
TELEPRAX: (619) 235-8850
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
LENGTH: 8220 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA (genomic)
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-487-826B-11
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Best Local Si
Matches 59,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2004, Application US/09134001C
Sequence 2004, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
RAPPLICANT: Lynn Doucette-Stamm et al
APPLICANT: NUMBER: ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCCUS
TITLE REFERENCE: GTC-07
CURRENT FILING DATE: 1997-08-14
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 528
LENGTH: 528
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0
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                                                                                                                                                                                                                                                                                                                                                                                                           767 CAIAAATICCGAITAAAAAAGGGAGIGCITACAACAGCCAIAICAGIGGA-GCAACCIIC 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       727 GCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   787 GGGAGIGCTIACAACAGCCAIATCAGIGGAGCAACCIICCCIITGAITCITIGAIAAIGA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Gaps
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                Score 32.2; DB 4; Length 70000; Pred. No. 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.9%; Score 32; DB 4; Length 528; ilarity 55.4%; Pred. No. 9.3; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                              98;
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                       CURRENT APPLICATION NUMBER: US/09/851,896
CURRENT FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425 ATGATGAATCAATTAATATGGAAGTTAA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886 AATAGAAATGCATTTGTGTCGAGCTAAA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Staphylococcus epidermidis
US-09-134-001C-2094
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.1%;
Matches 91; Conservative
                                                                                FILE REFERENCE: RTS-0220
                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1709 AGAAAAACC 1701
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US-09-134-001C-2094
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US-08-568-459A-11
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                                                                                                                                                                                   70000
                                                                                                                                                                                                                                                  ; FEATURE:
US-09-851-896-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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us-09-438-185a-1_1199590_1200675.rni

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,288
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: ISTBELSEN, NG
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/487,826B
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PC-DOS/MS-DOS
                                                                                 FILING DATE:

CLASSIFTCATION:

NAME: FULLEr, MICHAEL

REGISTRATION UNBER: 36,516

REGISTRATION UNBER: 36,516

REFERENCE/DOCKET NUMBER: 36,516

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CRARACTERISTICS:

LENGTH: 8220 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 10-SEP-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 36
US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
STREET: 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-210-288-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Millis, Chetan
APPLICANT: Millis, Loudid S.
APPLICANT: Pau, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9%; Score 32; DB 2; Length 8220; 56.7%; Pred. No. 31; tive 0; Mismatches 45; Indels
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATA
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY ACENT INFORMATION:
NAME: Israelsen, Ned
NAME: Israelsen, Ned
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPONE: (619) 235-0176
INFORMATION POSEQ ID NO: 11:
SEQUENCE GIARACTERISTICS:
LENTH: 8220 base pairs
TYPE: Nucleicaid
STRANDEDRESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2849 TACAAAAACGTCTTTTTACCTCCCCGACGAGAACACATGTGTAC 2892
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NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach
CITY: Newport Beach
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UKGANISM: Plasmodium falciparum
US-08-487-826B-11
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Best Local Similarity 56.74
Matches 59; Conservative
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ORGANISM: Pla
                                                                                                                                                      92660
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US-09-210-288-11
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Sequence 13, Application US/08487826B
Patent No. 599387
GENERAL INFORMATION
APPLICANT: Sim, Kim L.
APPLICANT: Miller, Louis, Chetan
APPLICANT: Miller, Louis, H.
APPLICANT: Peterson, David S.
APPLICANT: Peterson, David S.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 GATGTATTGAAGGGAAGACGAATAATCTGATCCAATTCTAAAGGGAGAAACAGGTACGTTA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.9%; Score 32; DB 4; Length 8220; Best Local Similarity 56.7%; Pred. No. 31; Matches 59; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2849 TACAAAAACGTCTTTTTACCTCCCGACGAGAACACATGTGTAC 2892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEE: Knobbe Martens Olson & Bear
1: 620 Newport Center Drive 16th Floor
Newport Beach
California
NIH121.1FWDV1
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APPLICANT: Kondo, Keiji
APPLICANT: Kondo, Keiji
APPLICANT: Inouve, Masayori
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
TITLE OF INVENTION: APPLICATIONS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207 GTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCAT 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 CTAAITTIGAAGIGAGTICTACCAGTICATCAAAATGICTTATTGAAAATAAAGICTCIT 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 CTAATAAGATAAAAAGATTTATGAATCAATTAATTCGAGGTATTAAACATTGTCATTCTC 421
                               APPLICANT: Draetta, Guillo
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins from
TITLE OF INVENTION: Human Pathogens, and Uses Related Thereto
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.9%; Score 31.8; DB 1; Length 1002; Best Local Similarity 47.3%; Pred. No. 14; Matches 96; Conservative 0; Mismatches 107; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 4.2.
ATTORNEY/AGRAT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRAATION NUMBER: 36,70
REFERENCE/DOCKET NUMBER: MIV032.01
TELEPHONE: (617) 832-129
TELEPHONE: (617) 832-700
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleit caid
                                                                                                                            E: Foley, Hoag & Eliot, LLP
One Post Office Square
                                                                                                                                                                                                                                                                                                             SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,090B
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 1, Application US/07667276A
; Patent No. 5470971
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        Cottarel, Guillaume
                           Veronique
                                                                                                                                                                                                                                                                                                                                                              05-JUN-1995
N: 435
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LOCATION: 43..993
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CLASSIFICATION:
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                                                                                                                                                                                                        USA
                                                                                                                                                                    Boston
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US-08-463-090B-3
                                                                                                                                  ADDRESSEE:
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                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                         831 GATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAATAG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               771 AATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTT 830
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                                                                                                                                                                                                                                                DB 2; Length 19124;
                                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.9%; Score 32; DB 2
Best Local Similarity 56.7%; Pred. No. 44;
Matches 59; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence 3, Application US/08463090B; Patent No. 5801015; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Saccharomyces cerevisiae US-09-356-952-12
; INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERESTICS: LENGTH: 19124 base pairs TYPE: nucleic acid STRANDEDNESS: single TOOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 32262 TTCTGGAT 32255
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                                                                                                                                                            MOLECULE TYPE: CE
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13
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STATE: Michigan COUNTRY: U.S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-952-014C-51
                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                             Query Match
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OTHER INFORMATION: corresponds to base -474 of the sequence listed in
OTHER INFORMATION: Figure 4 of the application"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1296 AATTGTCAAGAAAGGAAACATTTCTTACGGATTGGGAAGAAGCACTAATCTCGAAAAAGA 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666 CTAAGAAATCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAAT 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             606 AAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGT 665
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Best Local Similarity 51.9%; Pred. No. 17;
Matches 95; Conservative 0; Mismatches 87; Indels 1; Gaps
                                                                                                       COMPUTER: USC.

ZIP: 19102
COMPUTER READABLE FORM:
MDDIUM TYPE: FLOPPY disk
MDDIUM TYPE: FLOPPY disk
MDDIUM TYPE: BM PC Compatible
COMPUTER: DEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENT REAPARTION:
APPLICATION NUMBER: US/07/667,276A
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTONEY/AGENT INPORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 377.5351P
TELECOMMUNICATION INFORMATION:
TREEPARE: 215-875-8383
TELECOMMUNICATION INFORMATION:
TREEPARE: 215-875-8384
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
EDROTH: 1894 base pairs
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREFT: 230 S. Fifteenth Street, Suite 500
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UKGANISM: Saccharomyces cerevisiae STRAIN: S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1254 LLL.
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genor
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LOCATION: 475..1104
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ORIGINAL SOURCE:
ORGANISM: SACC
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                                                            CITY: Ph
STATE: P.
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; US-07-667-276A-1
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RESULT 40 US-08-642-274D-51 Sequence 51, Application US/08642274D Patent No. 6200749 ; GENERAL INFORMATION:

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APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
TITLE OF INVENTION: MCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 229000033
CURRENT APPLICATION NUMBER: US/08/642,274D
UNMBER OF SEQ ID NOS: 220
SOFTWARE PARTIAL DATE: 196-05-03
LENGTH: 679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         926 TTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGG 985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: genomic US-08-642-7440-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match 2.9%; Score 31.6; DB 4; Length 679; Local Similarity 50.0%; Pred. No. 13; 79; Indels on 79; Conservative 0; Mismatches 79; Indels on 79; Conservative 10; Mismatches 79; Indels on 79; Conservative 10; Mismatches 79; Indels on 79; Conservative 10; Mismatches 79; Mismatches
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TITLE OF INVENTION: ARAXIA-TELANGIECTASIA GENE AND ITS
TITLE OF INVENTION: GENOMIC ORGANIZATION
TORRESPONDENCE 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6265158thwestern Hwy., Suite 410
CITY: Farmington Hills
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,014C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    986 AGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTG 1023
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: ROIN, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 2290.
TELECOMMUNICATION: TELECHONE: 810-539-5050
INFORMATION FOR SEQ ID NO: 51:SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      679 base pairs
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143 TCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTGATCCAATTCTAAAGGGAGA 202
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                                                                                1016 ACACTAAGGCAACTCATGGAGGGGTCTTCAAAGACCTTGCAAGAAGTACTATGG 1073
                                                        203 ACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGG 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.9%; Score 31.6; DB 3; Length 1734;
                                                                                                                                                                                                                                                   APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvl
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTYRUL-COENZYME A
TITLE OF INVENTION: HUMAN 3-HYDROLASE
NUMBER OF SUGURNES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNETWARE: LISTEM: DOS
UNETWARE: FASTEED FOR Windows Version 2.0
APPLICATION NUMBER: US/No/NTELING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 54.2%; Pred. No. 20;
Matches 64; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             3: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0294 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/858,052
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AUGM.

NAME: Billings, Lucy 0.

REGISTRATION NUMBER: 36,749

REGISTRATION NUMBER: PF-0.

REFERENCE/DOCKET NUMBER: PF-0.

TELECOMMUNICATION INFORMATION:

--- PEHONE: 415-855-0555
                                                                                                                                                                          US-09-200-284-2
; Sequence 2, Application US/09200284
; Patent No. 6110507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHRACATERISTICS: LENGTH: 1734 base pairs TYPE: nucleic acid STRANDEDRESS: single TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIBRARY: U937NOT01
CLONE: 1187
                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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US-09-484-970B-60
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                                                                                                                                           83 AAGTITGCAATAGTICATATAATITAGCTAGCITTTATATGTATATAAGTTTAAATITTAG 142
                                                                                                          926 TIATITICCITITICIAGAATGATICGGTAGTAGGAATAIGGGGICGAGTAIGCACGTIGG 985
                                                                                                                                                                                                                           143 IGTATTACCTTAATTTGAGTGATTCTTTAGATGTATTTAGTATTTGTAATATAATTAA 202
                                                                    0; Gaps
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                          Score 31.6; DB 4; Length 679; Pred. No. 13; 0; Mismatches 79; Indels (
                                                                                                                                                                                                                                                                                                                                                                                          % Sequence 2. Application US/08858052
; Sequence 2. Application US/08858052
; Patent No. 5849498
; Patent No. 5849498
; RAPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Nell J.
TITLE OF INVENTION: HUMAN 3-HYDROXYISOBUTYRUL-COENZYME A
                                                                                                                                                                                                                                                                      986 AGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTG 1023
                                                                                                                                                                                                                                                                                                203 ATTGGTTGTGTTTTCTTGAAGGCAGTAGAAGTTGCTGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Faster for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,052
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
RELING APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF-0294 US
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-02
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1734 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                              Query Match 2.9%;
Best Local Similarity 50.0%;
Matches 79; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: U937NOT01
CLONE: 1187
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Best Local Simi
Matches 64;
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: NAME/KEY: CDS

: LOCATION: (127009)...(127130)

: NAME/KEY: CDS

: LOCATION: (128910)...(129139)

US-09-426-290-1
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US-09-428-034-1/C
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US-09-004-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 11987 AAAGAGATACGAATTTCTATAGACTGACTTTTTCCATTTTTTAAATGTTCATGTCACATC 12046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               765 ACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTT 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       885 AAATAGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAA 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.9%; Score 31.6; DB 4; Length 13977; Best Local Similarity 46.1%; Pred. No. 50; Matches 106; Conservative 0; Mismatches 124; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12047 CTAATAGAAAGAAATTACTTCTAGTCATCCAGGCTTACCTGCTTGG 12096
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                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 229357.11CB1
Sequence 60, Application US/09484970B
Patent No. 6426186
GENERAL INFORMATION:
APPLICANT: Jones, Karen A.
APPLICANT: JONES, Karen A.
APPLICANT: VOLKMULH, WAYNER.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
SOFTWARE: 113977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Berglind Ran olafsdottir
APPLICANT: Berglind Ran olafsdottir
APPLICANT: Deffrey Gollcher
TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REPERENCE: 2345.2001-000
CURRENT APPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOSTWARE: FESSESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: unsure
; LOCATION: 11721-11761, 12294, 13969
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-9708-60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
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(95252)...(95430)
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                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 168575
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US-09-426-290-1
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NAME/KEY:
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                                                                                                                                                                                                          744 ACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGAGTGCTTACAACAG 803
                                                                                                                                                                                                                                                                                                                804 CCATATCAGTGGAGCAACCTTCCCTTTGATTTTTGATAATGACAGAAGATGAACAAAGA 863
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Query Match 5.9%; Score 31.6; DB 4; Length 168575; Best Local Similarity 50.0%; Pred. No. 1.4e+Q2; Matches 105; Conservative 0; Mismatches 104; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 31.4; DB 4; Length 1364; 52.7%; Pred. No. 21; tive 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cheng, Kuo-Joan
APPLICANT: Liu, Jin-Hao
APPLICANT: Tay, Cheng-Fang
APPLICANT: Tay, Yih-Chin
TITLE OF INVENTION: CELLULASE ENZYMES
TITLE OF INVENTION: CELLULASE ENZYMES
CURRENT APPLICATION NUMBER: US/09/428,034
CURRENT FILING DATE: 1999-10-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   78297 TTGCAGACTTGTGAGGTGGTTAAATAACAA 78326
                                                                                                                                                                                                                                                                                                                                                                                                               864 GTAAGTTTTTGAAAATTCTAAAATAGAAA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-004-838-116; Sequence 116, Application US/09004838; Patent No. 6350933; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09428034; Patent No. 6428996; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Piromyces rhizinflata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 2.9%
Best Local Similarity 52.7%
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)...(1128)
US-09-428-034-1
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183 KNKNRSRNRNRSRNRNRSRNRNRSRNRNRSRCRARGRCRURGRCRGRURARARC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    508 GGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTG 567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             628 IGITICTAATICGAAGAAITIAATGACTGCTTGAIGGTCTAAGAAATCAGAAAGGAGACC 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SZOSLEK, Jack W.
APPLICANT: ROBERTS, RICHARD W.
APPLICANT: ROBERTS, RICHARD W.
APPLICANT: AND ROBERTS, RICHARD W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: EVELONE
FILE REFERENCE: 00706/350007
CURRENT APPLICATION NUMBER: 00/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-27
EARLIER PLING DATE: 1997-01-37
EARLIER PLING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.9%; Score 31.2; DB 4; Length 289; Best Local Similarity 9.3%; Pred. No. 12; Matches 26; Conservative 111; Mismatches 142; Indels
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FUSIONS
TITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
FULE REFERENCE: 00786/350003
CURRENY APPLICATION NUMBER: 05/09/007,005B
CURRENY FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER APPLICATION NUMBER: 60/064,491
SARLIER APPLICATION NUMBER: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASLESC for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Translation template
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/09244796 Patent No. 6281344 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature

: LOCATION: (1)...(289)

: OTHER INFORMATION: n = A,T,C or G

US-09-007-005-17
                                                                                                                                                                                                                                                                                                                                                                         TYPE: RNA
ORGANISM: Artificial Sequence
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SEQ ID NO 17
LENGTH: 289
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 17
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2.9%; Score 31.4; DB 4; Length 7521;
Best Local Similarity 48.5%; Pred. No. 43;
Matches 116; Conservative 0; Mismatches 121; Indels 2;
                                                APPLICANT: Meyers, Blake
TITLE OF INVENTION: Procedures and Materials for
TITLE OF INVENTION: Conferring Pest Resistance in Plants
NUMBER OF SEQUENCES: 140
CORRESPONDENCES ADDRESS:
ADDRESSED: Townsend and Townsend and Crew Lip
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Prancisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Elnhorn, Gregory P.
REGISTRATION NUMBER: 36,40
REFERENCE/DOCKET NUMBER: 023070-078810US
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 116:
LENGHE: 7521 base pairs
LENGHE: 7521 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 09-JAN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
FILING DATE: 10-JAN-1997
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: -
; LOCATION: 1..7521
; COTHER INFORMATION: /note= "RG2N"
US-09-004-838-116
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                                                                                                                                                                                                                                                                                                                               ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               APPLICANT: Michelmore, Richard W. APPLICANT: Shen, Kathy
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US-09-007-005-17
                                                                                                                                                                                                                                                                              STATE: CA
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Search completed: January 9, 2003, 11:51:00 Job time : 476 secs

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APPLICANT: LIFORRATION:
APPLICANT: LYON DOUGETEE-SEAMN et al
APPLICANT: LYON DOUGETEE-SEAMN et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: UNDER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PELING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PRI
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2.9%; Score 31.2; DB 4; Length 289;
Best Local Similarity 9.3%; Pred. No. 12;
Matches 26; Conservative 111; Mismatches 142; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 747 GTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAA 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-134-001C-1809; Sequence 1809, Application US/09134001C; Patent No. 6380370
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1809
                                                                                                                                                                                                                                                                                                                          , LUCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature LOCATION: (1)...(289)
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: January 9, 2003, 06:35:28 ; Search time 1940 Sei (without alignments) 9066.133 Million cell Title: US-09-438-185A-1_COPY_1199590_1200675	Scoring table: IDBNITYLNUC Searched: 16154066 segs, 8097743376 residues Total number of hits satisfying chosen parameters: 32308132 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries BAXIMUM Match 100% Listing first 150 summaries EST:* 2: em_esthum:* 3: em_esthum:* 4: em_esthum:* 5: em_estpl:* 6: em_estpl:* 7: em_estri:* 11: 9D_ests:* 11: 9D_ests:* 12: 9D_ests:* 13: 9D_ests:* 13: 9D_ests:* 14: 9D_ests:* 15: em_estin:* 16: em_estin:* 17: 9D_ests:* 18: em_gss_in:* 18: em_gss_in:* 19: em_gss_in:* 10: 9D_ests:* 11: 9D_ests:* 12: em_gss_in:* 13: 9D_ests:* 14: em_gss_in:* 15: em_gss_in:* 16: em_gss_in:* 17: em_gss_in:* 18: em_gss_in:* 18: em_gss_in:* 19: em_gss_in:* 10: em_gss_in:* 10: em_gss_in:* 11: em_gss_in:* 12: em_gss_in:* 13: em_gss_in:* 14: em_gss_in:* 15: em_gss_in:* 16: em_gss_in:* 17: em_gss_in:* 18: em_gss_in:* 18: em_gss_in:* 19: em_gss_in:* 10: em_gss_in:*	1

ALIGNMENTS	RESULT 1			ACCESSION AL063921 CT-4941778	S GSS.	SOURCE Drosophila melanogaster. ORGANISM Drosophila melanogaster		Ephydroidea; Drosophilidae; Drosophila.	REFERENCE 1 (bases 1 to 1101)	Direct Submission	JOURNAL SUBMILTEROR (12-10)-1999) GENOSCOPE - CENTIFO NATIONAL DE SEQUENCAGE : BP 191 91006 EVRY CEGEX - FRANCE (E-mail : segrefégenoscope.cns.fr	- Web : www.genoscope.cns.fr) COMMENT Determination of this BAC-end sequence was carried out as part of a		The BAGE is constructing a physical map of the Drosophila melanoaster denome using these BACs. For further information	please see http://www.fruitfly.org The BDGP Drosophila	metanogaster bac ilorary was prepared Dy Kazucoyo Usoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of	Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,	N: The Library is named ReVL-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BGCP from the	isogenic strain y2; cn bw sp, the same strain used for the BDGF's	and how to order individual BAC clones, the entire library, or	filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.	FEATURES Location/Qualifiers Source 1. 1101	/organism="Drosophila melanogaster"	/UD_AIDET	/clone_lib="RPCI-98" /note="end : TET3"	BASE COUNT 201 a 64 c 131 g 202 t 503 others ORIGIN	The state of the s	Query March Quert Local Similarity 16.0%; Pred. No. 6.86-05; Marches 09: Conservative 270; Mismatches 242; Indole 1: Cane 1:	מתרכווכם ססי כסווספד לתרכו של שני שדמוות ככווכם די פתקס	Qy 353 AGGGTTTGTATGCGTTTGTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTG 412	Db 1096 WGDDTWDRDTRKDDWDWTKWWTWWKDRADDRRWAGDADRWAWDDGAGTWWTATWWWWWW 1037	Qy 413 AAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGATGTAGAAGCCAAGGCACG 472	Db 1036 WATWDIWWDKWWWATAAKIDTAWIWWRTAWRADWAGRDRGAGKRDRDAATDADGAGRRD 977	Qy 473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532	THE STATE OF THE S		CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGA	Db 917 DGAGDKDDDGKGKDADDDTDGTKDDDDKDKWDDWDKAKGTWGDATWAWAATDWWWGWAD 858	Oy 593 GCIACAAATCCIGAAAGGGATAATAGGAAAAATGGTTTCTAATTCGAAGAATTAATG 652	Db 857 ADWWTWDAAADDWWADDRWDAWAWGMRTADRRDWGDRAGKRGGARKRRDRKR 798	Oy 653 ACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAA 712
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Direct Submission
Submitted (23-001-1999) Genoscope - Centre National de Sequencage :
Submitted (23-001-1999) Genoscope - Centre National de Sequencage :
Br 191 91006 EVRY cedex - FRANCE (E-mall : seqrefégenoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Geneyleve Payan. It has been constructed in the vector
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Drosophila melanogaster.
Eukaryota, Hetanogaster
Eukaryota, Metanogaster
Eukaryota, Retenogaster
Enkaryota, Endopteryota, Diptera; Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae; Drosophila.

[ Pases 1 to 1001)
409 AGTGAAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGG 468
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                                                                                                                                                    469 CACGIGCCCIAAAAGGICAIGGAIGAGAICAGGAGITAAAGGAGAAAITAICIITAAICGAG
                                                                                                                                                                                                                         858 GRRRRRGRAGRRARAGAGGRAGRRGRGRRRRARARRRAGAARARARGR-RARAARARAR
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence TET3 end of BAC # #ASCR12K22 of RPCI-98 library from Drosophila melanogaster (fruit AL060767
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                                                                                                                                                                                                                                                                                                                                                                 677 WDRTDAWWADAAWWTTTDTDTDDWDKRDRRRKGARRRRRTTARAAWDWWTWKAWDWAKWD 618
                                                                                                                                                                                                                                                                                                                                                                                                                                           833 ITCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAA 892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617 WKTRADRWDRWAADTWTDARKADRDWAKARAWRARRDRARAARADRRWTTKGKTTTATWT 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster.
Drosophila melanogaster.
Bruszoda, Arthropoda; Hexapoda; Insecta; Pterygota;
Brusryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                       713 AATCTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAA 772
                                                                                                                                                                                                                                                                                      773 TICCGAITAAAAAAGGGAGTGCTTACAACAGCCATAICAGTGGAGCAACCTICCCTTIGA 832
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4.7%; Score 51.4; DB 17; Length 997;
Best Local Similarity 18.6%; Pred. No. 0.019;
Matches 103; Conservative 162; Mismatches 288; Indels 1.
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/db_xref="taxon:7227"
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/note="end : TET3"
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Direct Submission
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CNS005TE/c
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37F10 of DrosBAC library from Drosophila melanogaster (fruit AL10817).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     854 TGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATTAGAAATGCATTTGTGTCGAGCTAAA 913
                                                                                                                                                                                                                                                        434 AAAAATTCAGAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAAAAGGTCATGGATG 493
                                                                                                                                                                                                                                                                                                  525 AAAAWAAAAAAAWAAAAAAGWGKARGAAGGGRRGRBVGAGRGDATAATAAAAAAADDTK 584
                                                                                                                                                                                                                                                                                                                                               494 AGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGA 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      614 TAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAA 673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 AAAAAAAAAAAAAAAAKKKKKKKKGDGKATKTAAWAKGRKDWGTATAWWTWDATWADTWK 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          674 TCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTC 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       765 AATDTDAKRAAAGRRKKDARKTARDGGRRARTRRRAWAAGGKRARAGARRARAARRAADD 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    734 CATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTG 793
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Buxosophila melanogaster

Eukaryota; Metanogaster

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Repydroidea; Drosophilidae; Drosophila.

(Pass 1 to 1101)
                                                                                                                                                                                                                Gaps
                                                                                                                                                              11arity 20.4%; Score 51.2; DB 17; Length 1101; Pred. WO. 0.022; Conservative 209; Mismatches 249; Indels 2;
                                                                                            358 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       974 TATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAG 1011
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                                                                                               ų
/clone="BACN37D10"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                                               128 g
                                                                    /note="end: SP6"
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                                                                                                                                                                                      Similarity
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es 118;
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VERSION
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- Web : www genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a

Genoscope.

Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

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COMMENT

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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
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collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37A07 of DrosBAC library from Drosophila melanogaster (fruit fly), agnomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 GGAAGAGCTTGTACTTTTCTATGACTTTAGTGAAGAGTCTTCCCATGTTTATGAAAAAT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 TCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAAAAGGTCATGGATGAGATCA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   988 WWRDTDWWDKWDTKWKDDRWTKRWATRGDGRAGRAKRRDDRRGDRGRRRRRRTRKWRWW 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        500 GGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAA 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          928 RRAAWWTAWTTWWWGTTKGAWWTKTRKRKGGGAAAAADWGRTDDWRWDKRAAAAGKDGG 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           560 CGGTCCTGCAACAGAGACAAGTATTGATGGGGGAGCTACAAATCCTGAAACGGGATAATAG 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             868 KGKKARTWGAAAAAAAAWDTKKTATKRKKRTKTGRAWWAAGTRTTWDAATAWKTKRAAAA 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               620 GAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAA 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              808 AGRRAAAAWAKDRGTKRGKGRKKRGTDDGKGTKWKTRTTWTKTAAAARRAAAKGWTK 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                680 AGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGA 739
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Drosophila melanogaster.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidas; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6%; Score 50.2; DB 17; Length 1101;
                                                                                                                                                                                                                                                                                                                                                                                          348 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ilarity 22.4%; Pred No. 0.039;
Conservative 135; Mismatches 181; Indels
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    .1101
    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"

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                                                                                                                                                                                                                                                                                   /clone="BACN37F10"
/clone_lib="DrosBAC"
/plasmid="pbeloBAC11"
/note="end: SP6"
a 84 c 159 g ;
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Direct Submission
                                                                                                                                                           pBeloBAC11
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CNS017LB
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Drosophila melanogaster genome survey sequence SP6 end of BAC BACN13C23 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
By 191 91006 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     957 ККDКАКDКБКБКБАБАКАВАКАКАБАБАКАКАКАКАКАКАВББААВБАКАКАВБАКАКАК 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1017 AKADDAAKAKAKAKABABABAAKAKAAKRAAKRAAKAABABAAKAKAKABDKDKDKBAKKDDADK 1076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   660 GATGGTCTAAGAAATCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTG 719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               837 AAAKAKADAAGDAKAKRRAGDKDKAKADAKAAKKAKAKDDDDAKAATKAKKATKAKKDK 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       780 TAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTG 839
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Eukaryota; Metanogaca; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Metanogaca; Arthropoda; Hexapoda; Insecta; Pterygota;

Endoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

(bases 1 to 1001)
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                                                                                                                                                                                                                                                                                                                                                                 480 AAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTA 539
                                                                                                                                                                                                                                                                                                                                                                                                        661 ARKDKDTAKDAWKWDKATKAKAKKKRAKAKAKARARAKTATGKDARKAKAKAKAK----ATK 716
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                                                                                                                                                                                                                                                                Similarity 19.4%; Pred. No. 0.11; Length 1101; 33; Conservative 178; Mismatches 163; Indels 4;
                                                                                                                                                                                                      501 others
                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                 /clone="BACN03K20"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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                      Location/Qualifiers
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pBeloBAC11.
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CNS0155H
                                                                                                                                                                                                                    BASE COUNT
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEBH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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        http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     746 CGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAAGGGAGTGCTTACAACAGCC 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          806 ATATCAGTGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAGAGT 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      814 AAAAWATKIWWWTWTAAWTWKKATTWRTGTTTWAAWWDWATGDGGKGGGGDRRAAAAAG 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 CCGAAAGCITCTAAGIAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAAC 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                694 RAGWAARGADSGKWMVAAANGRWAAAARTWTTTMWAWMTHYHHTHARDAWAAWAAAWG 753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634 IGAGKITCKKGKWKGKGTWTTTWAWCKGKKGKGTGSGDKDGKWTGWYTYKTDCVAGGAGG 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626 IGIGITICIAATICGAAGAATITAATGACTGCTIGAIGGICTAAGAAATCAGAAAGGAGA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17; Length 987;
                                                                                                                                                                                                                                                                                                                                              250 others
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 30.5%; Score 50; DB 17; Length 98. Similarity 30.5%; Pred. No. 0.044; 142; Indels 16; Conservative 77; Mismatches 142; Indels
                                                                                                                                                                                              /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN37A07"
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/plasmid="pBeloBAC11"
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VERSION
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                                                                                                                                                                                                                                                                                                                                                         COUNT
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CNS0106X
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d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of EAC
BACNSA12 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :: | | : | | ::|: | | | ::|: | | | ::|: | | | : | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|: | | ::|:
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                                                                                                                                                                                                                                                                                                                                                                                                                          494 SGRCGCGKGGGBTDTYYKKGKBBBBYKKGRMGAGADARAAKTGAGTAAAWRAAAGACAAA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440 TCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAAAAGGTCATGGATGAGATCA 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  560 CGGTCCTGCAACAGAGACAAGTATTGATGGGGGAGCTACAAATCCTGAAACGGGATAATAG 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             680 AGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGA 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 800 ACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACA 859
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Bukaryote, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 GGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614. ARGGAAAAAAAGWDADDAATWMRKAARAAKADADWAAAAACAAAAANVHNAAWAAARGKAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   734 AAAAAATTAWWTAAWWWWAAWWWWAAATAAAADTTWTATWAAATAAAAAWWTAAA
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                                                                                                                                                                                                                                            232 others
                                                                                                                                                                                                                                                                                                                                              Conservative 106; Mismatches 257; Indels
                                                                                                                    /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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                                                                                                                                                             /clone="BACN13C23"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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                                                                                 Location/Qualifiers
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Direct Submission
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRV cedex - FRANCE (E-mail : seqref@genoscope.cns.fr web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project Grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 06-MAR-2002
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BJ345426 Dictyostellum discoldeum cDNA library, AF Dictyostellum
discoldeum cDNA clone dda23117 3', mRNA sequence.
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1 (bases I to 615)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the aggregation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         939 GTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGT 998
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66; Conservative 146; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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Contact: Tadasu Shin-i
Center For Genetic Resource Information
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18.2%; Pred. No. (
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/clone_lib="DrosBAC"
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By 19 91000 EARL CHECK. ITAINLY (T. M. M. M. M. W. W. GENGCOPE. CAST.)

- Web: www.genGcOPE.CAST.)

Determination of this BAC-end sequence was carried out as part of Determination of this BAC-end sequence was carried out as part of Collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fuitfiy.org The BDGP Drosophila please see http://www.fuitfiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucyo Googeawa and Maron Mammoser in Picter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. EcoRI digestion of Drosophila DNA provided by the BDGP from the EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp. the same strain used for the BDGP's Ind EST libraries. A more detailed description of the library and how to order individual BAC clones the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster genome survey sequence T7 end of BAC # BACH4019 of RPCI-98 library from Drosophila melanogaster (fruit Lity), genomic survey sequence.
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TAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGAT 252
                         253 AAGAACGGCTCCATATGCTTTTCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGT 312
                                                                                                               Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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35.2%; Pred. No. 0.32;
Live 55; Mismatches 157;
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/note="end : T7"
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BJ345414 GI:19215921
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Lebasos 1 to 635)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                                                                                                                                                                                                                  /db_xref="taxon:44689"
/db_cxref="taxon:44689"
/clone='dda23117"
/clone=lib='Dictyostelium discoideum cDNA library, AF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 AAGAACGGCTCCATATGCTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACAGT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 TAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGAT 252
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                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 47.2; DB 13; Length 615; 59.8%; Pred. No. 0.22; tive 0; Mismatches 53; Indels 0;
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Center For Genetic Resource Information
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                              1. 615
/organism="Dictyostellum discoideum"
                            National Institute of Genetics Ill Yate, Mishina Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-685 Email: tshini@genes.nig.ac.jp. Locatlon/Qualifiers
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95 c 105 g 218 t
                                                                                                                                                                                                                                                                                                                     /dev_stage="Aggregation stage"
94 c 103 g 210 t
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Location/Qualifiers
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Dictyostelium discoideum
                                                                                                                                                                                                          /strain="AX4"
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Best Local Similarity 59.83
Matches 79; Conservative
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AUTHORS :
                                                                                                             ACCESSION
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Caenorhabditis elegans

Eukaryota; Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

I (basea: 1 to 588)

Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Suzuki,Y.
and Sugano,S.
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were closed into pPC86"
                                                                                            261 TCAAAATCTACAACTTCCGGCTTATCACTCAACGCATATTGAAGCTCTCCCAAATGAACTC 320
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                                                                       821 CCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAGAGTAAGTTTTTGAAAAAT 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191 TCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTG 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon.6239"
| /clone="yklo97h08"
| /clone="upublished oligo-capped cDNA library, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
761 CGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAA
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59.1%; Pred. No. 0.56;
tive 0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A complementary view of the C.elegans genome Unpublished (2002)
Contact: radasus Shin.
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
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                                                                                                                                             881 TCTAAAATAGAAATGCATTTGTGTCGA 907
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BJ135240.1 GI:18295397
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nes 78; Conservative
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Drosophila melanogaster genome survey sequence SP6 end of BAC BAC BAC 03504 of DrosBAC library from Drosophila melanogaster (fruit AL098379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre drouged up Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357 ITIGIAIGCGTIGITITITACTAGGAAGAGCTIGIACTITITCTATGACTITAGIGAAGA 416
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                                                                                                                                                                                                                                                                     Drosophila melanogaster.

Bucsophila melanogaster.

Bukaryotia metanogaster.

Bukaryotia Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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a 108 c 131 g 1
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Dictyostelium discoideum.

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Dictyostelium discoideum

Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.M., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of development for the first first first finder stage of development for the first fi
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/dev_stage="slug"
/ 78 c 79 g 175 t
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E 9915627

Contact: Hideko Urushihara

Contact: Hideko Urushihara

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1-1-1 Tennoudai, Tsukuba, Ibaraki 305-8572, Japan

Tel: 81-298-53-664

Fax: 81-298-53-664

Fax: 81-298-53-661.tsukuba.ac.jp

PROJECT - 'Dictyostelium discoideum cDNA project in Japan'.

rce

1. 529/Qullifiers
                                                                                                                                                                                                                                       /strain="AX4"
//strain="AX4"
//db.xref="taxon:44689"
//clone=ddal2al8"
//clone=lib="Dictyostelium discoideum cDNA library, AF"
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4.1%; Score 45; DB 9; Length 529;
Best Local Similarity 61.5%; Pred. No. 0.79;
Matches 72; Conservative 0; Mismatches 45; Indels
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Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6856 Email: tshini@genes.nig.ac.jp.
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/organism="Dictyostelium discoideum"
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72 c 83 g 171 t
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 485)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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Dictyostelium discoideum.
Dictyostelium discoideum
Bukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 348).
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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/clone="dda12b22"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
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Centect For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mashima, Shizuoka 411,8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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50 c 53 q 137 t
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Location/Qualifiers
1. .348
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Sp. Dictyostelium discoideum.

Bukaryota: Mycetozoa; Dictyosteliida; Dictyostelium.

E Lobasa: 1 to 546)

S Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length CDNA of Dictyostelium discoideum at the slug stage to 11 length CDNA of Dictyostelium discoideum at the slug stage.

Contact: Tadasu Shin-i

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National Institute of Genetics

Ill Yata Mashima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6855

Fax: 81-559-81-6855
                                                                                                                                                                                                  BJ400438 546 bp mRNA linear EST 10-MAR-20 BJ400438 Dictyostelium discoideum cDNA library, SF Dictyostelium discoideum cDNA clone dds13e07 3', mRNA sequence.
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/bd.xref="taxon:44689"
/clone="ad613607"
/clone_lib="lictyostelium discoideum cDNA library, SF"
/sex="mat A"
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Dictyostelium discoideum
Eukaryota, Mycetozoa, Dictyosteliida; Dictyostelium.
I (bases 1 to 54).
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the slug stage
Unpublished (2002).
Contact: Tadasu Shin-i
                     248 TGCTTTATCAGTTAAAAAGTGTTCCATTTCACCTGTTGATGATAAAAATACCTGCACCATA 189
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tive 0; Mismatches 45; Indels
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84 c 95 g 184 t
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Location/Qualifiers
1. .546
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BJ376869 Dictyostelium discoideum cDNA library, CF Dictyostelium
discoideum cDNA clone ddc30g10 3', mRNA sequence.
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1 (bases 1 to 562)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the culmination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.1%; Score 45; DB 13; Length 547;
61.5%; Pred. No. 0.79;
tive 0; Mismatches 45; Indels
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
TTE1: 81-559-81-6856
Fax: 81-559-81-6855
                                                                                                                                                                                                                 /organism="Dictyostelium discoideum"
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84 c 93 g 192 t
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84 c 94 g 185 t
                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 547
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Location/Qualifiers
1. 562
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BJ376869.1 GI:19286252
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EST 08-MAR-2002
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BJ376868. I GI:19286251
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota: Mycetoza: Dictyosteliida: Dictyostellum.
1 (bases 1 to 596)
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Pred. No. 0.8;
0; Mismatches 45; Indels
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Contact Tadasu Shin-i
Contact For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Location/Qualifiers
1..596
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshiningenes.nig.ac.jp.
Location/Qualifiers
1. 590
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Local Similarity 61.5%;
nes 72; Conservative
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                                                                                                                                                                  EST 07-MAR-2002
                                                                                                                                                                  BJ341943 Dictyostellum discoideum cDNA library, AF Dictyostellum discoideum cDNA library, AF Dictyostellum discoideum cDNA clone dda8h19 3', mRNA sequence.
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Dictyostellum discoideum.
Dictyostellum discoideum
Dictyostellum discoideum
Bukaryota: Mycetozoa; Dictyostellida; Dictyostellum.
Dictyostellum.
Upases 1 to 590)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length CDNA of Dictyostellum discoideum at the slug stage Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Illl Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                     Dictyostelium discoideum.
Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 584)
1 (bases 1, Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
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                         4.1%; Score 45; DB 13; Length 584;
llarity 61.5%; Pred. No. 0.8;
Conservative 0; Mismatches 45; Indels
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Contect: Tadasu Shin-i
Contect For Genetic Resource Information`
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum"
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91 c 101 g 192 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. 584
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                                                                                                                                                                                                                                                                                                                                                                                                                        stage
Unpublished (2002)
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es 72; Conserv
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BJ341943
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Dictyostellum discoideum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

(bases 1 to 653)

Morio,T., Uushihara,H., Saito,T., Ugawa,Y., Mizuno,H., Yoshida,M., Yoshiho,R., Mitra,B.N., Pi,M., Saco,T., Takemoto,K., Yasukawa,H., Yoshilams,J., Maeda,M., Takeuchi,I., Ochiai,H. and Tanaka,Y.

The Dictyostellum developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of
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/dev_stage="Slug stage"
a 88 c 99 g 207 t lothers
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PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
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DNA Res. 5 (6), 335-340 (1998)
9915627
Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
11-1 Tennoudal, Tsukuba ibaraki 305-8572, Japan
Fal: 81-298-53-464
Fax: 81-298-53-6614
  1. .598
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ilarity 61.5%; Pred. No. 0.8;
Conservative 0; Mismatches 45
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107 c 98 g
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Eukaryota: Mycetozca: Dictyostellida; Dictyostellum.

E 1 (bases 1 to 598)

S (urushihara: H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Full length cDNA of Dictyostellum discoideum at the slug stage

L Unpublished (2002)

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Fax: 81-559-81-6856

Email: tshini@enes.nig.ac.jp.

Location/Qualifiers
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BJ402538 Dictyostellum discoideum cDNA library, SF Dictyostellum
discoideum cDNA clone dds17c11 3', mRNA sequence.
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/clone_lib="bictyostelium discoideum cDNA library, SF"
/sex="mat A"
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Conservative 0; Mismatches 45; Indels
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Dictyostelium discoideum
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Matches 72; Conserv
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Dictyostellum discoideum.

SM Dictyostellum discoideum.

Dictyostellum discoideum.

Dictyostellum discoideum.

Eukaryota: Mycetozoa: Dictyostellida; Dictyostellum.

Eukaryota: Mycetozoa: Dictyostellida; Dictyostellum.

SG Turushinara: M.: Tanaka, Y.; Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the slug stage Unpublished (2002)

Unpublished (2002)

Contect: Tadasu Shin-i

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BJ401060 GI:19313977
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/db_xref="taxon:44689"
/db_xref="taxon:44689"
/clone="ddc20i13"
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/sex="mat A"
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Pred. No. 0.8;
0; Mismatches 45; Indels
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/strain="AX4"
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/clone="dds22c02"
                   Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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Fax: 81-559-81-6855
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1 (bases 1 to 663)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the culmination
                                                                                                                        BJ343976 Bictyostelium discoideum cDNA linear EST 06-MAR-20 BJ343976 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda17e22 3', mRNA sequence.
BJ343976 BJ343976 G:19214483
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1 (bases 1 to 654)

1 (urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostelium discoideum at the aggregation
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/clone_lib="Dictyostelium discoideum cDNA library, AF"
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Mational Institute of Genetics
1111 Yeta, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855

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    /organism="Dictyostelium discoideum"
/strain="AX4"

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    96 c    109 g    226 t
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Location/Qualifiers
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BJ375941
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                                                                                           RESULT 26
BJ343976
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COMMENT
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BJ343093
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BJ399159
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                    BJ434901 dictyostellum discoideum cDNA library, VF Dictyostellum discoideum cDNA library, VF Dictyostellum discoideum cDNA clone ddv25j11 3', mRNA sequence.
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S Urushihara, M., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the slug stage (brushihara, H., Tanaka, Y., Kohara, Y., and Shin-i, T.

Full length cDNA of Dictyostellum discoideum at the slug stage (brushihara, H.) (brushished (2002)

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I. Cocation/Qualifiers

ree 1. 675
                                                                                                                                                                              Eukaryota, Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases I to 665)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the vegetative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_"ddv25jll"
/clone_lib="blotyostelium discoideum cDNA library, VF"
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4.1%; Score 45; DB 13; Length 665;
Best Local Similarity 61.5%; Pred. No. 0.8;
Matches 72; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 others
                                                                                                                                                                                                                                                                           Unpublished (2002)
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1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fas: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Dictyostelium discoideum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Growth phase" 99 c 113 g 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:44689"
                                                                                                                                                                                                                                                                                                                                                                                                                         Email: tshini@genes.nig.ac.jp.
                                                                                                                                           Dictyostelium discoideum.
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BJ401293.1 GI:19314210
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BJ434901
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BJ443093 Dictyostellum discoldeum cDNA library, AF Dictyostellum
discoldeum cDNA clone dda22c04 3', mRNA sequence.
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Dictyostellum discoideum.
Dictyostellum discoideum
Eukaryota; Wycetoza; Dictyostellida; Dictyostellum.
1 (bases 1 to 680)
Urushihara, Y., Kohara, Y., Rohara, Y. and Shin-i, T.
Full length CDNA of Dictyostellum discoideum at the aggregation
                                              /strain="AX4"
/db_xref="taxon:44689"
/clone="dds22232"
/clone_lib="Dictyostelium discoideum cDNA library, SF"
/sex="mat A"
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/db_xref="taxon:44689"
/clone="daa22c04"
/sex="mat A"
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4.1%; Score 45; DB 13; Length 680;
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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Best Local Similarity 61:5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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Unpublished (2002).
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/organism="Dictyostelium discoideum"
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99 c 122 q 232 t
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                                                                                                                                                                                                                                                                                           /dev_stage="Slug stage"
101 c 119 g 2:
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SM Dictyostelium discoideum.

EDKATYOCE: Wycelozo: Dictyosteliida: Dictyostelium.

EDKATYOCE: Wycelozo: Dictyosteliida: Dictyostelium.

E 1 (bases 1 to 698)

C Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.

Full length Cohn.

C Unushished (2002)

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Contact: Tadasus Shin-i

Contact: Tadasus Shin-i

L Ontact: For Genetic Resource Information

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Fax: 81-559-81-6855
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BJ400818 BJ400818
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BJ401883 I GI:19314800
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/sirain="das 9p14"
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/clone="dda6d03"
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/sex="mat A"
                                                                                                                                                                                                                                  208 TACGTTATCAATGAAAGCGTGTCCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
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                                                                                                                                                4.1%; Score 45; DB 13; Length 691;
ilarity 61.5%; Pred. No. 0.81;
Conservative 0; Mismatches 45; Indels
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                                                                     /dev_stage="Aggregation stage"
101 c 121 g 238 t
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103 c 119 g 244 t
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Location/Qualifiers
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Matches 72; Conservative
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Matches 72; Conserv
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BJ400818
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BJ401883
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                                                                                                   BASE COUNT
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Envaryoces Mycetozoa; Dictyostellida; Dictyostellum.

E 1 (bases 1 to 688)

S Grushlara, H., Tanaka, Y., Kohara, Y. and Shin-1, T.

Full length cDMA of Dictyostellum discoldeum at the slug stage

L Onbublished (2002)

L Onbublished (2002)

Contect: Tadasu Shin-1

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Fax: 10-56-81-685
                 EST 10-MAR-2002
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Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozca; Dictyosteliida; Dictyostelium.
1 (bases 1 to 691)
1 (bases 1 to 691)
1 Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostelium discoideum at the aggregation
                      BJ399159 Bictyostelium discoideum cDNA linear EST 10-MAR-20
BJ399159 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds4p10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:44689"
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/clone_lib="blottyostellum discoideum cDNA library, SF"
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Contact: Tadasu Shin-i
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Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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102 c 114 g 240 t
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/db_xref="taxon:44689"
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BJ341290.1 GI:19249652
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BJ399159.1 GI:19312076
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BJ341290
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BJ341261 Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA library, AF Dictyostelium discoideum cDNA clone dda5120 3', mRNA sequence.
BJ341261 BJ341261 GI:19249633
EST.
BJ341261.1 GI:19249633
BJ64Yostelium discoideum.
Dictyostelium discoideum
Urostelium discoideum
Urostelium discoideum
Urostelium discoideum
Urostelium discoideum
Urostelium discoideum
Urostelium discoideum discoideum discoideum at the aggregation
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                                                                                                                208 TACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
                                                                                                                                  /db_xref="taxon:44689"
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    724
/organism="Dictyostelium discoideum"

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106 c 124 g 251 t
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Location/Qualifiers
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Dictyostelium discoideum
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Best Local Similarity 61.5*
Check 72; Conservative
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AUTHORS
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BJ341261
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BJ343890
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                                                         Eukaryota; Mycetozoa: Dictyostellida; Dictyostellum.

E 1 (Dasea: 140 718)

S Urushihara.H. Tanaka,Y., Kohara,Y. and Shin-i,T.

Eull length cDNA of Dictyostellum discoideum at the slug stage
Contact: Tadasu Shin-i
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Contact: Tadasu Shin-i
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BJ401195 Tctyostellum discoideum cDNA linear EST 10-MAR-2002 discoideum cDNA library, SF Dictyostellum BJ401195.1 GI:19314112
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M Dictyostellum discoideum.

Bukaryota: Mycetozoa; Dictyostellida; Dictyostellum.

E Ukaryota: Mycetozoa; Dictyostellida; Dictyostellum.

S Grushihara H., Tanaka, Y., Kohara, Y. and Shin-i, T.

L Unpublished (2002)

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Email: tShini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:44689"
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/clone="dds14p33"
/clone="dds14p33"
/sex="mat A"
/sex="mat A"
/dev_stage="Slug stage"
104 c 122 g 248 t 3 others
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                                                                                                                                                                                                                                                                                         /organism="Dictyostelium discoideum"
/strain="AX4"
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105 c 122 g 2
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Location/Qualifiers
                             Dictyostellum discoideum. Dictyostellum discoideum
 BJ400818.1 GI:19313735
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BJ401342 Brityostelium discoideum cDNA linear EST 10-MAR-2002 BJ401342 Dictyostelium discoideum cDNA library, SF Dictyostelium discoideum cDNA clone dds22019 3', mRNA sequence.
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Dictyostellum discoideum
Dictyostellum discoideum
Dictyostellum discoideum
Lukaryota: Wycetozoa; Dictyostellida: Dictyostellum.
1 (bases 1 to 744)
Urushihara. H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the aggregation
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Pred. No. 0.81;
0; Mismatches 45; Indels
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Dictyostelium discoideum
Eukaryota Mycetooa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 760)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
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Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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Unpublished (2002)
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Fax: 81-559-81-6855
Fax: 81-559-81-6855
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105 c 127 g 262 t
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ilarity 61.5%; Pred. No. 0.81;
Conservative 0; Mismatches
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/clone="dda26k16"
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Location/Qualifiers
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BJ401342.1 GI:19314259
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BJ347280.1 GI:19217787
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Matches 72; Conserva
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BJ401342
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BJ399243
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SM Dictyostellum discoideum.

Dictyostellum discoideum

Dictyostellum discoideum

E Ukaryota; Mycetozoa; Dictyostellida; Dictyostellum.

E Ubases 1 to 742)

S Urushinara H., Tanaka,Y., Kohara,Y. and Shin-i,T.

Full length cDnA of Dictyostellum discoideum at the slug stage

L Unpublished (2002)

L Ontact: Tadasus Shin-i

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         Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
1 (bases 1 to 734)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Full length cDNA of Dictyostellum discoideum at the aggregation
                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostellum discoideum"
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/clone="dda17d13"
/clone="bictyostellum discoideum cDNA library, AF"
/sex="mat A"
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                                                                                                                    Combished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tshiniqqenes.nig.ac.jp.
Location/Qualifiers
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105 c 126 g 256 t
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105 c 126 g 2
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Location/Qualifiers
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les 72; Conserv
                                                                                                            stage
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CNS0072R
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1 (bases 1 to 765)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                /db_xref="taxon:44689"
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/sex="mat A"
Full length cDNA of Dictyostelium discoideum at the slug stage Unpublished (2002)
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4.1%; Score 45; DB 13; Length 765;
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 4.1%; Score 45; DB 13; Length 766
Best Local Similarity 61.5%; Pred. No. 0.81;
Matches 72; Conservative 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                         1 others
                                     Contact: Tadasu Shin-i
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tahini@qenes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Email: tahiniqqenes nig.ac.jp.
Email: Location/Qualifiers
                                                                                                                                                                                                                           /organism="Dictyostelium discoideum"
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113 c 126 g 268 t
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109 c 127 g 2
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BJ371948.1 GI:19281331
                                                                                                                                                                                                                                                /strain="AX4"
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Print Jacob Evriced A France (E-Mail: Sequelegemoscope.us.it.)

- Web: www.gemoscope.cos.france (E-Mail: Sequelegemoscope.us.it.)

- Web: www.gemoscope.cos.france (E-Mail: Sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster agenome using these BACs. For further information please see http://www.fruithy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is mamed RPOI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; or bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR14E13 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                       623 AAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGG 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   683 AGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAA 742
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208 TACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTGATAAGAACGGCTCCATA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Droscophila melanogaster.
Droscophila melanogaster.
Droscophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Boptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Droscophilidae; Droscophila.
                                                                                                                                      268 IGCTITICTICCTICATGGTTTTCAATAAGTCCGCTTTCAACAGTAAACCAAAAGCA 324
                                                                                                                                                                             4.1%; Score 44.6; DB 17; Length 988; 39.3%; Pred. No. 1;
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/db_xref="taxon:7227"
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/note="end : TET3"
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Best Local Similarity
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- Web: www.genoscope.cns.ff)
- Web: www.genoscope.cns.ff)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (centre drough et Qront) and the Drosophila with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mall : segref@genoscope.cns.fr
                                                                                                                                           CNSOIGLI
Drosophila melanogaster genome survey sequence T7 end of BAC
BACNIGD22 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL106896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            875 AYAWWWWWWWWATATWWTAATAWWATTWTAATATATAWAAAATATATAWTWAAAAA 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853 ATGAACAAAGAGTAAGTTTTTGAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAA 912
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Poeptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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; Pred. No. 1.5;
71; Mismatches 206; Indels
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'Organism="Drosophila melanogaster"

/db_xref="taxon:7227"

/clone="BACN16D22"

/clone="BACN16D22"

/plasmid="pabloBAC11"

/note="end : T7"
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Best Local Similarity 28.6%;
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                                                                                                                                                                                        DEFINITION
                                                                                                     RESULT 45
CNS016LI/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                CNS0074D 958 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14F23 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        430 AANTINATATAAANNANTINNNNAANAAAWAWWWWWAAAWAAAATTAAAAAAATWAAAANNN 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   788 GGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGAC 847
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Bukaropta; Metanogaster.

Eukaryota; Metanogaster

Eukaryota; Metanogaster

Rooptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

[ Pass 1 to 958)
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Matches 115; Conservative 11; Mismatches 163; Indels
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/db_xref="taxon:727"
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/clone_lib="RPCI-98"
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39.8%; Pred. No. 1.3;
                                                                                                        780 AAAAAMAATYTYCCAAAAAAAAAACTWAAAYT 811
                                                863 AGTAAGTTTTTGAAAATTCTAAAATAGAAAT 894
                                                                                                                                                                                                                                                                                                                      tly), genomic survey sequence. AL066801
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11 c 80 g
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CNS0074D/C
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RESULT 47
AZ527921/c
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ORGANISM
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/strain="Maximss"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_"vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically heared to give a fight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for whole genome shoqeun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                        SM Entamoeba histolytica

Eukaryota: Entamoebidae; Entamoeba.

Eukaryota: Entamoebidae; Entamoeba.

Eukaryota: Entamoebidae; Entamoeba.

Softus, B., Van Aken, S. and Fraser, C.

Determination of Clone end sequences from Entamoeba histolytica
HMI:HMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

Fra: 301 838 0208

Fax: 301 838 9543

Email: Dijotusétigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared
                                                             A2550349 896 bp DNA linear GSS 14-NOV-2000 BNFEMP39TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     652 GACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAA 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 TCGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 592 AGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAAT 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 36
High quality sequence stop: 844.
Location/Qualifiers
1. 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA library
Seq primer: M13-Forward
Class: shotgun
                                                                                                                                                  AZS50349.1 GI:11175650
                                                                                                     genomic, DNA sequence.
AZ550349
                                                                                                                                                                                         Entamoeba histolytica.
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Best Local Similarity 52.55
Matches 96; Conservative
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                 RESULT 46
AZ550349
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/organism="Entamoeba histolytica"
/strain="HM1:IMSs"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
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/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Entamoeba histolytica Stellar Stellar Constructed at The Institute for Genomic Research (TIGR). Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Dlamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
AND 1921 BRITANNOP BNA linear GSS 03-NOV-2000 ENTCG17TR Entamoeba histolytica Sheared DNA Entamoeba histolytica preprior; DNA sequence.
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seg primer: M13-Reverse
                                                                                                                                                                                                                                                                                                              Ukaryota; Enterpolidae; Entamoeba.

1 (bases I to 899)

1 (bases I to 899)

Determination of clone end Sequences from Entamoeba histolytica HMI: HMS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fax: 301 838 9288
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4.0%; Score 43.8; DB 17; Length 899;
Best Local Similarity 52.5%; Pred. No. 1.7;
Matches 96; Conservative 0; Mismatches 87; Indels 0;
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High quality sequence stop: 808.
Location/Qualifiers
                                                                                                                                                                             AZ527921.1 GI:11080094
                                                                                                                                                                                                                                                 Entamoeba histolytica.
Entamoeba histolytica
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712 AAA 714
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AZ549336
                                                                                                                                                               ORGANISM
                                      DEFINITION
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TITLE
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                                                                               ACCESSION
                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                      REFERENCE
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AZ690917
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// Chone_lib="Intamocba histolytica Structed at The
// Chone_lib="Intamocba histolytica Structure for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamocba histolytica:
method for isolate identification. Exp. Parasitol.
// Afo.). The DNA was mechanically sheared to give a
// Tight size distribution (-2 kb). The v + i method used for
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and venter, J.C. (Maxhang small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barall, Oxford University Press, 1999)."
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            ....o.,ooo GSS 14-DEC-2000 BNT linear GSS 14-DEC-2000 BNT.72TF Entamoeba histolytica Sheared DNA Entamoeba histolytica genomic, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                          Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 91M)
Loftus, B., Van Aken, S. and Fraser, C.
Loftus, B., Van Aken, S. and sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fax: 301 838 9243
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High quality sequence stop: 869.
Location/Qualifiers
1. 914
/organism="Entamoeba histolytica"
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4.0%; Score 43.8; DB
Best Local Similarity 52.5%; Pred. No. 1.7;
Matches 96; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: M13-Forward
                                                                                                                                AZ687856.1 GI:11825002
                                                                                                                                                                         Entamoeba histolytica.
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              RESULT 48
AZ687856/c
                                                                      DEFINITION
                                                                                                                                                                           SOURCE
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KEYWORDS
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RESULT 49

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Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoceba histolytica: a method for isolate identification. Exp. parasitol.
77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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A2690917 924 bp DNA linear GSS 14-DEC-2000 ENTHV65TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: MJ-Reverse
Class: shotgun
                                                                                                                                                                                                  Entamoeba histolytica.
Entamoeba histolytica.
Entamoeba histolytica.
Entamoeba histolytica.
Eukaryota; Entamoebidae; Entamoeba.
I (bases 1 to 924)
Loftus, E., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica HM1: HSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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4.0%; Score 43.8; DB 17; Length 924;
Best Local Similarity 52.5%; Pred. No. 1.7;
Matches 96; Conservative 0; Mismatches 87; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Entamoeba histolytica"
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High quality sequence stop: 895.
Location/Qualiflers
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                                                                                                                                          AZ690917.1 GI:11828063
                                                                           genomic, DNA sequence.
AZ690917
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us-09-438-185a-1_1199590_1200675.rst

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Eukaryota: Entamoebalae; Entamoeba.

Eukaryota: Entamoebalae; Entamoeba.

RS Loftus.B., van Aken,S. and Fraser,C.

Loftus.B., van Aken,S. and Fraser,C.

Determination of Clone and sequences from Entamoeba histolytica
HMI:HNSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

Contact: Brendan J Loftus

Contact: Brendan J Loftus

The Institute for Genomics
Fax: 301 838 0208

Fax: 301 838 0208

Email: blloftus@tigr.org

Email: blloftus@tigr.org

Clones are derived from the Entamoeba histolytica HMI:IMSS sheared

DNA library

Seq primer: M13-Reverse

Class: shotgun

High quality sequence start: 15

High quality sequence stop: 907.

Location/Qualifiers

L. 94

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/organism:=Entamoeba histolytica Sheared DNA"

/organism:=Entamoeba histolytica: BET i; Constructed at The

/organism:=Entamoeba histolytica: BET i; Constructed at The

/organism:=Entamoeba histolytica: and bistolytica: and bistolytica: and bistolytica: and bistolytica: and method for isolated from broth cultures of Entamoeba histolytica: and method for isolated from broth cultures of Starsich and Diamond, L.S. (1993) Entamoeba histolytica: and method described in describe
ENTED22THB BITAMOREDA histolytica Sheared DNA Britamoeba histolytica AZ549336. DNA Sequence.
AZ549336.1 GI:11173846
GSS.
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4.0%, Score 43.8; DB 17; Length 944;
Best Local Similarity 52.5%, Pred. No. 1.7;
Matches 96; Conservative 0; Mismatches 87; Indels 0;
Matches 96; Conservative 0; Mismatches 97; Indels 0;
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Entamoeba histolytica
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TITLE
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COMMENT
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KEYWORDS
SOURCE
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Search completed: January 9, 2003, 11:40:55 Job time: 1961 secs

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	GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: January 9, 2003, 05:32:32 ; Search time 251 Seconds (without alignments)	9743.706 Million cell updates/sec Title: US-09-438-185A-1_COPY_1199590_1200675 Perfect score: 1086 Sequence: 1 ttggcaaagtacctcaaaacgttctctcgcagtagtgcac 1086	Scoring table: IDENTITY_NUC . Gapop 10.0 , Gapext 1.0	Searched: 2185239 seqs, 1125999159 residues Total number of hits satisfying chosen parameters: 4370478	Minimum DB seq length: 0	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries	Database: N_Geneseq_101002:* 1: /SIDS2/qcqdata/geneseq/geneseqn-embl/NA1980.DAT:* 2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:* 3: /SIDS2/gcgdata/geneseq/geneseqy-embl/NA1983.DAT:* 4: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*	 /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:* /SIDS2/gcgdata/geneseqr/geneseqr-emb1/NA1985.DAT:* /SIDS2/gcgdata/geneseq/genesegr-emb1/NA1986.DAT:* /SIDS2/gcgdata/geneseqr/genesegr-emb1/NA1987.* 	 /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:* /SIDS2/gcgdata/geneseqqn-emb1/NA1999.DAT:* /SIDS2/gcgdata/geneseqfyeneseqn-emb1/NA1990.DAT:* /SIDS2/gcgdata/geneseqqn-emb1/NA1990.DAT:* 	 13: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1992.DAT:* 14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:* 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:* 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:* 16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:* 	17: /SIDS2/gogdata/geneseq/geneseqn-embl/NA1996.DAT:* 18: /SIDS2/gogdata/geneseq/geneseqn-embl/NA1997.DAT:* 19: /SIDS2/gogdata/geneseq/geneseqn-embl/NA1998.DAT:* 19: /SIDS2/gogdata/geneseq/geneseqn-embl/NA1999.DAT:*	21: /SIDSZ/gogdata/geneseq/geneseqn-embl/NA2000.DAT:* 22: /SIDSZ/gogdata/geneseq/geneseqn-embl/NA2001B.DAT:* 23: /SIDSZ/gogdata/geneseq/geneseqn-embl/NA2001B.DAT:* 24: /SIDSZ/gogdata/geneseq/geneseqn-embl/NA2002.DAT:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query No. Score Match Length DB ID Description	C 1 1086 100.0 1089 24 ABL91284 Chlamydia pneumoni C 2 46.6 4.3 1642 21 AAA91624 Caenorhabditis ele C 3 43.4 4.0 6089 24 ABN80254 Caenorhabditis ele C 4 41 3.8 868 20 AA217250 Human gene express C 5 41 3.8 9504 24 ABX28408 Chman gene express C 6 41 3.8 40.6 3.7 5152 24 ABL92307 Human polynucleoti B 40.6 3.7 37184 24 ABC49374 Human anglogenesis

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Chlamydial infection; antigen; immunogen; vaccine; diagnosis; human respiratory disease; cardiovascular disease; atherosclerosis; coronary artery disease; carotid artery stenosis; myocardial infarction; cerebrovascular disease; anottic aneurysm; claudication; stroke; strain CWL029; open reading frame; ORF; gene; ds.

Location/Qualifiers 1..1089 /*tag= a /product= "cp7380"

Chlamydia pneumoniae.

Chlamydia pneumoniae cp7380 ORF DNA, SEQ ID NO:202.

29-JUL-2002 (first entry)

ABL91284;

.284/c ABL91284 standard; DNA; 1089 BP.

RESULT 1 ABL91284/

\$3645 \$27012 \$5203 \$5496	L7022 S4548 L3401 K2841 BA905	H1121 25980 26690 21775 41775 87692 87692 88004	L05433 L0546 L0546 L0546 L0546 N7998 R72229 F72230	AAK8800 AAK8800 AAS5499 ABN8678 AAV746 ABN8027 ABS383	ABL34063 AAS25472 AAN61077 ABL21406 ABL33620 ABL33782 AAR17183 AAR17183 AAR16959 ABK28233 AAR16959 ABK28233 AAR16959 ABK28233 AAR16959 ABL70399 ABL70399	L3366 L49389 L649389 L649389 L61377 L61377 L70603 L72860 L72860 L72860 L72860
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Chemically treated
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11-JUL-2000; 2000GB-0017047. 21-JUL-2000; 2000GB-0017983. 077-MUG-2000; 2000GB-0019568. 18-AUG-2000; 2000GB-0020440. 14-SEP-2000; 2000GB-002583. 10-NOV-2000; 2000GB-002549. 22-DEC-2000; 2000GB-0031706.

WPI; 2002-154726/20. N-PSDB; ABB90626. Ratti G, Grandi G; (CHIR-) CHIRON SPA.

03-JUL-2001; 2001WO-IB01445. 03-JUL-2000; 2000GB-0016363

WO200202606-A2.

10-JAN-2002.

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Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia pneumoniae (strain CWL029), and ABL91184-ABL9173 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as atherosclerosis, coronary artery disease, carotid artery stenosis, myocardial infarction, cerebrovascular disease, actic aneurysm, claudication and stroke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions of the invention or treatment of chlamydia compositions, particularly Chlamydia pneumoniae, and the nucleic acids may be used in the detection of chlamydia pneumoniae, and the nucleic acids may be used in the detection of chlamydia ensured sease or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes
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Score 1086; DB 24; Length 1089; Pred. No. 1e-283;

100.0%; 100.0%;

Query Match Best Local Similarity

ALIGNMENTS

Fri Jan 10 12:01:27 2003

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Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-423022/36.
P-PSDB; AAB13327.
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         1081 GTGCAC 1086
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                            6 GTGCAC 1
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                                                                                                                181 CTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTG 240
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                                                             TAACAGACCTTGGTCGAGCATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAA 120
                                                                                                     121 ATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAAT 180
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   Conservative
   Matches 1086;
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The present sequence is the cod-5 gene from Caenorhabditis elegans. Cod-5 is the aromatic amino acid hydroxylase that synthesises serrotonin froom precursor Ltryptophan. The cod-5 gene was knocked out to produce mutants precursor Ltryptophan. The cod-5 gene was knocked out to produce mutants completely lacking in serotonin. These mutants were found to have defects in metabolic control. A number of c. elegans proteins that have defects can manalian homologues acting in the insulin signalling pathway were also manmalian homologue of the mammalian by 3 *kinase whilst daf-2 encodes a homologue of the mammalian proceptor. The C. elegans ART kinase and PKB kinase act downstream of insulin signalling The C. elegans PFEN lipid phosphatase homologue, C. c. elegans PFEN lipid phosphatase homologue, C. DAF-18, has been found to act upstream of ART in the pathway. This discovery has enabled mammalian PFEN action to be mapped to the insulin signalling pathway. Conserved DAF monologues and thus to identify individuals with a predisposition towards the development of glucose intolerance conditions,
                                                                                                                                                                                                                                                                                                                                                                                           ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity -
                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans; cod-5; daf-18; insulin signalling pathway; daf-2; age-1; insulin receptor; PI 3-kinase; PKB kinase; PTEN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes;
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                                                                                                                                                                                                                                              Caenorhabditis elegans cod-5 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "Cod-5"
AAA91624 standard; DNA; 1642 BP
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Matches 249; Conservative
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1464 TCTTCAAAATTTCTAGTATAGAAATACGCTGGAAAGTAGTAATGAGAACATTCTTGC 1405
                                                                                                                                                                                                                                                               1344 AACTCGCCAGCACTGCTCAGAAGTCCTGCTCCGTATACTTTAAATCTTTCATGATTTGAT 1285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 AAGAGTCTTCCCATGTTTATGAAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACG 472
                                                             473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGA 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      593 GCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, development, homeobox gene; HOX; diabetes; cancer; apoptosis; heart disease; epilepsy; histone deacetylation; muscular dystrophy; dwarfism; single nucleotide polymorphism; SNP; cytosine methylation; antidiabetic; cytostatic; anticonvulsant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABN80254 standard; DNA; 6089 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (EPIG-) EPIGENOMICS AG
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KW Human;
KW Homon;
AWARFI,
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The invention relates to a nucleic acid (I) comprising a sequence at least 18 bases in length of a segment of chemically pretreated DNA (II) of genes associated with development selected from 87 genes listed in the specification such as ACCPN, ADRN, or AFDL and comprising one of 350 sequences (ABN7984-ABN8033) or their complements. The invention is sequences (ABN7984-ABN80333) or their complements. The invention is genes (HCX), like diabetes, cancer, applyeis related to homeobox containing genes (HCX), like diabetes, cancer, applyeis related to homeobox containing genes (HCX), like diabetes, cancer, applyeis related diseases related to histone deacetylation, Currarino syndrome, diseases related with the complements of the genes are useful for detecting the methylation state of all Cpd dinucleotides within the 350 sequences or containing the methylatic or state of all Cpd dinucleotides within the 350 sequences or containing the specification of the 350 sequences, (II) and/or their complementary sequences, (II) and/or their complements and sequences as oligomer probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs).

Note: The sequence data for this patent did not form part of the printed specification but is based on sequence information supplied to Derwent by the containing specification but is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans; cod-5; daf-18; insulin signalling pathway; daf-2; ag-1; insulin receptor; pr 3 *kinase; PRB kinase; PRB kinase; PTRN lipid phosphatase; antidiabetic; anorectic; obesity; diabetes; ss.
associated with development genes such as diabetes, comprises a sequence of a segment of chemically pretreated DNA of genes associated with development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       621 AAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681 GGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAG 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        741 AAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAA 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   801 CAGCCATATCAGIGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAA 860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6089 BP; 1262 A; 219 C; 1585 G; 3023 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans cod-5 knockout cDNA.
                                                                                                Claim 1; SEQ ID NO 271; 27pp; English.
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AAZ17250;
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                                                                                                                                                                                                                                                                                                                                                     The present sequence is a Caenorhabditis elegans cod-5 knockout cDNA.

Most of the cod-5 gene has been deleted and this has caused a frameshift in the remaining coding region. Cod-5 is the aromatic amino acid in the remaining coding region. Cod-5 is the aromatic amino acid in the remaining coding region. Cod-5 is the aromatic amino acid hydroxylase that synthesises servicinin from precursor Liryptophan. The cod-5 gene was knocked out to produce mutants completely lackfing in a servicinin. The mutants were found to have defects in metabolic control. A number of C. elegans proteins that have mammalian homologues acting in the insulin signalling pathway were also identified. The C. elegans age-1 cancodes a homologue of the mammalian PI 3 kinase whilst daf-2 encodes a homologue of the mammalian pi 3 kinase whilst daf-2 cancodes a homologue of the mammalian pi 3 kinase whilst daf-2 cancodes a homologue of the mammalian pi 3 kinase whilst daf-2 cancodes a homologue act downstream of insulin signalling stream of the pathway. This discovery has been found to act upstream code was mapped to the insulin signalling pathway. Conserved DAF motific can be mapped to the insulin signalling pathway. Conserved DAF motific can be used to design probes to identify mammalian DAF homologues and thus to identify individuals with a predisposition towards the development of glucose intolerance conditions, such as obesity and diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 TCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        639 TCTTCAAAATTTCTAGTATAGAAATACGCTGACTGGAAAGTAGTAATGAGACATTCTTGC 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 AAAGAAGTAGAGGTTTGCAAGCTTCTTCAAA-----TCTTCCTCTGATGCTCCAAGA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Gaps
                                                                                                                                                                                                                                                                                       Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity ^{\rm -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; Length 817;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.8%; Score 41.4; DB 21; Length Best Local Similarity 45.2%; Pred. No. 0.39; Matches 239; Conservative 0; Mismatches 281; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 817 BP; 214 A; 197 C; 166 G; 240 T; 0 other;
                                                             /product= "Cod-5 frameshift mutant"
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                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 43; 402pp; English
                                                                                                                                                   99WO-US28529.
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                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
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                                                                                                                                                                               03-DEC-1998;
Synthetic.
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The present invention describes a library of human polynucleotides comprising the sequences given in AA21253 to AA417779. Also described is a method of detecting differentially expressed genes correlated with the cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample from a cell suspected of being cancerous, where the gene product is encoded by one of the 5248 polynucleotide sequences given in AA212532 to AA21779. The polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, mapping, tissue typing or profiling, forensics, genetic analysis and detection of polymorphisms. Polypeptides encoded by the polynucleotides can be used for raising antibodies for experimental, diagnostic and therapeutic purposes. The polynucleotides may also be used to construct arrays for diagnostics (which may be used to determine function of an
                                                                                                                                                                     288 TGACCCATGAGCTCGTGAACGGTGTCTGGTTCTGGAGTGTAAAATGGATCGCCATGATGG 229
                                                                                                                                                                                                                                                   533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGGA 592
                                                                                                                                                                                                                                                                                                                                     228 CGAACGTATTGAGTGCAGAAGAAGACACGATATGCAAGACCTGCCAAGAAATCACGAGCT 169
348 GAAGCTAATCCAATCTCTTGAGAAAACTGAGCAAAATCTGGATCAGCGAATAGAGCCATG 289
                                                                                  473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTT 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; gene; gene expression product; diagnosis; therapy; probe; detection; mapping; tissue typing; profiling; forensic; cancer; genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene expression product cDNA sequence SEQ ID NO:4721.
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Escobedo J, García PD, García V, Giese K, Innis MA;
Jones WL, Kassam A, Kennedy GC, Rita D, Labat I;
Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
Stache-Crain B, Sudduth-Klinger J, Williams LT;
                                                                                                                                                                                                                                                                                                                                                                                                                        593 GCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGA 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 GATAAGTATCCGGCGACTGGGCGAACACGGAATCCAGTTTTTGACACTA 120
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98US-0080114.
98US-0080515.
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98US-0072910.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9938972-A2
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24-FEB-1998;
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encoded protein); and to detect differences in expression levels between two cells (e.g. to identify abnormal or diseased lissue in a human, to identify a genetic predisposition or susceptibility to a disease such as cancer). The polynucleotides of the invention are especially used in the diagnosis, prognosis and management of colorectal cancer, breast cancer, and ing cancer. prepared in the polynucleotides can also be used to screen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                   625
                                                                                                                                                                                                                                                                                     446 AATGAGGATGTAGAAGCCAAGGCACGTGCCCTAAAAGGTCATGGATGAGATCAGGAGTT 505
                                                                                                                                                                                                                                                                                                                          575 AGNGNNNGANGANANAAATAAANNANAAGNNGAANAANANTGAGANNAAAANAGAGGNT 516
                                                                                                                                                                                                                                                                                                                                                                  506 AAGGAGAAATTATCTTTATCGAGAGTTCGCATTACAGAGGCAATGGGAAAGTAACGGTCC 565
                                                                                                                                                                                                                                                                                                                                                                                                         515 TAGGAGNNANAAANANANANANGAGNNNANNNTAGNNANTAAATGGNAANTGGANANNN 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455 ANTINAGGNANANAGNTINNGAGNNINGAGGNATGANANATTGANAGAANTNANNNNNAA 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                626 TGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGA 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395 NNNATNAATTATNAATGNNNNGNGAAGNGANANGAAAAANTTAAANNANTATNAATAAGN 336
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 566 TGCAACAGAGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA transcription associated complementary genomic DNA #141.
                                                                                                                                                                                                   Score 41; DB 20; Length 868;
Pred. No. 0.51;
0; Mismatches 180; Indels
                                                                                                                                                              Sequence 868 BP; 148 A; 148 C; 32 G; 284 T; 256 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             686 CCGAAAGCTTCTAAGTAATCAAGAAAAA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   335 NNGAAAGNINGNANGNATGNIANANANA 307
                                                                                                                         peptide analogues and antagonists.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK28408 standard; DNA; 9504 BP
                                                                                                                                                                                                        3.8%;
1 Similarity 33.1%;
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                Matches
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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sazary syndrome, memberological disorders, immunological disorders, where syndrome, tuberoulosis, developmental disorders; psoriasis, sporiasis, syndrome, nucleotion, hypertension, anglogenesis, erythropoiesis, congenital heart disease, HDNR syndrome, and for this patent did not form part of the printed syndrome. Sequence data for this patent did not form part of the printed European Patent Office.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8911 GTGGATGATATATATTGGTGTTATTTTGGTTTTTATTGGTATGGGGGTATTGTTTGTTT 8970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8971 ATTGTTATTGTGTTTTTTTTTAGATTTTTTATTGAAAAGGAAAGTGAGGGTTAGGTTTAGAG 9030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA repair: cytosine methylation; PMS2L1; PMS2L2; PMS2L2; PMS2L3; PMS2; L4; PMS2L5; PMS2L6; MGMT; MSH2; NUDT1; TDG; INPPL1; RFC4; DDTT1L; FNMCB; XCCG8; ataxia telangiectasia; aging; Bloom's syndrome; Cockayne syndrome; Nijmegen breakage syndrome; Werner syndrome; immunodeficiency; trichthiodystrophy; Fanconi's anaemia; solid tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 CTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACG 981
                                         New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chemically treated DNA repair gene fragment complementary to#58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9504 BP; 2775 A; 138 C; 2348 G; 4243 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           982 ITGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATT 1022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9031 AGATAGTGTTTTTGTTTTTAGGGGAATAAGGATATTAATT 9071
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0; Mismatches
                                                                                                                                                                        Claim 1; SEQ ID No 282; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL92307 standard; DNA; 5152 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to nucleic acids containing a sequence of at least an uncledides of chemically treated DNA of genes associated with DNA repair, and their complements. The invention also relates to nucleic acids comprising at least 18 base pairs of the chemically pretreated DNA of genes associated with DNA repair selected from PMSZLL, PMSZLL, PMSZLLS, PMSZLLS, PMSZLLS, PMSZLS, MSHY, MSHZ, NUCHI, TDG, INPPLI, RFC4, DDITIL, FANCB, Or XRCC8. Nucleic acids of the invention and related oligomers, are useful for diagnosis of diseases associated with gene or pair, specifically attaxia telanglectasia, aging, Bloom's syndrome, cockayne syndrome, Nijmegen breakage syndrome or Werner syndrome, communodeficiency, trichthiodystrophy, Fanconi's aneamla, solid tumours and cancer, particularly by determining status of cytosine methylation and/or by detecting single-nucleotide polymorphisms. Determination of individual methylation patterns may allow development of individualised therapies. The sequences given in records ABU52192-ABL92335 represent commically pre-treated DNA fragments from genes associated with DNA context is sequence data for this patent is not represented in the specification, but is based on sequence information supplied by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                               New nucleic acid derived from genes associated with DNA repair, useful for diagnosis, e.g. of ataxia telanglectasia, by determination of cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             644 AATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAA 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 GATTTTAAAATTTTTTATATTTTTTTTTTTTTAGGGAAAGTGGAAAATAAGGAACGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           764 TACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCT 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 ATTTTTATTTTTTTTTTTTAGAGGAATAAATTTTTAGAATAAGATATTTAATGTAATGTAGGATTTG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            824 TCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAAGAGTAAGTTTTTTGAAAAATTCT 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 rGTTGGGGTGGGAGGATTATTTATTTGAGTTTAGGAATTTGAAATTGTAGTGAGTCGTGA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             133 GTATTTTAGTTTGGGTAATAGTGTGAGATTTTGTTATAAAATAAGATTAGTTTAGTATAA 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 116; 25pp + sequence listing; English.
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0; Mismatches 249;
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                                                                                                                                                                                                                                        Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 44.6%;
Matches 201; Conservative
                                                                                     07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                 06-APR-2001; 2001WO-EP03972.
                                                                 06-APR-2000; 2000DE-1019058.
                                                                                                                                                                                                                                        Olek A, Piepenbrock C,
                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                      WPI; 2002-034446/04.
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The invention relates to nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation, selected from 94 genes (ABL49301-ABL49394) and/or complementary sequences associated with DNA replication, CENPB, DNA2L, ATR, CHDIL, ERCC3, SNRPAL, RAD50 and Ling2. The chemical pretreatment converts cytosine bases unmethylated at the 5-position to uracil or another base with hypridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations. The DNA sequences and method are useful in the cytosine methylations. The DNA sequences and method are useful in the cytosine methylations. The passociated with DNA replication and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes. They are especially useful in diagnosis and therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes. They are especially useful in diagnosis and therapy of eigh Ataxia telangiectasia, ATR-X, Bloom's syndrome, solid tumours and cancer.

CNOTE: The sequence data for this patent did not form part of the printed specification and was supposed to be available directly from WIPO at the vipo. Intrypub/published_pet_sequences. However, the sequence data did not correspond to that referred to in the specification. The present data is taken from EPO data for the patent.
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                                                                                                                                                                                                                                                                                                                                                                                     Human, cytostatic; neuroprotective; nootropic; immunostimulant; gene regulation; DNA replication; CRNBB; DNAZL; ATR; CHDLL; ERCC3; SNRPA1; RAD50; LIG2; cytosine methylation; Ataxia telangiectasia; ATR; ATR; Bloom's syndrome; tumour; cancer; methylation; gene; ds.
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432 GIGITITIACGAAAAAATATAATGITTTTTATTTTTAAGIGTTATAATTTTTAGT 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid sequences from chemically modified genes associated with DNA replication, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. Ataxia telangiectasia
                                                                                                                                                                                                                                                                                                                                             Human polynucleotide associated with DNA replication SEQ ID NO 74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 44.6%; Pred. No. 1.3; Sonservative 0; Mismatches 249; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 74; 23pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5152 BP; 1608 A; 36 C; 965 G; 2543 T; 0 other;
                                                1004 AAGAACAGGGAAAGTGATTGTCTCAGCTTTA 1034
                                                                           492 TAATATTTCGTAAGAAATTTTTTAGATTTTA 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berlin K;
                                                                                                                                                                                                            ABL49374 standard; DNA; 5152 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-APR-2001; 2001WO-EP03971.
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07-APR-2000; 2000DE-1019173.
30-dUN-2000; 2000DE-1035529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                    01-MAY-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-017471/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200177377-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                            ABL49374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                 RESULT 8
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                                                                                                                                                                                                                                                          944 ATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGG 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; angiogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.
133 GTATTTTAGTTTGGGTAATAGTGTGAGATTTTGTTATAAAATAAGATTAGTTTAGTATAA 192
                                                                           TCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGA 763
                                                                                                                       764 TACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCT 823
                                                                                                                                             253 ATTTTTATTTTTTTTTTTAGAGGAATAAATTTTAGAATAAGATATTAATGTAATGTAGGATTTG 312
                                                                                                                                                                                                                            372 TATTATAAAATTTATTATTTTATGTTTTAATTTATATATATATTTTTATATATTTGTTTA 431
                                                                                                                                                                                                                                                                      644 AATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAA 703
                                                                                                 193 GATTTTAAAATTTTTTAATATTTTTTTTTTTTTTAGGGAAAGTGGAAAAATAAGGAACGG 252
                                                                                                                                                                                        824 TCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCT
                                                                                                                                                                                                              884 AAAATAGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTCTTTATTTCCTTTTGTAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human angiogenesis associated polynucleotide SEQ ID NO 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 107; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                    1004 AAGAACAGGGAAAGTGATTGTCTCAGCTTTA 1034
                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                              ABO67077 standard; DNA; 37184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2000; 2000DE-1061338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2001; 2001WO-EP14320.
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-500450/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in andiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, dlabette retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     834 TCTTTGATAATGACAGAAGATGAACAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 37184;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37184 BP; 8680 A; 717 C; 9540 G; 18247 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.7%; Score 40.6; DE Best Local Similarity 57.5%; Pred. No. 2.7; Matches 73; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 16-230; 237pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Buchnera sp. genomic DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABA92787 standard; DNA; 640681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-APR-2000; 2000JP-0107160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6362 AGGAGGA 6368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              954 AGTAGGA 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP2001292771-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the expression protein of the objective protein is collected from the resultant culture. The DNA is useful for developing agricultural chemicals for exterminating cockroaches. The present sequence represents the specifically claimed Buchnera sp. genomic DNA sequence, from the
                                                                                                                                                                                                                                                                                                                                                       Db 190302 ACTAATTTAGTACAAAAAAAAATCATATCATAGAAGAAATAATCATATTCGATACGCAT 190361
                                                                                                                                                                                                                                                                                        DD 190242 AATCGAAACATCGTAACAACACGTGTAATAGATCTTTTTAATTTTTAATTATACAACAT 190301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 CCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGTAGGGTT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    419 CTTCCCATGTTTATGAAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479 AAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATT 538
                                                                                                                                                                                                                                                  119 AAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATA 178
                                                                                                                                                                                                                                                                                                                                  179 ATCIGAICCAATICTAAAGGGAGAACACGIACGITAICAAFGAAAGCGIGTCCAAGTICC 238
                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiatrefiosclerofic; antianaemic; cytostatic; nootropic; neuroprotective; antianaemic; cytostatic; obthalmologic; antirheumatic; antiarthritic; antidiabetic; antipsorlatic; antiflammatory; cancer; eye disease; arteriosclerosts; anemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                           Sequence 640681 BP; 237522 A; 83822 C; 84757 G; 234580 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 359 TGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTTCTATGACTTTAGTGAAGAGT
                                                                                                                                                               Score 40.6; DB 24; Length 640681;
Pred. No. 7.8;
0; Mismatches 244; Indels 0; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immune system associated gene SEQ ID NO: 1120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABL33147 standard; DNA; 6740 BP.
                                                                                                                                                               3.7%; Scc
Similarity 43.4%; Pro
37; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07537.
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                                                                                         present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200200928-A2
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                                                                                                                                                                                                             Matches 187;
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                                                                                                                                                                       Query Match
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cell cycle, human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                                                                                                                             The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chemically pretreated complementary DNA associated with cell cycle #49 \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       984 ATATAAGTTTGTTTTTGATGAAGCGTATATTTTTAAAAGGTGGATTTTTTGGTTATTAT 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 ATGACTITAGIGAAGAGICTICCCATGITTATGAAAATTCAGAAAATGAGGGATGIAGA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         341 AGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCT 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 50; Indels
                                                                                                                                                                                                 Claim 1; SEQ ID NO 1120; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6740 BP; 1717 A; 76 C; 1496 G; 3451 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%; Score 40;
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                                                               Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS45393 standard; DNA; 17419 BP.
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06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1033259.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 58.3%;
nes 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001; 2001WO-EP02945
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                               Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
                             (EPIG-) EPIGENOMICS AG
                                                                                                 WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200168911-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS45393;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                 olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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us-09-438-185a-1_1199590_1200675.rng

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                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                            Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for flagnosis and/or prognosis events which are disadventageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        972 AGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2266 ATTATTAGGTTGGAGTGTAGTGATGTAATTATAGTTTATTGTAATTTTTATTGGG 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                            852 GATGAACAAAGAGTTTTTGAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     912 AAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCG 971
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                         Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Immune system disease; cytosine methylation; antiasthmatic; antianteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; antianterint; anticonvalsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; artirosoriatic; antifhammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                   Length 17419;
                                                                                                                                                                                                                                                                                                                                                     Sequence 17419 BP; 5015 A; 311 C; 3864 G; 8229 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 1268.
                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.6%; Score 39.6; DB 22; Best Local Similarity 49.5%; Pred. No. 3.7; Matches 102; Conservative 0; Mismatches 104;
                                                                                                    Claim 1; SEQ ID No 98; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1032 TTAGAGCAATCTTCAGAATATACTTT 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2326 TTTAAGTTATTTTTTTTAGTTT 2351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL33295 standard; DNA; 17419
                                                                        associated with cell cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; ds
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albriemer's disease, ADS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cyclosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 24; Length 17419;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17419 BP; 5015 A; 311 C; 3864 G; 8229 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1268; 32pp + Sequence Listing; German.
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0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.6; Di
Pred. No. 3.7;
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Local Similarity 49.5%;
les 102; Conservative (
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                Olek A, Piepenbrock C,
                                                                                                          (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                      WPI; 2002-130909/17.
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Genomic library; bacteria; human upper airway; otitis media; sinusitis; bronchopulmonary; endocarditis; meningitis; ss.
              04-APR-2001 (first entry)
                                                                                                                                        Moraxella catarrhalis.
                                                Genomic fragment #37.
                                                                                                                                                                            WO200078968-A2.
                                                                                                                                                                                                               28-DEC-2000.
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                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from cone of 346 sequences, and an oligomer, in particular an oligomer theory or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical corrected properties associated with DNA of genes associated with DNA of consistency or to the chemically pretreated DNA of genes associated with DNA of cytosine methylation state and/or shape nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide deaminase (particularly with the methylation status), e.g. adenosine deaminase (contribution), retroviral infection, Sezary syndrome, hemmatological disorders, immunological disorders, Mernet syndrome, tuberculosis, developmental disorders, psorlasis, Rieger's syndrome, syndrome, nucleotical disorders, meurodegenerative disorders, wardenburg infarction, hypertreation, andyogenesis, erythropolesis, congenital heart disorders, mandogenesis, erythropolesis, congenital heart consenses, HDNS syndrome, arthritis, polyglutamine disorders, solid tumours cassociated genomic DNA molecules of the invention.

Concern Sequence data for this patent did not form part of the printed consense before the consense of the consense of the printed of specification but was obtained in electronic format directly from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 AGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           852 GATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             912 AAGCTTGCTTCTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGGTCG 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                  New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 17419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17419 BP; 5015 A; 311 C; 3864 G; 8229 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 39.6; DB 24; Length
19.5%; Pred. No. 3.7;
Lve 0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 112; 32pp; English.
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                                                                                                                                                                                                   Berlin K;
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                                                                       06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1035529.
01-SEP-2000; 2000DE-1043826.
                                       06-APR-2001; 2001WO-EP03973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 49.5
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Patent Office.
                                                                                                                                                                                                   Olek A, Piepenbrock C,
                                                                                                                                                                 (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                    WPI; 2002-090046/12.
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ID AAF2
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AC AAF2
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AAF28550;

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The present invention relates to a Moraxella catarrhalis genomic library comprising of a combination of 41 nucleic acid molecules (see AAF20514 AAF20554). The library has a number of uses described in the specification e.g. is useful for aidentifying diagnostic and therapeutic compositions. M. catarrhalis (Branhamella catarrhalis) is a large aerobic, gram-negative diplococus, normally found among the bacterial flora of human upper airways. M. catarrhalis is known to cause acute, localised infections such as cuttis media, sinusitis and bronchopulmonary infection and life-threatening, systemic diseases including endocarditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               803 GCCATATCAGTGGAGCAACCTTCCCTTTGATTGATAATGACAGAAGATGAACAAAG 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HV; anticonvulsant; opthalmological; antiinfammatic; antiarthritic; antidiabetic; antipsoriatic; antiinfammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                  Genomic library for identifying diagnostic and therapeutic compositions, and for identifying virulence factors, regulatory elements and drug targets, comprises Moraxella catarrhalis nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39.6; DB 22; Length 99629;
Pred. No. 7.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 391-415; 545pp; English.
                                                                                                                                          Patterson C, Berg KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL32333 standard; DNA; 8895 BP
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16-JUN-2000; 2000WO-US16649.
                                                99US-0140121.
                                                                                                (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                          WPI; 2001-041427/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
                                             18-JUN-1999;
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SS.

pharmacogenomic marker; gene;

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ABK33948
ID ABK3
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                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrimer's diseases, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7006 AAAAAAAAATAAAATAATATGGAAAAACCTAAAATACTACTACCTAAAAACCCTCTTACAT 6947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6946 CTCCCAAAACCACTTTTACCCATCTATAAAACAATAACCAATCTAAGTTTAATATTCTAA 6887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695 TCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     755 AGGAGTCGATACCATAAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTG 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     815 GAGCAACCTTCCCTTTGATTCTTTGATGACAGAGATGAAGAGAGAAGAAGTTTTTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     635 AATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCT 694
                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 24; Length 8895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%; Score 39; DB 24; Length 88
46.2%; Pred. No. 4.2;
Live 0; Mismatches 150; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8895 BP; 2269 A; 62 C; 1898 G; 4665 T; 1 other;
                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 306; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6886 AAATAACCTAAAATCAAAAACAACCTCTTTCGTCATACA 6848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     875 AAAAATTCTAAAATAGAAATGCATTTGTGTGGGGTAAA 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human prostate expression marker cDNA 61117
                                                                                                                                                                                               Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV61126 standard; cDNA; 326
                                                                                                                                  30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                          02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 46.2 tes 129; Conservative
                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                     WPI; 2002-130909/17
                                                          WO200200928-A2
                                   Homo sapiens
                                                                                  3-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
            dene; ds
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                                                                                                                                                                                               olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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comprising
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(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;

(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;

(f) assessing the prostate cell carcinogenic potential of a compound;

(f) assessing the prostate cell carcinogenic potential of a compound;

(g) determining whether prostate cancer has metastasized in a patient;

(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       735 ATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGC 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  795 TTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 GAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAATGAAATGCATTTGTGTGGAGCTAAAG 914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 326 BP; 100 A; 48 C; 37 G; 140 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 11610; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            915 CITGCITCTTTATTTTCCTTTTGT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88 TTTTTTTTTTTTTTTTTTTTTTTTTT
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                                                                                                                                                                                                                                                                                                                                    16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
18-UUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
                                                                                                                                                                                                                           20-FEB-2001; 2001WO-US05171.
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                                                                                                                                                                                                                                                                                                 17-FEB-2000; 2000US-183319P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-662795/76.
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                                                                 WO200160860-A2
Homo sapiens.
                                                                                                                                                23-AUG-2001.
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Gaps

ABK33948;

0;

0; Gaps

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WO200202808-A2
                    astrocytomas
      Homo sapiens
         10-JAN-2002.
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer, s disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                            856 AACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGC 915
                                                                                                                                                                                                                                                                                     916 TYGCTICTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTA 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human, immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV, anticonvulsant; ophthalmologic; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiframmatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                      DB 24; Length 18997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;
         Sequence 18997 BP; 4675 A; 299 C; 4016 G; 10007 T; 0 other;
                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 543; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immune system associated gene SEQ ID NO: 543.
                                                                                                                            99
                                                                         Score 38.4; DI
Pred. No. 8.2;
                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          4137 TGTTTTTCGGGTTTTTCGACGTT 4160
                                                                                                                                                                                                                                                                                                                                                                                                    976 TGCACGTTGGAGTGGCTGTT 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL32570 standard; DNA; 18997 BP.
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2000DE-1043826.
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                                                                                               54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
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                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-JAN-2002.
                                                                                                                               78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABL32570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olek A,
                                                                            Query Match
                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
ABL32570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
XX
                                                                                                                                                                                                                                                                                                     δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid comprising a sequence (I) of at least 18 bases in length of a segment of chemically pre-treated genomic DNA whitch has any one of the sequences of (ABKA31919-ABKA4032) or its complement. Also included are an oligonuclectides which hybridises to (I), probes for detecting oytosine methylation or single-complements (SNP) in (I), an array of oligomers to (I), probes for detecting oytosine methylation or single-complements (SNP) in (I), an array of oligomers or peptide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing oytosine methylation states of the CpG dinuclectides of (I). The array is useful cor peptide nucleic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astroychomas, or the predisposition to astrocychomas by analysing openetic and/or epigenetic parameters, classification, differentiations, involves obtaining a biological sample containing genomic CDNA, extracting the genomic DNA, converting cytosine bases which are methylations, involves obtaining a biological sample containing genomic CNNA, extracting the genomic DNA, converting cytosine bases which are monther base which is dissimilar to cytosine in terms of hybridisation canother base which is dissimilar to cytosine in terms of hybridisation containing genomic DNA fragments using the array and a polymerase, where the analysing methylation status of the cytosine positions by reference to analysing methylation status of the cytosine positions by reference to analysing methylation status of the cytosine positions by reference to bisulphite, hydrogen sulphite or disulphite. The amplificates are detachable made or or more cytosine positions by the cytosine positions or tissues, as opposed to background DNA. The amplificates are detachable molecule fragments by any any assisted laser desorption/ionally, the labels of the indicates are detachable molecule fragments and positioned for a better detection mass spectrometer
                                                                                                                                  Human; ds; astrocytoma; cytostatic; staging; cysteine methylation; CpG; bisulphite; brain tissue; MALDI; ESI; electron spray mass spectrometry; matrix assisted laser desorption/ionization mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel chemically modified genomic DNA sequences, useful in the characterisation, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                      Human DNA for staging of Astrocytomas #16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 31; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                   18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
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The invention relates to an isolated polynucleotide which is a polymcrphic variant of glutamate receptor, metabotrophic 3 (GRM3) is a receptor for glutamate, the major excitory neutotraphic variants of glutamate receptor, metabotrophic 3 (GRM3) is sogene. GRM3 is a receptor for glutamate, the major excitory neutotransmitter in the mammalian central nervous system. Human GRM3 coated no chromosome 7421.1-q21.2 is expressed in human fotall and adult whole brain especially in the caudate nucleus and corpus collosum. GRM3 CMM3 is useful in gene therapy and also for studying the expression and function of GRM3. GRM3 polypeptide is used for screening drugs. A recombinant non-human organism is used to study expression of GRM3 SC in vivo screening and testing of drugs targetted against GRM3 protein, and for testing the efficacy of therapeutic agents and compounds for neurological disorders in a biological system. GRM3 compounds for testing diseases associated with GRM3 activity, e.g., neurological disorders. The present sequence is human GRM3 gene fragment containing polymorphic sites.
                                                                                                                                                                                                                                                                                                                                     and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "This degenerate base represents polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "This degenerate base represents polymorphic site
(PS) 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human GRM3 gene fragment #1 allelic variant containing polymorphic site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727 GCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAA 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               787 GGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTGTTGTTAATGA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               847 CAGAAGATGAACAAAGAGTATTTTGAAAATTCTAAAATAGAAATGCATTTGTGTCG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; glutamate receptor metabotrophic 3; GRM3; neuroprotective; nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2; drug screening; neurological disorder; polymorphic site; Ps; ds.
                                                                           New isolated polynucleotide, a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat {\tt GRM3} activity-related disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.5%; Score 38.4; DB 24; Length 50000; Best Local Similarity 51.9%; Pred. No. 12; Matches 110; Conservative 0; Mismatches 101; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 50000 BP; 15337 A; 9556 C; 9289 G; 15817 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         907 AGCTAAAGCTTGCTTCTCTTTATTTTCCTTTT 938
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                                                                                                                                                                                 Example 1; Fig 1; 165pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    437/c
AAD26437 standard; DNA; 50000 BP.
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4192
                               WPI; 2002-090198/12.
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//rtag= involectide Y is present at this location in the
sequence shown in sequence listing of the specification
26032..50000
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/note="Nucleotide R is present at this location in the
sequence shown in sequence listing of the specification"
4667.4528
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/*tag= c
/*tog= Nucleotide R is present at this location in the Shoure shown in sequence listing of the specification 4529..25175
/*tag= d
25176..26031
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                                                                                                                                                                                                                                     916 TIGCTICTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTA 975
                                                                                                  856 AACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGC 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; glutamate receptor metaborrophic 3; GRM3; neuroprotective; nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2; drug screening; neurological disorder; polymorphism; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human glutamate receptor, metabotrophic 3 (GRM3) gene fragment #1.
Query Match 3.5%; Score 38.4; DB 24; Length 18997; Best Local Similarity 54.2%; Pred. No. 8.2; Matches 78; Conservative 0; Mismatches 66; Indels 0;
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/partial
replace (26157, A)
/*tag= h
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replace (4006, A)
                                                                                                                                                                                                                                                                                                                                     replace (25586, T)
                                                                                                                                                                                                                                                                                                        976 TGCACGTTGGAGTGATTGGCTGTT 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD26400 standard; DNA; 50000 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-2001; 2001WO-US19447.
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AAD26400/Cc
IAA AAD2641
AXX AAD2641
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XXX AAD2641
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28-AUG-2002 (first entry)

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The invention relates to an isolated polynucleotide which is a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) is areceptor for glutamate, the major excitory sequence GRM3 is a receptor for glutamate, the major excitory neurotransmitter in the mammallan central nervous system. Human GRM3 located on chromosome 7421.1.421.2 is expressed in human foretal and adult whole brain especially in the caudate nucleus and corpus collosum. GRM3 or located on GRM3 of GRM3 (GRM3 GRM3) in the caudate nucleus and corpus collosum. GRM3 crecombinant non-human organism is used to study expression of GRM3 GC in vivo, for in vivo screening and testing of drugs targetted against compounds for neurological disorders in a biological system. GRM3 compounds for treating diseases associated with GRM3 and compounds for treating diseases associated with GRM3 activity, expression of GRM3 chuman GRM3 gene fragment containing polymorphic sites (PS):
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                                                                                              /*tag= d
/note= "This degenerate base represents polymorphic site
(PS) 4"
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/note= "This degenerate base represents polymorphic site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 727 GCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATAACCATAAATTCCGATTAAAAAA 786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.5%; Score 38.4; DB 24; Length 50000; Best Local Similarity 51.9%; Pred. No. 12; Matches 110; Conservative 0; Mismatches 101; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide, a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat GRM3 activity-related disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20; Page 135-153; 165pp; English.
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                                                                                                                                                                                                                                                                                                                                                                      Tanguay DA;
                                                                                                                                                                                                                                                                                                                               (GENA-) GENAISSANCE PHARM INC.
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                                                       (PS) 3
26157
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misc_feature
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ABQ67094
ID ABQ670
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AC ABQ670
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The invention relates to a nucleic acid (1) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67718) or their complements. (1), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, necvascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, psoriasis, arteriopathy, macular degeneration caused by neovascularisation, psoriasis, arterioscierosis, inflammation well diseases, ulcers and companion and companion and companion and companion and control of the companion and companion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 ACTITAGTGAAGAGTCTTCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGC 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid fragments from chemically treated angiogenesis associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 83391 BP; 24547 A; 665 C; 16953 G; 41209 T; 17 other;
                                                                              Human angiogenesis associated polynucleotide SEQ ID NO 124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 124; 41pp. + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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ABL32294/c
ID ABL32294 standard; DNA; 9415 BP.
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01-SEP-2000; 2000DE-1043826.
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                                                                               2854 AGAGAGAGAGATT 2868
                                                 746 CGTGAGGAAAGGAGT 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                            ABL32294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chamically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (Ss). The nucleic acid may be eptide nucleic acid coligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and cumours. The probes can also be used in a method for ancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases associated with CpG dinucleotides e.g. canneers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific compared to another set of genetic and/or epigenetic parameters may be differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                              Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2674 TGTATTAATAAAAATTTTATTTTAGAATTTTTAATTTTGGGAGAAAATAAGATAAA 2733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626 TGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGA 685
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              Tumour suppressor gene derived chemically modified sequence #55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 3.5%; Score 38.2; DB 22; Length 7667; Best Local Similarity 49.7%; Pred. No. 6.6; Matches 97; Conservative 0; Mismatches 98; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                       06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1035529.
01-SEP-2000; 2000DE-1043826.
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                                                              cancer; tumour; CpG dinuc
cytosine methylation; ds
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                                                                                                                                            WO200168912-A2
                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               655 TGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAA 714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                            Human: immune system disease; cytosine methylation; antiasthmatic; antiatrefioscierofic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant: ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiflammatory; cancer; eye disease; arterioscialorosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.5%; Score 38.2; DB 24; Length 9415; Best Lacocal Similarity 48.8%; Pred. No. 7.1; Matches 103; Conservative 0; Mismatches 108; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 267; 32pp + Sequence Listing; German.
Human immune system associated gene SEQ ID NO: 267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berlin K;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/alcerative bowel diseases. The present sequence is a gene of the invention.
                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
715 TCTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATT 774
                                                                                                                                                                                                                                                                                                                                   Human, immune system disease; cytosine methylation, antiasthmatic; antiatrefiosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologici; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antifanmatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 15373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 440; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 440.
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Pred. No. 8.
                                                                                                       3869 АААААТАААААТААТТАТАААТАААТСС 3839
                                                                      775 CCGATTAAAAAGGGAGTGCTTACAACAGCC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K;
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ABL32467 standard; DNA; 15373 BP.
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2000DE-1043826.
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                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Olek A, Piepenbrock C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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01-SEP-2000;
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The present invention relates to chemically modified DNA sequences of signal transduction associated genes. The DNA sequences are chemically modified using a solution of bisulphite, hydrogen sulphite or modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonotteotides and/or PNA oligomers of disulphite. Also disclosed are oligonotteotides and/or PNA oligomers of or detectoring the cytosine methylation state (ppG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular scomponents which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible compinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and sequences of different genes associated with signal transduction, or their complementary sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; signal transduction associated gene; cytosine methylation state; CpG island; signal transduction associated disease; solid tumour; cancer; antitumour; cytostatic; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction
                                        10146 CITCICCICACAAAAAAAAATATAAAAAAAAAATCAAITACCIAAITCAAAATAC 10087
                                                                                                                               10086 CTCTATAAACTCCAAATTATAAAACGTTAAACTAACCATAACTATACTTTTTACATTACT 10027
                                                                                                                                                                                                    10026 TABABABATAATGCGGTTATATATATTTTABABATCTATBABTTABATAAAAATATTCTT 9967
                                                                                      786 AGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATG 845
                                                                                                                                                                        846 ACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTC 905
726 AGCTITICCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal transduction associated gene modified DNA #177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID No 353; 24pp; English.
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                                                                                                                                                                                                                                                                                                          9966 ATACTAACTTATTTCATATTAA 9944
                                                                                                                                                                                                                                                                 906 GAGCTAAAGCTTGCTTTTA 928
                                                                                                                                                                                                                                                                                                                                                                                                                       ABK31510 standard; DNA; 47108
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01-SEP-2000; 2000DE-1043826.
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666 CTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAAT 725

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ABL34174;
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ID ABL
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the European Patent Office.
                                                                                                                                                                                                                                                                                                                       43962 TAAAAAATTCTTCATAAAATTTTAAAATTTTTCGATATAAAACTTTTCAATATCGCATTTA 43903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 TAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAA 673
                                                                                                                                                                                                                                                                                                                                                                                                  674 TCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTC 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 734 CATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTG 793
                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               794 CTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAAGA
                                                                                                                                                                        Length 47108;
                                                                                                                    Sequence 47108 BP; 13283 A; 429 C; 9740 G; 23656 T; 0 other;
                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                        Score 38.2; DB 24;
Pred. No. 13;
0; Mismatches 143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          854 TGAACAAAGAGTAAGTTTTTGAAAAT 880
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                                                                                                                                                                            3.58;
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2000DE-1043826.
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                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                        Query Match
Best Local Similarity
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01-SEP-2000;
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                                                                                                                                                                                                                                Matches 124;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albriemer's disease, AlbS, eplilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                             13766 TTTGAGTTTAGTGTATATTGTTAAGGTGATAGATGTATATAGAATTTTATAAATTATATATATAT 13825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13826 AAAGAATTTATTTAGTAGGGGCTAGTTTATGTTATTATTATTTTAGTATTTTGGGAGGT 13885
                                                                                                                                                                                                                                                                                                                                                   828 TTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAATTCTAAAA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                             888 TAGAAATGCATTTGTGTCGAGCTAAAGCTTGCTTCTTTATTTTTCCTTTTGTAGAATGA 947
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarchritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic;
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for diagnosis and treatment of diseases associated with abnormal
cytosine methylation -
                                                                                                                                                                                                                                                       DB 24; Length 17213; 10;
                                                                                                                                                                                                             Sequence 17213 BP; 5148 A; 333 C; 3659 G; 8073 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 2147; 32pp + Sequence Listing; German.
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                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                          3.5%; Score 38;
54.2%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      948 TTCGGTAGTAGGAATATGGGGT 969
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                 Local Similarity
les 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Gaps

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2689 AATCAAATTTAAAAACTAAAAATAATATATAAAAAACTTTATTTCCTTAATTTTAACGTT 2630
                                                                                                                                                      2629 ICTAAAAAAAAAAAATATAATAAAAAAAAAAAAAATATAACGTTCTATAACAATTTAAA 2570
                                                                672 AATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTT 731
                                                                                                                          732 TCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAG 791
                                                                                                                                                                                    792 IGCITACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
        DB 24; Length 7690;
      Score 37.8; DB 24; Length
Pred. No. 8.5;
0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                          2509 AACAAAAGCCAAAAACAACAATAATAACTAATACTTCGAAATCC 2465
                                                                                                                                                                                                                                              852 GATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAATAGAAATGC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 29351.
                                                                                                                                                                                                                                                                                                                                                     AAC40730 standard; DNA; 870 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0123180.
99US-012548.
99US-0126264.
99US-0126785.
99US-0126785.
99US-012834.
99US-012834.
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99US-0131449.
99US-0132048.
          3.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0130077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000EP-0301439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0121825
                                                                                                                                                                                                                                                                                                                                                                                                                 17-OCT-2000 (first entry)
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana.
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                         Similarity
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29-MAR-1999;
01-APR-1999;
06-APR-1999;
08-APR-1999;
16-APR-1999;
21-APR-1999;
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30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000
                         Best Local Sim
Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                    AAC40730;
             Query Match
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                                                                                                                                               ;
0
                                                                                                                                                                                                        including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia. Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ducerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                           343 ATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAGAGCTTGTACTTTTTCTAT 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; immune system disease; cytosine methylation; antiasthmatic; antiatrefiosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmologici; antirheumatic; antiarthritic; antidlabetic; antipsoriatic; antiinfammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer; disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                      Sequence 113515 BP; 31803 A; 1174 C; 24020 G; 56518 T; 0 other;
                                                                                                              Score 38; DB 24; Length 113515;
Pred. No. 21;
0; Mismatches 40; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7690 BP; 1804 A; 225 C; 2151 G; 3510 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1095; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                       Human immune system associated gene SEQ ID NO: 1095.
                                                                                                                                                                                                                                        403 GACTTTAGTGAAGAGTCTTCCCATGTTTATGAAAATTCAGA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin K;
                                                                                                                  3.5%; Scc
Similarity 60.8%; Pre
52; Conservative 0;
                                                                                                                                                                                                                                                                                                                                            ABL33122 standard; DNA; 7690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2001; 2001WO-EP07537.
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01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Olek A, Piepenbrock C,
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                                                                                                                                                   62;
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                                                                                                                     Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                RESULT 29
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     SSSSSX
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9904S - 0146386 9904S - 0146388 9904S - 01472038 9904S - 01472036 9904S - 01472036 9904S - 01472035 9904S - 01473035 9904S - 01473035 9904S - 0148319 9904S - 0148319 9904S - 0148319 9904S - 0148319 9904S - 01494226 9904S - 0151046 9904S - 015104739 9904S - 0151046 9904S - 0161046 9904S - 0161046	100000
02-AUG-1999; 02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AU	25-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999; 26-0CT-1999;
	P P P P P P P P P P P P P P P P P P P
990S - 0135124 990S - 013523 990S - 013629 990S - 013629 990S - 013629 990S - 013722 990S - 013722 990S - 013722 990S - 013745 990S - 013445 990S - 014182 990S - 014082 990S - 014182 990S - 014182 990S - 0144132 990S - 0144132 990S - 0144132 990S - 0144132 990S - 0144132 990S - 0144132 990S - 0144133 990S - 0144133 990S - 0144132 990S - 0144133 990S - 0144133 990S - 0144135 990S - 0145088 990S - 0145088	000000
22 - MAY 1999 24 - MAY 1999 25 - MAY 1999 25 - MAY 1999 26 - MAY 1999 26 - MAY 1999 27 - MAY 1999 28 - MAY 1999 28 - MAY 1999 29 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 28 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 28 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 26 - JUN 1999 27 - JUN 1999 27 - JUN 1999 28 - JUN 1999 28 - JUN 1999 29 - JUN 1999 20 - JUN 1999 20 - JUN 1999 21 - JUN 1999 22 - JUN 1999 23 - JUN 1999 24 - JUN 1999 25 - JUN 1999 27 - JUN 1999 27 - JUN 1999 28 - J	, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	. 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7

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Gaps

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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arterlosclerosis, anomana, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                  2002 TITAAAATIGATATGAAAAAATIAATGIATAAGAATAGITAATAATITAAAGIIAYAGI 2061
                                                                                                                            1942 ATTAATTAATTTATTTAATATAATAATAATAAAAAGTTTTAGAATAAGTTAAGTTGAT 2001
                                                                                                                                                                            402 TGACITIAGIGAAGAGICTTCCCAIGTTATGAAAAATTCAGAAAATGAGGGATGTAGAA 461
                                                                                                          342 GATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTTA 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant: ophthalmologici; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antifrlammatory; cancer; eye disease, arteriosclerosis; anemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                462 GCCAAGGCACGTGCCCTAAAAGGTCATGAATGAGATCAGGAGTTAAGGAGAAATTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                          DB 24; Length 6237;
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 503; 32pp + Sequence Listing; German.
      Sequence 6237 BP; 2071 A; 77 C; 1289 G; 2800 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 503.
                                                                        91;
                                                                            0; Mismatches
                                        Score 37.4;
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL32530 standard; DNA; 7644 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                            3.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAR-2002 (first entry)
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
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                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200200928-A2.
                                                                                                                                                                                                                                                                                                                                                       2062 AAT 2064
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                                                                                                                                                                                                                                                                                                                      522 TAT 524
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                                                                                92;
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                                              Query Match
                                                                  Local
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                                                                                Matches
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                                                                                                                                  0;
                                                                                                                                                                                                    168 ATTICITCCGGTGGTGGAGGCGACGCCGTACCAAGGAATCTAGAGGAGCGAGTCATTTG 109
                                                                                                                                                                                                                                      90 ATTITICAAGTICAGTICTACCAGTICATCAAAATGICITAATTGAAAATAAAAGTCTCTTGIG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                    Gaps
                                                                                                                                                                  30 ATTICICITICALIGIAAAGGGGAATIGATICIAACAGACCITGGICGAGCAICCATICIA 89
                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiateriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant: ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinfammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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0
                                                                                                  DB 21; Length 870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 332; 32pp + Sequence Listing; German.
                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                          150 GAGTIGATGTATIGAAGGGAAGACGAATAATCIGATCCAATICTAAA 196
                                                                                                                                                                                                                                                                                                                                         48 ACTTIGITGITIAGAGGAGAAGAAGAATCTGATCCAAGTTATAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 332.
                                                                                                                                    81;
                                                                                                              4.8;
                                                                                                                                      Mismatches
                                                                                                  3.4%; Score 37.4;
51.5%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berlin K;
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990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                    86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS AG
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                                                                                                                        Similarity
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  26-OCT-1999;
28-OCT-1999;
                                                                    29-OCT-1999
                                    28-OCT-1999
                                                      28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL32359;
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                                                                                                      Query Match
Best Local
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990S - 0.139119
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990S - 0.139456
990S - 0.139466
990S - 0.139461
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990S - 0.139461
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990S - 0.139617
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990S - 0.140823
990S - 0.14287
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990S - 014400S
990S - 0144086
990S - 0144086
990S - 0144331
990S - 0144331
990S - 0144334
990S - 0144334
990S - 0144334
990S - 0144334
990S - 0144336
                                                                                                  99US-0138094.
99US-0138540.
99US-0138847.
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99US-0147204
    99US-0136782
28 - MAY 11999;

01 - JUN 11999;

04 - JUN 11999;

06 - JUN 11999;

10 - JUN 11999;

110 - JUN 11999;

110 - JUN 11999;

110 - JUN 11999;

110 - JUN 11999;

111 - JUN 11999;

112 - JUN 11999;

113 - JUN 11999;

114 - JUN 11999;

115 - JUN 11999;

116 - JUN 11999;

117 - JUN 11999;

118 - JUN 11999;

119 - JUL 11999;
                                                                                                                                                                                   338 ATCAGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTT 397
                                                                                                                         Gaps
                                                                                                                       .;
0
                                                                           Query Match 3.4%; Score 37.4; DB 24; Length 7644; Best Local Similarity 60.2%; Pred. No. 11; Matches 62; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
    diseases. The present sequence is a gene of the invention.
                                         Sequence 7644 BP; 2187 A; 53 C; 1625 G; 3779 T; 0 other;
                                                                                                                                                                                                                                                                 3030 TGTTTATTTTTAGATAAGTTTTGTTTTGTGATTATAATGAATT 3072
                                                                                                                                                                                                                                        398 TCTATGACTTTAGTGAAGAGTCTTCCCATGTTATGAAAATT 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana DNA fragment SEQ ID NO: 14105.
                                                                                                                                                                                                                                                                                                                                                                  518/c
AAC36518 standard; DNA; 522 BP
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PR 05-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147260.

PR 06-AUG-1999; 99US-0147416.

PR 09-AUG-1999; 99US-0147416.

PR 11-AUG-1999; 99US-0147416.

PR 11-AUG-1999; 99US-0147419.

PR 11-AUG-1999; 99US-0148119.

PR 13-AUG-1999; 99US-0148119.

PR 13-AUG-1999; 99US-0148119.

PR 13-AUG-1999; 99US-0148119.

PR 23-AUG-1999; 99US-014916.

PR 23-AUG-1999; 99US-014918.

PR 23-AUG-1999; 99US-0151066.

PR 23-AUG-1999; 99US-015206.

PR 24-CCT-1999; 99US-015206.

PR 24-CCT-1999; 99US-015206.

PR 13-CCT-1999; 99US-01506.

PR 24-CCT-1999; 99US-016076.

PR 22-CCT-1999; 99US-016076.

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Query Match 3.4%; Score 37.2; DB 21; Length 522; Best Local Similarity 51.9%; Pred. No. 4.5; Matches 84; Conservative 0; Mismatches 78; Indels 0;
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to
                                                                                                                                                 1826 GAACACCCCAATATTAAACAAAACCACTTTTACTCTAACTCTAAATAAAAACCACTTTT 1885
                                                                                                                                                                                                                                                                                                                               1886 GITTAATTAAGTGTGAAATTCTTCTTCATCATATTTTTCTGATAAAAAATAACCTGGGAC 1945
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                                          Score 37.2; DB 22; Length 3152;
Pred. No. 8.8;
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                                                                                         0; Mismatches 128; Indels
         Sequence 3152 BP; 995 A; 616 C; 431 G; 1110 T; 0 other;
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Similarity 47.1%;
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                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis \dot{}
                                                                                                                                                                                                                                     30 ATTICICITIGATIGIAAAGGGGAATIGATICIAACAGACCITGGICGAGCATCCATICIA 89
                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. epidermidis genomic polynucleotide sequence SEQ ID NO:4056.
                                   ch 3.4%; Score 37.2; DB 21; Length 869; 1 Similarity 51.9%; Pred. No. 5.4; 84; Conservative 0; Mismatches 78; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                                                                                  150 GAGTIGATGTATIGAAGGGAAGACGAATAATCIGATCCAATT 191
                                                                                                                                                                                                                                                                                                       46 ACTITGITGITGITAGAGGAGAAGAATCIGAICCAAGI 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; Page 1740-1741; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        AAH54692 standard; DNA; 3152 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-2000; 2000WO-US30782.
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  99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccination; endocarditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-316495/33.
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    29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH54692;
                                            Query Match
                                                               Local
                                                                                  Matches
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AAH55090 represent specifically claimed S. epidermidis genomic DNA polymoleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonoclectide sequences and primers which are used in the exemplification of the present invention.

N.B. The present invention specifically claims all the polymucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4455 to 4472, no sequences are present for SEQ ID NO:4455 to 4472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2971 GAACACCCCAATATTAAACAAAACCACTTTTTACTCTAACTCTAAATAAAAACCACTTTT 3030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3031 GTTTAATTAAGTGTGAAATTCTTCTTCATCATATTTTTCTGATAAAAATAACCTGGGAC 3090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               574 AGACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        634 TAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            694 TICTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                      3.4%; Score 37.2; DB 22; Length 3345; 47.1%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                          Sequence 3345 BP; 1108 A; 485 C; 551 G; 1201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immune system associated gene SEQ ID NO: 775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 9;
0; Mismatches 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL32802 standard; DNA; 6113 BP.
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 47.1
Matches 114, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dene;
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AEB132802
ID AEB132802
XX AEB132802
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Albrimer's disease, AIDS, epllapsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                 860 AAGAGTAAGTTTTTGAAAAATTCTAAAATGGAATGCATTTGTGTGGGGGTAAAGCTTGC 919
                                                                                                                                                                                                                                                                                                                                                                                                                     920 TICTCTTTATTTTCCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCA 979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; opthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds.
Nucleic acid comprising fragment of chemically modified gene, usfor diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                            DB 24; Length 6113;
                                                                                                                                                                                                                                                                        Sequence 6113 BP; 1487 A; 157 C; 1487 G; 2982 T; 0 other;
                                                                                                                                                                                                                                                                                                          3.4%; Score 37.2; DB 24; Length (53.4%; Pred. No. 11;
tive 0; Mismatches 68; Indels
                                                                     Claim 1; SEQ ID NO 775; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immune system associated gene SEQ ID NO: 1693.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                980 CGTTGGAGTGATTGGCTGTTCTGGAA 1005
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01-SEP-2000; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                        Local Similarity 53.4 tes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                              Query Match
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ID ABL3
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comprising

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Gram positive bacteria; dnaE; dnaX; dnaB; PolC; dnaN; dnaG; helicase; alpha subunit; DNA polymerase III holoenzyme; gamma subunit; tau subunit; clamp loader; glue protein; replication; antibiotic; ss.
                                                         The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: or assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (f) assessing the prostate cancer has metastasized in a patient; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated dnaE, dnaX and dnaB genes from Gram positive bacteria, used to develop screening assays for identifying antibiotic compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 CAATAGCGATCAGATTGCTTTGTAGGGTTTGTATGCGTTGTTTTTTACTAGGAAGAGCTT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 37; DB 23; Length 619; 0.04%; Pred. No. 5.4; ve. 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 619 BP; 265 A; 95 C; 107 G; 149 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 GTACTTTTTCTATGACTTTAGTGAAGAGTCTTCCCATGTTT 430
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/note= "Dna N gene product"
Claim 1; Page 10116; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ31005 standard; DNA; 1134 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 60.49 Solution 15 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                   The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosinos. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlbS, epilepsy, neurofibromatosis, rheumatoid arthritis, psorlasis and inflammatory/alcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        957 AGGAATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAA 1016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         837 TTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAATAGAAATGC 896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 ATTICICICGAGCIAAAGCIIGCIICCITITAITITICCITITGIAGAAIGAITCGCIAGI 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24; Length 7190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7190 BP; 1434 A; 310 C; 2114 G; 3261 T; 71 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                         Claim 1; SEQ ID NO 1693; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 52120.
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Pred. No. 12;
0; Mismatches
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2000US-189862P.
2000US-207454P.
2000US-211314P.
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ilarity 49.5%;
Conservative
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2000US-255281P
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90; Conserv
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09-JUN-2000; 2
18-JUL-2000; 2
13-DEC-2000; 3
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16-MAR-2000;
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99US-0146178.

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This sequence is the partial dnaw gene of Staphylococcus aureus. The invention relates to a number of isolated DNA molecules from Gram CC invention relates to a number of isolated DNA molecules from Gram positive bacterium, corresponding to dnaE (AAZ31001), dnaX (AAZ31004-231006) are also identified. The PolC, dnaw and dnaG genes (AAZ31004-231006) are also identified. The dnaE gene corresponds to the alpha subunit of the Escherichia coll, DNA polymerase III holocoryme, and corresponds to the alpha subunit is the actual DNA polymerase, the gamma complex forms the clamp loader and tau is a "glue protein". DnaX encodes complex forms the alpha subunit is the actual DNA polymerase, the gamma complex forms the alpha subunit is the full gene, while gamma is the product of the first two thirds of the gene. DnaN forms the beta subunit which forms the sliding clamp, and dnaG encodes a primase. The DNA sequences of the invention can be used to identify agents that inhibit or promote DNA replication by acting on various parts of the gram positive bacterial DNA polymerase holocoryme. The products and methods of the invention can be used for identifying pharmacological agents or lead computing pharmacological agents or lead computing pharmacological agents or lead computed for identifying pharmacological agents or lead computed for agents active at the level of a replication protein forms and particularly DNA replication. The agents identified can be used computed for identified can be used computed to the invention can be used fo
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dnaG; dnaB; antiblotic; replication; cell growth; cell death;
bacterial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 TGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGT 153
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/product= "dnaN protein"
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                       Example 8; Page 30; 132pp; English.
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AAF54735
ID AAF54
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Human; secreted protein; proliferative disorder; cancer; feetal abnormality; heematopoietic disorder; feetal abnormality; heematopoietic disorder; lummune system disorder; AlDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AlZhehimer's disease; skinflammation; allergy; neurological disorder; AlZhehimer's disease; skin disorder; psoriasis; sepsis; diabetes; atheroscleroais; cardiovascular disorder; angiogenic disorder; kidney disorder; angiogenic disorder; stops disorder; pregnancy-related disorder; pregnancy-related disorder; infection; wound healing; vulnerary; endocrine disordaris; cell culture; chemotaxis; findey disorder; bindication; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a dnaN polypeptide. The specification describes DNA molecules from Gram positive bacteria, which comprise a coding region from a polC, dnaE, holB, dnaX, dnaN, ssb dnaG or a dnaB gene. These sequences encode proteins that replicate the chromosome of Gram positive bacteria. They are used for sequencing and amplification of DNA and in drug discovery to identify compounds which have antibiotic activity through interference with replication. They are used in methods for identifying compounds that are active at the level of DNA replication and result in arrest of cell growth or cell death of bacteria to treat bacterial infections in animals.
                                                                                                                                                                                   Isolated DNA molecule from a Gram positive bacterium encoding DNA replication proteins used to identify compounds which have antibiotic activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 TGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              834 CTCTTTATTAGCACGTGAAGGTGGTAATAACGTTATTAAATTAAGTACAGGTGATGACGT 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 CTCTTGATTGTAAAGGGGAATTGATTCTAACAGACCTTGGTCGAGCATCCATTCTAATTT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein gene 27 cDNA clone HJAAJ58, SEQ ID NO:100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 1134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 6.8;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1134 BP; 411 A; 176 C; 194 G; 353 T; 0 other;
                                                                                   Whipple R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.4%; Score 37; Best Local Similarity 50.3%; Pred. No. (Matches 91; Conservative 0; Mismatc)
                                                                                                                                                                                                                                                                     Disclosure; Page 39-40; 239pp; English.
                                                                                 O'Donnell ME, Bruck I, Zhang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 611/c
AAH32611 standard; cDNA; 1075 BP.
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                                           (UYRQ ) UNIV ROCKEFELLER.
                                                                                                                       WPI; 2001-147453/15.
P-PSDB; AAB31935.
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us-09-438-185a-1_1199590_1200675.rng

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RESULT 43
                                                                                       protein genes, and AAG73346-AAG73448 represent the proteins they encode protein genes, and AAG73346-AAG73448 represent the proteins they encode protein genes, and AAG73346-AAG73348 represent the proteins they encode and Their corresponding secreted proteins are useful for preventing, and their corresponding secreted proteins are useful for preventing, therapy. Pathological conditions can be diagnosed by determining the mouth of the new protein in a sample or by determining the presence of amount of the new protein in a sample or by determining the presence of the languages, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of the last season on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of the last season of the diagnosis or treatment of the last season of the disorders, cancer, tumours, foetal and developmental chormalities, haematopoietic disorders, diseases of the immune system, allergies, neurological disorders (e.g., Alzheimer's disease, alterosalis, cardiovascular disorders, e.g., alzheimer's disease, alterosalis, cardiovascular disorders, pregnancy-related disorders, endocrine disorders, and infections. The proteins can also be used to aid wound chasing and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to cidentify their cognate ligands or binding partners, and in chemotaxis, and can be used in diagnostic immunosassay endocrate the invention can be used in diagnostic immunosassay endocrate in preservative to medity storger properties.

Antibodies specific for a protein of the invention can be used in diagnostic immunosassay endocrate envent expresents a human cognity and envent assay (ELISA). The present sequence represents a human cognity and protein-encoding cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 ITGTTTGTAAAAAAAAAAAAATTAACAAATGTTTAGCTAAACAAAGTAAGAAAAAG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         754 AAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                432 AAAGACTCAAATAAATGAAATCAGAAATGAAAAAGGAGACATGACAATTGATACCACAGA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGA-TGAACAAAGAGTAAGTTTT
                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 1075;
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                                                                                                                                                                                                     Ni J, Moore PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36.8; DE
Pred. No. 7.5;
0; Mismatches
                                                                                                                                                                                                     Ruben SM, Komatsoulis GA, Birse CE,
                                                                                                                                                                                                                                                                                                                                        preventing, diagnosing and/or treat
disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 504; 604pp; English.
                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
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                                                08-NOV-2000; 2000WO-US30653.
                                                                                       12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 52.6
Matches 103; Conservative
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     17-MAY-2001.
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AMH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein grade and AAG73346-AAG7348 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be disgnosed by determining the mount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the mount of the new genes. Specific uses are described for each of the amount of the new genes. Specific uses are described for each of the proliferative disorders, cancer, tumours, foetal and developmental enformations autoimmune diseases (e.g., rheumatoid arrthritis), inflammation, allergies, neurological disorders, disbetes, achieroscherosis, candiovascular disorders (e.g., Alzhelmer's disease) candiovascular disorders (e.g., Alzhelmer's disease) candiovascular disorders, angiogenic disorders, and infections. The proteins can also be used to aid wound closured and disorders, pregnancy-related disorders, endocrine closurders, and infections. The proteins can also be used to aid wound closure of primary tissues, to regenerate tissues, to identify their connected ligands or binding partners, and in chemotaxis, and connected in chemotaxis, and connected in the invention can be used in
                                                                                                                                                                                                                                                         Human secreted protein-encoding gene 27 cDNA clone HJAAJ58, SEQ ID NO:98
                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; proliferative disorder; cancer; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allorgy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsils; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM, Komatsoulis GA, Birse CE, Ni J, Moore PA;
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AAH32609 standard; cDNA; 1724 BP.
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27-JUL-2000; 2000US-0221193.
                                                                                                                                                                                         10-AUG-2001 (first entry)
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                                                                                               AAH32609;
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alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding CDNA of the invention.
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                                                                                                                                                                                                                              694 TTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoletic; immune/haematopoletic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                           Query Match 3.4%; Score 36.8; DB 22; Length 1724; Best Local Similarity 52.6%; Pred. No. 9; Matches 103; Conservative 0; Mismatches 92; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23239.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1724 BP; 433 A; 242 C; 279 G; 770 T; 0 other;
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44-FEB-2000; 2000US-0186528.

22-FEB-2000; 2000US-0186564.

16-MAR-2000; 2000US-0189874.

17-MAR-2000; 2000US-0189874.

18-APR-2000; 2000US-0199874.

19-MAY-2000; 2000US-025515.

20-JUN-2000; 2000US-0214886.

30-JUN-2000; 2000US-0214886.

30-JUN-2000; 2000US-0214886.

30-JUL-2000; 2000US-0214886.

11-JUL-2000; 2000US-0214887.

11-JUL-2000; 2000US-021487.

14-AUG-2000; 2000US-0225213.

14-AUG-2000; 2000US-0225213.

14-AUG-2000; 2000US-0225214.
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PR 14-AUG-2000; 2000US-022526B

PR 14-AUG-2000; 2000US-0225270

PR 14-AUG-2000; 2000US-0225767

PR 14-AUG-2000; 2000US-0225767

PR 14-AUG-2000; 2000US-0225757

PR 14-AUG-2000; 2000US-0225757

PR 12-AUG-2000; 2000US-0225759

PR 22-AUG-2000; 2000US-02256B

PR 22-AUG-2000; 2000US-02256B

PR 22-AUG-2000; 2000US-02256B

PR 23-AUG-2000; 2000US-02258B

PR 23-AUG-2000; 2000US-022981

PR 01-SEP-2000; 2000US-022991

PR 14-SEP-2000; 2000US-023991

PR 14-SEP-2000; 2000US-023144

PR 14-SEP-2000; 2000US-023144

PR 14-SEP-2000; 2000US-023149

PR 14-SEP-2000; 2000US-023149

PR 29-SEP-2000; 2000US-023149

PR 20-CCT-2000; 2000US-0
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Fri Jan 10 12:01:27 2003

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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1) amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins and polynucleotides may be used to produce the secreted (1), by inserting claspinose and treat immune/haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic-derived cells. AAK64703 concers from the present invention. AAK654942 to AAK64950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 23239; 3071pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Barash SC, Ruben SM;
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08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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1;
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                                          699 TIGTTTGTAAAAAAAAAAAAAATAACAAATGTTTAGCTAAACAAAGTAAGAAAAAAG 758
                                                              754 AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                        814 GGAGCAACCTTCCTTTGATTCTTTGATAATGACAGAAGA-TGAACAAAGAGTAAGTTTT 872
                                                                                                             694 TTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23240.
        1; Gaps
       92; Indels
Best Local Similarity 52.6%; Pred. No. 9;
Matches 103; Conservative 0; Mismatches
                                                                                                                                                                                                            AAK68428 standard; DNA; 1761 BP.
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2000US-0220964.
2000US-0224518.
2000US-0224518.
2000US-0225213.
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2000US-0215135
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                                                                                                                                           873 TGAAAATTCTAAAAT 888
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2000US-0226681

3.4%; Score 36.8; DB 22; Length 1761;

Query Match

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20000S - 022824
20000S - 022834
20000S - 0229343
20000S - 0229343
20000S - 0229343
20000S - 0231244
20000S - 0231244
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2000US-0249207
22 - Aug. - 2000 | 22 - Aug. - 2000 | 23 - Aug. - 2000 | 24 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 | 25 - 2000 |
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AAX AAX64951 to AAX64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAAM8120 to AAA91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectic-derived cells. AAK6401 cancers and cancer metastases of haematopoietic-derived cells. AAK6401 to AAK878494 represent human immune/haematopoietic acids ind AAK6402 sequences from the present invention. AKK6442 to AAK6400 and AAK81699.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     694 TICTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 23240; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.4%; Score 36.8; DB 22; Length 1761; Best Local Similarity 52.6%; Pred. No. 9; Matches 103; Conservative 0; Mismatches 92; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1761 BP; 809 A; 297 C; 253 G; 402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben SM
17-NOV-2000; 2000US-0249208.
17-NOV-2000; 2000US-0249209.
17-NOV-2000; 2000US-0249210.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249211.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249218.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-0249245.
17-NOV-2000; 2000US-024929.
17-NOV-2000; 2000US-0250391.
01-DEC-2000; 2000US-0251988.
05-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-483426/52.
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RESULT 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, angiogenesis, methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; mancular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.
814 GGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGA-TGAACAAAGAGTAAGTTTT 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                   DB 24; Length 7857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human angiogenesis associated polynucleotide SEQ ID NO 105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7857 BP; 2110 A; 218 C; 2100 G; 3429 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 105; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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54.4%; Pred. No. 16;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ67075 standard; DNA; 7857 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                             873 TGAAAATTCTAAAAT 888
                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-500450/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-JUN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ67075;
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 46
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The present sequence is the genome sequence of Listeria monocytogenes EGD-e. This sequence and fragments of this sequence are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and to study genetic polymorphisms and other genomes. Proteins (ABB47297-ABB50149) expressed from the present sequence are monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis, identification of L. biodegradation, especially biosynthesis of Vitamin B12. This sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, this sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organisms.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Cetcuani F, Nedjari H, Glaser P, Kunst F, Cossart P; Geobel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; sernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; T, Domann E, Hain T, Berroe P, Charbit A, Durant L; J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and
Sequence 2944528 BP; 914202 A; 563301 C; 555061 G; 911964 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                   Listeria monocytogenes EGD-e genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 1; 192pp; French.
                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                              ABA03041 standard; DNA; 2944528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dussurget O, Chetouani F, I
Daniels J, Goebel W, Krefet
Dominguez-Bernal G, Garridor
Chakraborty T, Domann E, Hi
Perez-Diaz J, Baquero F, Gs
Maduenio E, De Pablos B, W
Rose M, Voss H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-APR-2000; 2000FR-0004629.
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                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                            3627 AAGGTAGGTGGATTAT 3642
                                                                                      949 TCGGTAGTAGGAATAT 964
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listeria monocytogenes.
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related polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200177335-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Buchrieser C,
                                                                                                                                                                                                                                                                                                              05-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-OCT-2001.
                                                                                                                                                                                                                                                                   ABA03041;
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Length 2944528;

DB 24;

3.4%; Score 36.8;

Query Match

829 TIGATICITIGATAATGACAGAAGATGAACAAAGAGTAAGTITITIGAAAAATTCIAAAAT 888

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0; Gaps

Indels

62;

Local Similarity 54.49 les 74, Conservative

Matches

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Query Match

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2501177 AAAAGGACACTGTGGGGGGGAATTATGAAGAAAAAAATAACTATATTGATGTTAAGTATA 2501118
                                                                                                                                                                                 2501117 ACAGCCGCACTACTCCTTGCATCGT-GTGGAAATGATACGACAACTGATATGAATAATGA 2501059
                                                                                                                                                                                                                                                                      bb 2501058 AACAACAAAAAACGGAAAATAAATCGCAAGCGCCTCTAACGATTACAGATATGGCCGGGCG 2500999
                       Ϊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the oplynucleotide which comprises a 1'-end sequence of a polynucleotide which comprises a 1'-end sequence of sequence complementary to a polynucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence; where the complementary to a sequence/3'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length CDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs -
                                                                479 AAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAATTATCTTTATCGAGAGTTCGCATT 538
                                                                                                                                                       539 ACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAGACAAGTATTGATGGGGAGCTACA 598
                                                                                                                                                                                                                                               599 AATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCT 658
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto J;
                       ;;
Best Local Similarity 51.4%; Pred. No. 1.3e+02;
Matches 109; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID 4186; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                             Db 2500998 TGATGTTTTTTTTAAAAAACCAGAACGAA 2500967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ogai T, Nishikawa T, Hayashi K, S.
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cDNA clone (5'-primer) SEQ ID NO:4186.
                                                                                                                                                                                                                                                                                                                                 659 TGATGGTCTAAGAAATCAGAAAGGAGGCGGAA 690
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in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-iength cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH1842 represent human cDNA sequences; AAB92446 to AAH13631 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                     816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New KUZ polypeptides, members of the ADAM family of metalloprotease - useful in neural partitioning and development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kuzbanian; kuz; neurogenic; KUZ protein; neuronal partitioning;
development; WOTCH protein processing; regulation; cell function;
signal transduction pathways; screening; receptor binding;
metalloprotease; soluble; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence is that of the human soluble (lacking a transmembrane domain) Kuzbanian gene, a neurogenic gene. THE KUZ protein that it encodes is involved in neuronal partitioning and development. It is also involved in processing
                                                                                                                                                                                                          .;
0
                                                                                                                                                                              DB 22; Length 771;
                                                                                                                                                                                                          Indels
                                                                                                                                                 Sequence 771 BP; 246 A; 131 C; 124 G; 264 T; 6 other;
                                                                                                                                                                                                        29;
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                                                                                                                                                                            Score 36.6; DF
Pred. No. 7.5;
                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens soluble kuzbanian (kuz) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/product= KU2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Pages 37-38; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                              876 AAAATTCTAAAATAGAAATGCAT 898
                                                                                                                                                                                                                                                                                                                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                                                               AAV22649 standard; cDNA; 2098
                                                                                                                                                                              3.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US15099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                             1 Similarity 65.19
54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-179428/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9808933-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1997;
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29-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                             AAV22649;
                                                                                                                                                                               Query Match
                                                                                                                                                                                             Local
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AAV22649/c
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                                                                                                                                                                                                                                                       816 AGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGA 875
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of the NOTCH protein by cleaving the C-terminal portion. The KUZ protein can be used to screen for compounds that alter binding of KUZ to its receptor or the cleavage of the NOTCH protein, hence acting to requlate NOTCH signal transduction pathways and regulate cell functions.
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                                                                                                                    Sequence 2098 BP; 655 A; 353 C; 380 G; 710 T; 0 other;
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, Sugiyama T, Wakamatsu A, Nagai K,
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AAH17997 standard; cDNA; 2333 BP.
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12-740G-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-02813776.
09-JUN-2000; 2000JP-02418999.
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the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the fill-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH3633 to AAH1872 represent human cDNA sequences; AAB92446 to AAH13639 represent human amino acid sequences; and AAH3629 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the present invention.
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3.6 161625 2 AC121072 3.6 168710 9 AC021849 3.6 167353 2 AC1224471 3.6 178012 2 AC02467 3.6 192938 2 AC103908 3.6 19285 2 AC103908 3.6 208952 2 AC113302 3.6 208973 2 AC0265 3.6 208973 2 AC02663 3.6 256774 2 AC116964 3.6 256774 2 AC116964	ALIGNMENTS X349679 1089 bp equence 202 from Patent W00202606 X349679 1 GI:18615446 hlamydophila pneumoniae. hlamydophila pneumoniae acteria; Chlamydiae acteria; Chlamydiae neuti, G. and Grandi, G. munnisation against Chlamydia pneatent: W0 0202666-A 202 10-JAN-20 hiron S.p.A. (IT) Location/Qualifiers 1. 1099 is core 1086; Ab_xref="taxon:81558" 315 a 249 c 171 g 354	Similarity 100.0%; Douglands to Conservative 0; Mismatche 0; Conservative 0; Mismatche 0; Mismatche 111111111111111111111111111111111111
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AC119741 Homo sapi AC010640 Homo sapi AC008517 Homo sapi AF276990 Canis fam AC104182 Homo sapi AC024977 Homo sapi AC113169 Homo sapi AC131509 Homo sapi AC097700 Mus muscu AY040092 Dictyoste AX281209 Sequence	AX356482 Sequence AX458561 Sequence AC080017 Mus muscu AL355610 Human DNA AC097502 Human DNA AC107505 Rattus no AC107362 Rattus no AC107362 Rattus no AC107362 Rattus no AL160292 Human DNA AC1073761 Homo sapi AC1073761 Homo sapi AC012013 Homo sapi AC012013 Homo sapi AC01216784 Medicago AC012014 Homo sapi AC12366 Mus muscu AC021367 Human DNA AC12368 ACAPIOSPE CONTINUATION (4 Of AC091378 Rattus no CONTINUATION (3 Of AC109245 Rattus no AC10924 Rattus no AC10945 Rattus no AC10945 Rattus no AC10945 Rattus no AC1094660 Dictycyctes	AC069221 DATE OF CANADA ACO SADA MAND SADA ACO SADA MAND SADA ACO SADA SEQUENCE ACIO SADA SADA SADA ACO SA

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Chlamydophila pneumoniae CWL029
Chlamydophila pneumoniae CWL029
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1 (bases 1 to 10847)
Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W., Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.
Comparative genomes of Chlamydia pneumoniae and C. trachomatis
Nat. Genet. 21 (4), 385-389 (1999)
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Direct Submission
Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
1. 10847
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                                                                                                                                                                                          487
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                                                                                                                                                                       TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCTAA
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ALETICIPEDELATIONS OLD PPPODHS OGSISSPSKLRVLAITFLVFGMLLLISG
ALETICIPEDELATISTICA ALGOVILAS OLD PPPODHS OGSISSPSKLRVLAITFLVFGMLLLISG
ALETICIPEDELATISTICA ALGOVILANG SCHAMAGE ALETIOV REBELIPED PEGVSL
APSEEPALOAAG ATLACH ALGOVILANG ORD ALGOVILANG ALGOVILAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1306 AAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTATCGAGAGTTCGCATTAC 1365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1006 CTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCCAAGTTCCTG 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           946 ATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAAT 1005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TAACAGACCTTGGTCGAGCATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCAAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 GCTFTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGTAGGGTTTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421 TCCCATGTTTATGAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 CTGATCCAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 1086; DB 1; Length 10847; Best Local Similarity 100.0%; Pred. No. 4e-244; Matches 1086; Conservative 0; Mismatches 0; Indels 0;
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BSVPWILMFPLOGTPLQDOPPISFWEVLRTIATARYVFREMVRLAGGAFTIVEQQT
1CFLAGANSIFYGEKLITVENNDIDEDAEMIKLLGLIPRESFGIERGNFCYANNS"
3790. 4938
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IPGGLLTCPLTFLISDVWBIFGPRKARVMIFSAFIANLLASSIVQIFMFFPYASPEM
OTAWHGLEDLSBLRFLASLLAFTVSQQLDIVLYTFFRNRTPNSSLWLRSNGSTWISQI
PDTFIVDCILXFGMGLSFPQTLNIMFYSYIYKITFCVLTTPLEYLAVNTIRKFLGMP
2816. 3811.
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hydroxylase family protein"
hydroxylase family protein"
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YRILLOSRESHEWGISILEFFNALLFVHLISLSKNQREGCSTDMAVSTPF
NRNLMSYRESHKSYCPREFDYLEARGLISDFLHOLHOLHOFFEEDTHESYPV
SGFVARHOYLSLGORYPPIASWURTLDKONFSIPPDIHOLHOLHOLHOFFSEF
INMGRILTATWIEKVORIPERSKORIQTLGNDLIHOLHOFFSEF
INMGRILTATWIEKVORIPERDOJIRLAPORTSEF
VILSSPORELGHAFTDNVKVLPEEDOJIRLAPORTSEF
VLISSPORELGHAFTDNVKVLPEEDOJIRLAPORTSEF
MMLDOGILESIPLYNORKYLSGFEVLCQ"
                                                                                                                                                                                                                                                                                                                                                                                                                 //occe="biopterin-dependent aromatic amino acid hydroxylase family protein; identified by match to PFAM protein family HWM PF00351"
                                                                                                        /translation-"MGSSMHVGVIGCSGRTGKVIVSALEGSSEYTLGPGFSRSSALTL
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OVKOEDWGEBYEVGQRDSSKRTIEVGSSRVGDIPGEHEVAPISSGDQILVRHTVFSRN
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PID:490219 GB:U00096; identified by sequence similarity;
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/gene="CP0807"
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/product="conserved"
/pro
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/codon_start=1
/transl_table=11
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/3790. /arr
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2816. 3211
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/gene="CP0808"
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832. .1920
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/gene="CP0806"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE002240 22589 bp DNA linear BCT 30-MAY-2000 Chlamydophila pneumoniae AR39, section 68 of 94 of the complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1846 TIGICICAGCITITAGAGCAATCITCAGAATATACITITGGGTCCAGGGTTCTCTCGCAGAA 1905
                                                                                                    961 ATATGGGGTCGAGTATGCACGTTGGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGA 1020
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                                                                                                                                                                                                        841 TAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTT 900
                                                                                                                                                                                                                                                                                                                                                  781 AAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGA
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Chlamydophila pneumoniae AR39
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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/note="synonym: Chlamydia pneumoniae AR39"
complement(161. .955)
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Nucleic Acids Res. 28 (6), 1397-1406 (2000)
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/gene="CP0805"
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AE002240.2 GI:8163502
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AE002240/c
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AUTHORS
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CVESKEITVTGSSQLQRRPMAPLLQALRNFGASFHFSSDKSVLPFTMSGPLRSAYSDV
EGSDGQFASALAYAGCSTATIEPKERWPDLSLWAMEKHLHFSGSDYTYSF
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GDSR.HNTACVRTPRNYQTLAIMERRIEBCHDNYSMMSTHKRKYFARGSFG
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                                                                                                                   100.0%; Score 1086; DB 1;
100.0%; Pred. No. 3.7e-244;
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                                                                                                                                 Similarity 100.
6; Conservative
                                                                                                                                          Matches 1086;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP002548 325865 bp DNA linear BCT 25-MAY-2002
Chlamydophila pneumoniae J138 genomic DNA, complete sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shirai,M., Hirakawa,H., Kimoto,M., Tabuchi,M., Kishi,F., Ouchi,K., Shiba,T., Ishii,K., Hattori,M., Kuhara,S. and Nakazawa,T. Comparison of Whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWLO29 from USA
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Shiral, M. Direct Submission
Direct Submission
Submitted (04-JUL-2000) Mutsunori Shiral, Yamaguchi University School of Medicine, Department of Microbiology; 1-1-1
Minamikogushi, Ube, Yamaguchi 75-8505, Japan (E-mail:mshiral@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-227, Fax:81-836-22-2415)
On or abefore Sep 15, 2000 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                    AP002548 AB033788 AB033789 AB033799 AB033791 AB033818 AB036083 AB036084 AB036084 AB036085 AB036088 AB036089 AB038350 AB0038351 AB038352 BA000008 AB038352 BA0005848.2 EACO02648.2
                                                                                                            /db_xrref="taxon:138677"
/note="grnonym:Chlamydia pneumoniae (strain J138)"
221. .1318
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                                                                         Chlamydophila pneumoniae J138 (strain:J138) DNA.
Chlamydophila pneumoniae J138
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
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221. 1318
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/trans1_table=11
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/translation="MIQVTCDQKNYEVLEGTTAAELAKQLKNSHQFIGVLINERPRDL

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                                                                                                                  295293 TIGGCAAAGTACCTCAAAACCAGAAAGATATTTCTCTTGATTGTAAAGGGGAATTGATTC 295352
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                                                                                                                                                                                                                                                                                                295473 CTGATCCAATTCTAAAGGGAAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTG 295532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 295713 TCCCATGTTTATGAAAAATCAGAAAATGAGGGATGTAGAAGCCAAGGCACGTGCCCTAA 295772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 TATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTGAAGAGTCT 420
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                                                                                                                                                                                61 TAACAGACCTTGGTCGAGCATCCATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAA 120
                                                                                           1 TTGGCAAAGTACCTCAAAACCAGAAAGATATTTCTCTTGATTGTAAAGGGGAATTGATTC
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     Length 325865;
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Query Match 100.0%; Score 1086; DB 1; Best Local Similarity 100.0%; Pred. No. 2.7e-244; Matches 1086; Conservative 0; Mismatches 0;
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Homos sapiens, clone Nell Zimis
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E (bases 1 to 15112)
E (b
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Homo sapiens clone RP11-21M15, WORKING DRAFT SEQUENCE, 5 unordered
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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*NOTE: This is a "working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary caps between the contigs are represented as runitars of N, but the exact sizes of the gaps are unknown. This secord will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center clone name: 21_M15
Center clone name: 21_M15
Sequencing vector: M13; M77815; 2% of reads
Sequencing vector: Plasmid; n/a; 98% of reads
Sequencing vector: Plasmid; n/a; 98% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 140254 bases at least Q40
Consensus quality: 140194 bases at least Q20
Consensus quality: 140194 bases at least Q20
Insert size: 150000; agarose-fp
Insert size: 150720; sum-of-contigs
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                                                                                                                                                                                                                                                                                                         AC015814
AC015814 GI:13940724
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Pri
1 (bases 1 to 151120)
1012 GGAAAG 1017
                                                         848 GTGAGG 843
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                                                                                                                                                        RESULT 6
AC015814
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                                       1088 RRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCCCTCGACCTGCAGCCAGCTCGGAATT 1029
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          1021 ITGICICAGCITIAGAGCAAICTICAGAAIATACTITGGGTCCAGGGTTCTCGCAGTA 1080
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                                                                                                                                                                                                                                                                                                                                                           linear
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Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fourbox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
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Sequence 14 from patent US 5670367.
166494.1 GI:2724471
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1491 c 1486 g
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1. 193804
/Organism=Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
/map="15621.1"
/clone="RP11-40816"
/clone="RP11-40816"
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RP11-691911 AC064813, RP11-313A9 AC025843 and CTD-2150N2
AC023905. Data from overlapping BACs were added and the consensus sequence was determined from RP11-408J6 to the extent possible"
           2 (bases I to 193804)
Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S.,
Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A.,
Discheft, R., Traicoff, R. and Hood, L.
Direct Submission
Submitted (28-NOV-2000) Multimegabase Sequencing Center, Institute
for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA
98105, USA
                                                                                                                                                                                                                                                             Rowen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A., Madan, A., Nebitt, R., Traicoff, R. and Hood, L.

Direct Submission
Submitted (22-MAR-2001) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA
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                                                                                                                                                                                                                                                                                                                                                                                                            98105, USA
On Mar 22, 2001 this sequence version replaced gi:11386266.
Center: Multimegabase Sequencing Center
Center code: UNMSC
Web site: http://chroma.mbt.washington.edu/msg_www
Contact: leerowen6systemsbiology.org
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10350. .104040
113550. .13700
110550. .13700
110705. .193804
110705. .193804
1152960. .152980
1152960. .152980
110404 quality data"
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misc_feature 177480. .193804

Anote="overlap with CTD-2050N2, AC023905"

BASE COUNT 57860 a 35778 c 37171 g 62995 t
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Homo sapiens chromosome 15 clone RP11-408J6 map 15q21.1, complete
sequence.
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1 (bases 1 to 19380).

Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A., Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13385 AAATCCAAAATTAGTACAAGGAGAAAAATAGCAAAGATCAAAGCAAAAATAAAATA 13444
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4931 5030: gap of 100 bp 5031 89503: contig of 80373 bp in length 85904 86003: gap of 100 bp 86004 97975: contig of 11073 bp in length 9797 98077 147748: contig of 49672 bp in length 147749 14748: contig of 49672 bp in length 147749 14748: contig of 3272 bp in length 151120: contig of 3272 bp in length Location/Qualifiers
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                                                                                                                                                                                                                                              /organism="Homo sapiens"
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1. -4930
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47047 a 27918 c 27085 g 48670 t
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5031..85903
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147849..151120
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ACO84882.2 GI:13430989
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1464 TCTTCAAAATTTCTAGTATAGAAATACGCTGACTGGAAAGTAGTAATGAGACATTCTTGC 1405
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1. .1531
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Caenorhabditis elegans
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AF119388/c
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FELLERHCGYSENNIPQLEDICKFLKAKTGFRVRPVAGYLSARDFLAGLAYRYFFCTO
YVRHHADPPTYFEDTYHFLMGHMALFADPDFAQFSQEIGLASLGASEEDLKKLATLY
FFSIERGLSSDDAANSPYKENGSNHERFKVYGAGLLSSAGELQHAVBGSATIIRFDPI
RVVEQECLITTFQSAYFYTRNFEEAQOKLRMFTNNWKRPFIVRYNPYTESVEVLNNSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDSIFQMASAMKFQYYSKKAAGKTWSNSVSMSSDNRWEDFKRRF
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SSTIRPTAIREQTTEGSSDDATTGSEWFPKSIYDLDICAKRVIMYGAGLDADHFGFKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
birect Submission
Submitted (16 MAR-1999) Department of Molecular Biology/Department
of Genetics, Massachusetts General Hospital/Harvard Medical School,
Boston, MA 02114, USA
Location/Qualifiers
                                                                                                                                                                                                            Db 104432 AGGTGAAAAAGGAAACATTAAAACTGACACCACAGTAATACAACGATCACAAGAGACTAT 104373
                                                            113 TCATCAAAATGTCTTATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGA 172
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                            658 TTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCT 717
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                                                                                                                                                                                                                                                                        DD 104372 TATGAACAACTGTATACCAACAAATTGGAAAATCTAGAAAA 104331
                                                                                                                                                                                                                                                     838 TGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAA 879
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Matches 249;
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KEYWORDS
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AF119388 1531 bp mRNA linear INV 23-MAY-1999
Caenorhabditis elegans phenylalanine hydroxylase (KO8F8.4) mRNA,
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Submitted (12-7AN-1999) Dept. of Biology, University of San Diego,
5998 Alcala Park, San Diego, CA 92110, USA
Location/Qualifiers
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Loer,C.M., Davidson,B. and McKerrow,J.
A phenylalanine hydroxylase gene from the nematode Caenorhabditis elegans is expressed in the hypodermis
J. Neurogenet. (1999) In press
2 (bases 1 to 1531)
                                      1284 CCATTITCTTITACIGGAG-AATCGGCAGCGICATCAGACGAGAGACCAAATTCAATGGA 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1113 İGACCCATGAGCTCGTGAACGGTGTCTGGAGTGTAAAAATGGATCGGCATGATGG 1054
                                                                                                                                                                                                                                                                                                                                                                                                              1225 AAAGAAGTAGAGGTTGCAAGCTTCTTCAAA-----TCTTCCTCTGATGCTCCAAGA 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         473 TGCCCTAAAAGGTCATGGATGAGATCAGGAGTTAAGGAGAAATTATCTTTTATCGAGAGTT 532
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                                                                                                               233 AGTICCIGAGGAGAACIGATAAGAACGGCTCCATAIGCTTTTCTTCCTTCATGGTTTTCA 292
                                                                                                                                                                                                                                   293 ATAAGICCGCTTTCAACAGTAAACCAAAAGCAGCGTACAATAGCGATCAGATTGCTTTGT 352
                                                                                                                                                                                                                                                                                                                                                      353 AGGGTTTGTATGCGTTGTTTTTACTAGGAAGAGCTTGTACTTTTTCTATGACTTTAGTG 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          413 AAGAGTCTTCCCATGTTTATGAAAAATTCAGAAAATGAGGGATGTAGAAGCCAAGGCACG 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            993 GATAAGTATCGGCGACTGGGCGAACACGGAATCCAGTTTTGCTTTCAAAAACTTGCAG 934
1053 cGaacgtattgagtgcagaagagacacacgatatgcaagacctgccaagaaatcacgagct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       533 CGCATTACAGAGGCAATGGGAAAGTAACGGTCCTGCAACAGAACAAGTATTGATGGGGA
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unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone KOBFB. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone KOBFB is at 260B1 in sequence Z66499.

The true right end of clone KOBFB is at 101 in sequence Z66499.

The start of this sequence (1. .100) overlaps with the end of sequence Z66499.

The end of this sequence (41146. .41246) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(14261. __14391,14466. __14841,15072. __15294,15377. __15633,
15707. __15805,15894. __16013)
/gene="K08F8.2"
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15707. 15805,15894. 16013)
/gene="K08F8.2"
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Location/Qualifiers
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RLTHHEAMAPLVTGEPTYPGKHITTAAAIPGADESECGGGYFDDGFIYBEBEFPDTV
ABILDPVRSGNFETBGVKAPRLHSIQEEVGRAMEINRMGTDQVYIKNPTASCNNLFER
RRAVHLSIPRVYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence Z68314.
For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?nmmpaex(08F8)
IMPORTANT: This sequence is www ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contains similarity to Pfam domain: PP00069 (Eukaryotic protein kinase domain), Score=215.4, E-value-2.8e-61, N=1 comes from this gene cDNA EST EMBL: M8996 comes from this gene cDNA EST yill867.3 comes from this gene cDNA EST yill867.5 comes from this gene cDNA EST yill867.5 comes from this gene cDNA EST yill367.5 comes from this gene cDNA EST yill5107.5 comes from this gene cDNA EST yill510.5 comes from this gene cDNA EST yill510.5 comes from this gene cDNA EST yill507.5 comes from this gene
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8333. .8410,8631. .8755,8864. .9078,9128. .9346)
/gene="KO8F8.1"

    .41246
    .70.ganism="Caenorhabditis elegans"
/db_xref="taxon:6239"
/chromosome="II"

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                                                                                                                                                            /note="similar to sequences presented in GenBank Accession
Numbers C65545 and C55069; phenylalanine-4-hydroxylase;
phe-4-monooxygenase; PAH; PheH"
                                                                                                                                                                                                                                                                                                               /product="phenylalanine hydroxylase"
/product="phenylalanine hydroxylase"
/product="gl:4883167"
/db_xref="gl:4883167"
/db_xref="gl:4883167"
/db_xref="gl:4883167"
/db_xref="gl:4883167"
/reaslation="MPPAGDDLDFLKYAMESYVADVNADIGKTTIVFTLREKAGALA
ETLKLEQAHDVNLSHIESRPSRLAKDAMRCSELLAADHPGFKDMTYRERRKF
FADIARNEKHGBK TPTITYTDEETATWRTYVNELTWYPKNACQEENYTFPLLQONG
FGPDRIPQLQDVSDFLKTTITYTDEETATWRTYVNELTWYPKNACQEENYTFPLLQONG
FGPDRIPQLGHVGLASVEGLAADVERGAGGSGEGIGAASLGAADFRYFHSAPY
YTPEPDICHELLGHVPLADVEFGAGGSGEGIGAASLGAADFRYFHTEVQPKTALTYWTIEFGIG
QQDGEKKAXGAGLLSSFGEGLAALSORFELYANSTORFLASSF
ASAKNKLKSWAATINRPFQIRYNAYTQRVEILDKVAALQRLARDIRSDISTLEEBALGK
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Submitted (12-007-1995) Nematode Sequencing Project, Sanger
Institute, Hinton, Cambridge (210 15A, England and Department of
Genetics, Mashington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode wustl.edu
On Dec 12, 1996 this sequence wustl.edu from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
available information.
Current sequence finishing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1132 AAAAGTCCGGCTCCGTAAGCTTTTTTCTCCCCATCTTGTTGACAGATTCCAAATT 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 ATAAGAACGCCTCCATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCAACA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 TCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAACTG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.2%; Score 45.6; DB 3; Length 1531;
59.1%; Pred. NO. 2.5;
Live 0; Mismatches 54; Indels 0; Gaps
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                                                                              /function="biopterin-dependent aromatic amino acid
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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2 (bases 1 to 41246)
                                              /EC_number="1.14.16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 g
                                                                                                                                                                                                                                                                                             /codon_start=]
                                                                                                                            hydroxylase"
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Best Local Similarity 59.14
Matches 78; Conservative
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CEKO8F8
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AUTHORS
TITLE
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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ECATVALNGSVTQLDGGPVKSIMVLCRKEMAETMLI"
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Uppublished
Cobklob. Kim, D. and Roe, B.A.
Shaull,S., Kim,D. and Roe,B.A.
Direct Submission
Submitted (16-MAY-2002) Department of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 (bases 1 to 109206)
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Direct Submission
Submitted (23-AuG-2002) Department Of Chemistry And Biochemistry,
The University of Oxlahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25306 TCAAAATCTACAACTTCCGGCTTATCACTCAACGCATATTGAAGCTCTCCAAATGAACTC 25365
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1 (bases 1 to 109206)
Shaull,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,
Cook,D., Kim,D. and Roe,B.A.
Medicago truncatula BAC Clone mth2-34p9
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HTG; HTGS_PHASE2; HTGS_DRAFT.
barrel medic.
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Best Local Similarity 59.1%;
Matches 78; Conservative
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complement(join(24990. .25164,25210. .25439,25484. .25610,
25786. .25921,25972. .26168,26281. .26443,26496. .26688,
27097. .27213,47309. .27344))

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RSPDSSTDVMMPOPLOPGCSSYTQOIGOPARSGTPOPPYLOAVQGEPSLIEAALISQRRB
SPVPPOSTTBHISGLNSPRHTGNKSDCESYSSASFSYSHSSEDHSNYSNKSPOYVD
RRRRNNABAARRCRANRRAVFEYRSRRVQLLEGENDDLRTQIETLKAEIAHFKSVLAOR
ASVYTALHP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(18851. .19061,19149. .19267,19316. .19421,
19473. .19561,19609. .19713,19799. .19939,19989. .20176,
20245. .20482,20530. .20599,20934. .21022))
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//gene=**K08P82. 28. Zimilarity to pfam domain: PF00852
//note=**contains similarity to pfam domain: PF00852
CDNA EST yk78d11.3 comes from this gene
CDNA EST yk78d11.5 comes from this gene
CDNA EST yk34d045.3 comes from this gene
CDNA EST yk34d045.5 comes from this gene
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cDNA EST yk273b10.5 comes from this gene"
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/db_xref="GI:3979833"
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/db_xref="GI:3878362"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This is a "working draft" sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 5534 5734 app of unknown length 5535 1734; app of unknown length 15442 26435; contig of 11394 bp in length 15442 26435; contig of 11394 bp in length 26436 26535; app of unknown length 1543 26335; contig of 11394 bp in length 1543 26335; contig of 11896 bp in length 1543 26335; contig of 11896 bp in length 1543 26335; contig of lenknown length 1543 26335; contig of lenknown length 1543 26335; contig of 1865 bp in length 58432 26331; app of unknown length 1543 26335; contig of 50675 bp in length 15832 109206; contig of 50675 bp in length.
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/clone=lb=mkdicago truncatula BAC library H2"
37237 a 17162 c 18248 g 36159 t 400 others
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ilarity 46.1%; Pred. No. 1.6; Conservative 0; Masmatches 179; Indels 0;
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/db_xref="taxon:3880"
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Sequence 22 from Patent W00111061.
AX083744 AX083744.1 GI:13185472
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1. .109206
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/note="consensus sequence of A.t., L.a., and B.n. FAE1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 ATTCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCTTATTGAAAATAAAGTCT 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               400 NNNGTIMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKNKKMWTYYKWKANNCKWRA 459
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Matches 114; Conservative 369; Mismatches 541; Indels 17;
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1 (bases 1 to 1141)
Kunst.L. and Clemens, S.
Regulation of embryonic transcription in plants
Pacant: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
Location/Qualifiers
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/db_xref="taxon:32630"
1. .1141
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11.0%; Pred. No.
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ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping afforts:
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons EST and cDNA sequences. Genes demonstrate at least two exons continuity across the splice lunctions. Sequences continuity across the splice junctions. Sequences that maintained sequence identical matches are annotated as similar.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tictagacag(C)aatgacaata
ctrittgaaa(C)tattatattg
gcattggttg(C)aacaggcccc
gcattggttg(C)acaggcccc
aaagactggtg(C)acaggattgg
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atattacctt(()taaaaattt
                                                                                                                                                                                                                                                                                                                                                      Submitted (11-JUL-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 11, 2001 this sequence version replaced gi:13492990.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                               Direct Submission Submission Submission Submitted (03-MAR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 172246)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171130
2.13165e-05
0.00600713
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Fraction of Phrap values less than 40:
Number of consensus changing edits:
Number of N's in consensus:
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ttctagacag(n)aatgacaata
ctctttgaaa(n)tattatattg
ggcatggtg(n)nacaggcccc
gcatggtgn(n)acaggcccca
aagaactggtgn(n)acaggcccca
tatattacct(a)ataaaaatnt
atattaccta(a)taaaaaatnt
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                                                           1 to 172246)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                       Worley, K.C.
Direct Submission
Direct Submission
Unpublished
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106704
106705
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Enkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

In (bases 1 to 17224)

Mary D.M., Adams, C., Addo-Oduola, B., Ali-Canno, F. Allen, C.,

Mary, D.M., Adams, C., Mado-Oduola, B., Ali-Canno, F., Buck, J.,

Benton, J., Birteva, M., Brawher, E., Brown, M., Bryant, N.P., Burk, J.,

Benton, J., Birteva, M., Browner, E., Brown, M., Bryant, N.P.,

Burch, P., Burkett, C., Burrell, K.L., Byta, N.C., Cleveland, C., Chen, Z., Coyle, M.D., Dathornes, S.R., Delaney, K. R., David, M. L., Davis, C.,

Davy, Carroll, L., Dederich, D.A., Delaney, K. R., Davis, M. L., Davis, C.,

Day, Carroll, L., Daderich, D.A., Delaney, K. R., Davis, M. L., Davis, C.,

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Elhaj, C., Emerling, S., Escotto, M., Falls, T., Berrad, C.C.,

Elhaj, C., Barring, S., Hamilton, K. J., Brander, C., Harris, M. Garner, T., Garnell, J. H., Guerara, M.

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Hadylak, P., Huber, J., Hullyk, S., Hume, J., Icshikhes, I., Jackson, L. E.,

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Loulsegad, H., Locado, R.J., Lu, X. M. Leal, B., Lee, E., Lewis, L.,

Marindale, A., Marthell, T., Wohabbak, R., Manhell, S., Massey, E., Mawhiney, E., Mccod, M. M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC024941 172246 bp DNA linear PRI 11-JUL-2001
Homo sapiens 12 BAC RP11-900F13 (Roswell Park Cancer Institute
Human BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                      983 WMITTRIIWYAATRWKINNAIGSMIRCNAIGWKNNNYWIGWKIRWIAYRMAIRWKAWWK 1042
                                                                                                                                                                                                                                                                                                                                                  984 GGAGTGATTGGCTGTTCTGGAAGAACAGGGAAAGTGATTGTCTCAGCTTTAGAGCAATCT 1043
   863 BAYTNNNNNRMAYYGAYADDYAYYMSDTCDAWMKWDATKMNNATTYNRGTAWRTNNNNN 922
                                                                       923 NMTMKTKYYBHAAWNNNNNGKMCTAHTWWVCKATKTTKGCWMNCTTTCRKYKNNCTWT
                                                                                                                                                                                                           924 CITIATITICCTTTTGTAGAATGATTCGGTAGTAGGAATATGGGGTCGAGTATGCACTT
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DEFINITION RESULT 13 AC024941

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VERSION KEYWORDS

ORGANISM

AUTHORS

REFERENCE

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AC034170 180563 bp DNA linear HTG 20-APR-2000 Homo sapiens chromosome 12 clone RP11-674J5, *** SEQUENCING IN PROGRESS ***, 89 unordered pieces.
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Materston, R.H.
Direct Submission
Submitted (04-APR-2000) Genome Sequencing Center, Washington
Noiversity School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 20, 2000 this sequence version replaced gi:7579885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180563)
Waterston, R. H.
                                                                                                                                                                   618 AGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
                                                                                                                                                                                                                   678 AAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                                                                                                                      738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 89 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: WUGSC
                                                                            DB 9; Length 172246;
                                                                                                                                                                                                                                                                                                                                                       Ouery Match
4 1%; Score 45; DB 9; Length 172;
Best Local Similarity 49.8%; Pred: No. 2.1; Indels
Matches 114; Conservative 0; Mismatches 115; Indels
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AC034170.3 GI:7622528
HTG; HTGS_PHASE1.
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ttttaaaaat(t)tatgottagt
ctctgactcc(t)tagottagtg
cttaacttat(a)aatgotgtag
acactctgct(c)atctgocctgg
caagactgaa(t)tc...
                                                                                                                                                               Distribution of Quality < 40 Bases ---
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Phrap Value Range
                    taataaaaal(n)tatgcttagt
ctctgactco(c)tagcttagty
cttaacttat(n)aatgctgtag
acactctgc(n)atctgcctgg
cagactgaa(a)tt....
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complement(836, .852)
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Location/Qualifiers
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# n i m i m i m i m i m i m i m i m i m i	100494; gap of unknown length 102562; contig of 2068 bp in 102567; contig of 2945 bp in 105607; contig of 2945 bp in 105607; contig of 2945 bp in 105707; gap of unknown length 108535; contig of 2828 bp in 11168; contig of 2533 bp in 111440; contig of 2533 bp in 114140; gap of unknown length 117073; contig of 2933 bp in 117073; contig of 2933 bp in 117173; gap of unknown length 119936; contig of 2933 bp in 117173; gap of unknown length 119936; contig of 2063 bp in 123089; contig of 2063 bp in 123189; gap of unknown length 125696; contig of 2507 bp in 125796; gap of unknown length 12569; contig of 2507 bp in 125796; gap of unknown length 12652; contig of 2826 bp in 128722; gap of unknown length
contig of 730 bp in length gap of unknown length contig of 688 bp in length contig of 705 bp in length contig of 705 bp in length contig of 705 bp in length contig of 713 bp in length gap of unknown length end of 1189 bp in length gap of unknown length contig of 755 bp in length gap of unknown length contig of 755 bp in length gap of unknown length contig of 755 bp in length gap of unknown length contig of 758 bp in length gap of unknown length contig of 758 bp in length gap of unknown length contig of 702 bp in length gap of unknown length contig of 1056 bp in length gap of unknown length gap of unknown length contig of 542 bp in length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length contig of 1038 bp in length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length gap of unknown length contig of 1038 bp in length gap of unknown length contig of 1038 bp in length gap of unknown length contig of 1038 bp in length gap of unknown length contig of 1048 bp in length gap of unknown length contig of 1048 bp in length gap of unknown length length contig of 1048 bp in length gap of unknown length length length length gap of unknown length len	gap continued and a continued
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/trans_ation="myrels.rnvs.perlifex.syknivkkDLODKFNKSIITINIA SRILTENNKKWYKXIYTSIFSGNKNPOKRERKNEEBNQKDNTKVDNDNNMENEMENH DDS.DDDPMDDLANDKWRHNSLEBRIKEYYTLTDPSSOGEENNSFKKLKLINNILDE VHSDLLINNSYTDGSIFSPELVPISVLSTMTLACPPIGTVTLPYINRINFLNNILDE NIHTEHDLKIFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product-"predicted integral membrane protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5186 ATAATAATAATTATAATTTTATAAATAATTATCATGTAATGCTATATTATTACATGT 5245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 673 ATCAGAAAGGACCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTT 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          733 CCATAGAGAAAACCGTGAGGAAAGGAGTCGATAACCATAAATTCCGATTAAAAAGGGAGT 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                793 GCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAG 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       853 ATGAACAAAGAGTAAGTTTTGAAAAATTCTA----AAATAGAAATGCATTTGTGTCGA 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%; Score 44.8; DB 3; Length 12029; 47.7%; Pred. No. 3.1; tive 1; Mismatches 173; Indels 5;
                                                                                                                                                                                                                            complement (4238. .4798)
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9309. 10001
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Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 12029)

2 dardner, M., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L., Koonin, E.V., Shallom, S., Mason, C., Lai, Z., Schwartz, D.C., Pertea, M., Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O., Fasser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L. Chromosome 2 sequence of the human malaria parasite plasmodium Science 282 (5391), 1126-1132 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE001431 12029 bp DNA linear INV 16-APR-2002 Plasmodium falciparum chromosome 2, section 68 of 73 of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="pFB0975c"
/note="pFEMP1 fragment; identified by sequence similarity;
putative; weak similarity to DBL1 domain of PEMP1"
                                                                                                                                                                                                                                                                                                                       Db 114415 AGGAAAAAAGCTTTTCAAAATTGGATTAATCAATAATAGCATGAGTGACGAATAGTATTG 114474
                                                                                                                                                                                                                                                                                                                                                                                                                 Db 114475 AAAGTATTCAAGTAAAAATTAGATAATCATGAAATAACTTTCTACCCAGTGTGTAAATG 114534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 114535 TTGAATTCCCTGAGTTGTAAATGGTAGCCTGCTATTTCCATAAGAAAAACATCCCCCATC 114594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 12029)
Gardner, M.J.
Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
1. 12029
                                                                                                                                                                                                                                                                                                                                                                       678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                                                                                                              618 AGGAAAAATGTTTTTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGGGGTGCTTA 797
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 114595 CCTCCTGTCCACCTGGGACATAGCCCTGCTCTTGTTCAGTTTAAAGGA 114643
                                                                                                                                                                                       DB 2; Length 180563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    798 CAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGA 846
contig of 3222 bp in length gap of unknown length contig of 3286 bp in length gap of unknown length contig of 3201 bp in length gap of unknown length gap of unknown length contig of 4290 bp in length
                                                                                                                                                                                                         ed. No. 2.1;
Mismatches 115; Indels
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/gene="PFB0980w"
2754. ?£^^
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135330:
135430:
138631:
138731:
143021:
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Best Local Similarity 49.8%;
Matches 114; Conservative
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AE001431 AE001362
AE001431.1 GI:38
                       131945
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138732
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AE001431
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TION Plasmodium falciparum MAL4P2, complete sequence.

AL033475

N AL033475

SHTG; DNA polymerase alpha; DnaJ; flap exonuclease; protein
plossphatase; replication A protein; ribosomal protein; ribosomal protein; rifin; transcription factor; var.

Plasmodium falciparum 3D7.

ISM Plasmodium falciparum 3D7.

Elkaryota; Alvoolata; Apicomplexa; Haemosporida; Plasmodium:

Devlin, K., Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Olin, M. and Barrell, B.

L Shhmitson

L Shhmitson
                                                                                                                                                                                                                                                                         Direct Submission

Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium,
The Sanger Centre, Wellcome Trust Genome Campus, Hinkton, Cambridge
CB10 1SA, UK
On Dec 12, 1999 this sequence version replaced gi:5731898.
For more information about this sequence or the Malaria Project,
see http://www.sanger.ac.uk/Projects/P.falciparum. IMPORFANT: This
sequence is not the entire insert of clone MALA22. It may be
shorter because we only sequence overlapping sections once, or
longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5644. .6063
/gene="MAL4P2.02"
/note="WAL4P2.02, very hypothetical protein, len: 139 aa"
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> 1130 aa, contains NKSKPDD repeat sequence"
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-tract upstream of MAL4P2.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Plasmodium falciparum 3D7'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1. .3390)
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complement(1. .3390)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="MAL4P2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="3D7"
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          RESULT 17
PFMAL4P2/c
                                                             DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                            HSA343706 783 bp DNA linear PRI 18-JUL-2002
Homo sapiens genomic sequence surrounding NotI site, clone
NR5-FITR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1'to 783)
Zabarovsky,E.R.
Direct Submissary.
Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Rarolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
1 (bases 1 to 783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGCIICACCIAAIAIACAIAATICTICCAGNGIACAIAIAIAIATAICAAAAAAA 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    891 AAATGCATTTGTCGAGCTAAAGCTTGCTTCTTTATTTTCCTTTTGTAGAATGATTC 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         714 ATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTC---GATACCATA 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             831 GATICITIGATAATGACAGAAGATGAACAAGAGTAAGTITITGAAAAATICTAAAATAG 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 CTGCTTGATGGTCTAAGAAATCAGAAAGGAGCCGAAAGCTTCTAAGTAATCAAGAAAA 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 AATICCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTT 830
            396 ACAACCCCATGAAAAAGGAAGGGCTATAGAATACCCATCTATTAACCAATAAATGGTTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 783;
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                                                                                      of the human genome
Nucleic Acids Res. 30 (14), 3163-3170 (2002)
                                                                 908 GCTAAAGCTTGCTTCTTTTTTTTCCTTTTGTAGAATGATT 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 154;
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Pred. No. 5.8;
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1. 783
/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="NR5-FI7R"
a 154.c 141 g 202 n
                                                                                                                                                                                                                                                                     AJ343706.1 GI:15918898
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Best Local Similarity 48.7%;
Matches 149; Conservative
                                                                                                                                                                                                                                                                                                      Homo sapiens.
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576 GGGAAT 581
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8065. :8070 //gene="Mark4P2.03" //note="potential splice donor sequence, caa/gtaaaa, for exon 5 of Mark4P2.03" exon 5 of Mark4P2.03" //note="predicted splice acceptor sequence for exon 6 of Mark4P2.03" //note="predicted splice acceptor sequence for exon 6 of Mark4P2.03" //note="potential splice donor sequence, cag/gtagga, for exon 6 of Mark4P2.03" //note="potential splice donor sequence, cag/gtagga, for exon 6 of Mark4P2.03"	acceptor sequence for exon 7 donor sequence, tat/gtatat, f	//note="predicted splice acceptor sequence for exon 8 or MALAP2.03" 9610. 9615. 9610. 9615. //note="predicted splice donor sequence, acc/gtaaat, for exon 8 of MALAP2.03" //note="mALAP2.03" //note="alternative splice donor sequence, acc/gtaaat, for exon 8 of MALAP2.03" //note="alternative splice donor sequence, acc/gtaaat, for exon 8 of MALAP2.03" //note="mALAP2.03" //note="mALAP2.03" //note="predicted splice acceptor sequence for exon 9 f MALAP2.03" //note="predicted splice acceptor sequence for exon 9 f	e splice acceptor sequence fo splice donor sequence, cac/gt 03".	splice donor sequence, aag/gtaata, fc 2.03" splice acceptor sequence for exon 11	tch 4.1%; Score 44.2; DB 3; Length 234112; sol Similarity 50.2%; Pred. No. 3.1; Oscoretyative 0; Mismatches 108; Indels 0; Gaps 0; ACAGGAGAGAGATTGATGGGAGATCTGAAATCTGGAAAAGGGGAAAAATGGGAAAAAGGGAAAAAATGGGAAAAAGGGAAAAAA	TITCTAATICGAAGAATITAAIGACTGCTTGAIGGTCTAAGAAATCAGAAAGGAGACCGA 689
misc_feature misc_feature misc_feature		misc_feature misc_feature misc_feature	misc_feature misc_feature	misc_feature misc_feature	Query Match Best Local Simil Matches 109; C QY 570 ACAGAGAC OY 222724 ATAAAAAT	0y 630 TTTCTAAT
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misc_feature gene	CDS		misc_feature	misc_feature misc_feature	misc_feature misc_feature	misc_feature

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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                     ACO08008 167257 bp DNA linear PRI 16-MAY-2002 Homo sapiens Xp22 PAC RPCI6-102 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
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Submitted (16-Man 2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 30, 1999 this sequence version replaced gi:5441911.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.

Direct Submission (Submission)

Submitted (30-JUL-1999) Human Genome Sequencing Center, Department Submitted (30-JUL-1999) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

( pases 1 to 16725)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submitted (10-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 167257)
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Worldy,K.C.

Direct Submission
Submitted (31-JUL-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

5 (bases 1 to 167257)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Worley, K.C.
Direct Submission
Submitted (09-OCT-1999) Human Genome Sequencing Center, Departmen Submitted (19-OCT-1999) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA

( bases 1 to 167257)
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                      Db 222544 ATAAAAATTTTAATTAAATAACAAAAAAAAAAAAA 222508
750 AGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAA 786
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2 (bases 1 to 167257)
Worley, K.C.
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Worley, K.C.
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Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Proports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT-

Distribution of Quality < 40 Bases

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10001	1006	8001	1007

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758 AGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAG 817
                 698 AAGTAATCAAGAAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGG 757
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0; Mismatches 155; Indels
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/db_xref="dbS7S:64811"
complement(8394..8628)
/rpt_famlly="Alusg"
complement(9633..9771)
/rpt_famlly="MIR"
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3178. ..3178. ..3178. ..3178. ..3178. ..3178. ..3178. ..3178. ...
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... family="L2"
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complement(11720. .11846)
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complement(11924. .12374)
/rpt_family="MER31B"
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'110, 7102
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/rpt_family="Charlie5"
1531. .1578
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/rpt_family="MIR"
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7144. .7353
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1244. .11549
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2470. .2525
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/rpt_family="L
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PRI 01-MAR-2002
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Submitted (20-0CT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 198230)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-OCT-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 198230)
Sulston,J.E. and Waterston,R.
Homo sapiens BAC clone RP11-510H11 from 2, complete sequence. AC092662 AC02578 AC092662.2 GI:16303564 HTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (19-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
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Harris,A., Abbott,A., Dixon,R., Dignan,G. and Phillips,A.
The sequence of Homo sapiens BAC clone RPl1-510Hll
Upublished (2001)
3 (bases 1 to 198230)
Waterston,R.H.
                                                                                       818 CAACCTTCCCTTTGATTCTTTGATAATGACAAGATGAACAAAGAGTAAGT 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998)
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Drafting Center: WIBR
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Waterston, R.H.
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6 (bases 1 to 198230)
Waterston, R.
Direct Submission
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AC092662
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Length 198230;
                                                                                                /683. .7843 ... / / / note="sinilar to Homo sapiens EST BE874285 (NID:91023061)" 8827. .8861
7683. .7975
/note="similar to Homo saplens EST BG253627
(NID:912763443)"
7683. .7975
                                                         4.1%; Score 44; DB 9;
46.4%; Pred. No. 3.5;
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008. .17085
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7092. .17417
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9860. .1907.
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23469. 2365.
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6603. .16761
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8846. .9142
/rpt_family="Alu"
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9383. .10565
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24064. 24407
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5066. .16328
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24567. .25448
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0016. .20038
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8268. .19500
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9660. .19697
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5770. 1601
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7423. .17913
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7912. 1777.
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6329. .16602
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6587, 1641
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2152. 1736?
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1347. .9395
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\2528. 13
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                                                                                                                                                                                    MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping on formation of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
                                                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The clone sequenced to the left is RP11-569P21, 2000 bp overlap; the clone sequenced to the right is RP11-727011. Actual start of this clone is at base position 1 of RP11-510H11; actual end is at base position 1.
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Mote="simlar to Homo sapiens EST BE874285
:NDF.g10323061)"
:805. .6607
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/note="similar to Homo sapiens EST BE874285
NID:910323061)"
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/db_xref="taxon:9606"
/chromosome="2"
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3654 .3683
/rpt_family="AT_rich"
3782, .4214
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1. .198230
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4246. .4282
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076. .7108
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                                                                                                                                                                          /organism="synthetic construct"
/db_xxef="taxon:32630"
1. 1141
/note="consensus sequence of A.t., L.a., and B.n. FAE1
                                                                                                                                                                                                                    187 CAATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGA 246
                                                                                          67 ACCTTGGTCGAGCATCCTAATTTTGAAGTGAGTTCTACCAGTTCATCAAAATGTCT 126
                                                                                                                                                        127 TATTGAAAATAAAGTCTCTTGTGGAGTTGATGTATTGAAGGGAAGACGAATAATCTGATC 186
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                              7 AAGTACCTCAAAACCAGAAAGATATTTCTCTTGATTGTAAAGGGGAATTGATTCTAACAG 66
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 0; Mismatches 165; Indels
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Regulation of embryonic transcription in plants
Patent: Wo 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
Location/Qualifiers
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Sequence 22 from Patent W00111061.
AXO83744 1GI:13185472
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Location/Vualifiers
1. 6089
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
1. 219 c. 1585 g. 3023 t.
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648 TAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACGGAAAGCTTCTAAGTAATCAA 707
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Sequence 271 from Patent WO0200927.
AX348846 AX344846.1 GI:18492732
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Submitted (01-MAR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA on Jan 3, 2002 this sequence version replaced gi:16077045.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 14667).
Sulston, J. E. and Waterston, R.
                                                                                                                                                                   62988 CCAAGCTAAAGGTTTTTTTGAAAAGATCAACAAAACTAAACAGACATTTATCTATATG 62929
                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate
                                                                                                                                                                                                                                                          738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                         678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
618 AGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAG 677
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4444 Forest Park Parkway, St.
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Homo sapiens BAC clone RP11-354024 from 4, complete sequence.
ACO93810 ACO23636
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Kalicki, J. and Hagjund, K.
Kalicki, J. and Hagjund, K.
The sequence of Homo sapiens BAC clone RP11-354024
Unpublished (2001)
3 (bases 1 to 146671)
Waterston, R.H.
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Waterston, R.H.
Direct Submission
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AC093810/c
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Submitted (28-APR-2000) Shih-Feng Tsai, National Yang-Ming
Submitted (28-APR-2000) Shih-Feng Tsai, National Yang-Ming
University, Institute of Genetics: 155 Li-Rong St. Section 2,
Peitou, Taipel, Taiwan 11221, Republic of China
These sequences are draft human sequence. Yn these sequences are represented as 100 N.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AP001943 88966 bp DNA linear HTG 09-AUG-2000 Homo sapiens chromosome 4 clone 2185P9 map 4q22-q24, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 88966)
                                                                                                                  Gaps
                                                                               801 CAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAA 860
                                                                                                                                                                                                         861 AGAGTAAGTTTTTGAAAAATTCTAAAATAGAAATGCATTTGTGTCGAGCTAAAGCTTGCT 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Pred. No. 5.9;
0; Mismatches 88; Indels 0;
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AP001943.1 GI:7678833
HTG; HTGS_PHASE1.
Homo sapiens DNA, clone:2185P9.
                                                                                                                                                                                                                                                                                                                                                                                                           1050 TAATCAAATTTTTATTTCAAAAAT 1026
                                                                                                                                                                                                                                                                                                                                              921 TCTCTTTATTTTCCTTTTGTAGAAT 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /map="4q22-q24"
/clone="2185P9"
a 15563 c 16501
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Matches 96; Conservative
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ORIGIN
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VERSION
KEYWORDS
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AP001943/c
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AUTHORS
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JOURNAL
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Louis,

Louis,

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Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC087607; the clone sequenced to
the right is RPI1-484F3, 2000 bp overlap. Actual start of this
clone is at base position 1 of RPI1-354024; actual end is at base
position 34976 of RPI1-484F3.
                                                                                                                                                                                                                                                                          The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao,B., Frengen,E., Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone, and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="ERV1"

/rpt_family="L1"

1644_ 1728

1746_ 2036

//rote="match to EST T41120 (NID:9648688) ya3la05.s2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of AC023636 has been incorporated into AC093810.

Location/Qualifiers

L. .14671

/organism="Homo sapiens"
/dLxref="taxon:9606"
/chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1943. .2237
/note="match to EST T40287 (NID:g647923) ya3le05.r2"
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/rpt_family="AT_rich"
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6532. .6553
/rpt_family="AT_rich"
6748. .6776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -"AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="RP11-354024"
/clone_lib="RPCI-11"
1, 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="ERV1"
341. .503
/rpt_family="ERV1"
515. .667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="ERV1"
681. .1056
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/rpt_family="L1"
4121. .4623
/rpt_family="L1"
4199. .4220
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4891
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4638. 4865
                                                                                                                                                 MAPPING INFORMATION:
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27186. .27799
/rpt_family="L2"
28814. .28850
/rpt_family="AT_rich"
28906. .29115
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32734. 33108
/rpt_family="MaLR"
33109. 33153
                                                                                                                                                                                                                                                                             26984, .27033
'rpt_family="AT_rich"
7186, .27799
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/rpt_family="AT_rich"
)6984. .27033
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10463. .30505
rpt_family="AT_rich"
10555. .31651
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22953. .22993
/rpt_family="(TC)n"
24268. .24346
24359. .24406
                     8370. .8483
/rpt_family="AcHobo"
8562. .8954
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21531. 22139
/rpt_family="ERV1"
22360. 22425
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9150. .29507
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0271.
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33907. .33936
                                                                                                                                                                           'rpt_family="Alu"
6136. .16229
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8968. .9041
/rpt_family="MIR"
                                                                                                         -"MIR"
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7713. .1p^~
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9505. .29527
                                                                                                                              'rpt_family="L1"
5469. .15706
                                                                                                                                               /rpt_family="L1"
15759. 15000
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rpt_family="L1"
8782. .18840
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10903. .21254
                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="L2"
2477. 22646
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1663. .32733
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2109. .32133
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     /rpt_family="L2"
8370. 848?
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                                                                                                        /rpt_family
15296. .154
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29116. .29
repeat_region
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us-09-438-185a-1_1199590_1200675.rge

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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
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                                                                                                                                                           Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                              Worley, K.C.
Direct Submission
                               Gibbs, R.
Direct Submission
Unpublished
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EUKARYOTA: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla: Eutherla; Primates; Catarrhini; Hominidae; Homo.

EL (Dasea: 1 to 158066)

Muzny, D.M., Adams.C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrocks, S.L., Amaratunge, H.C., Arel-J.R., Ayele, M., Banks, T., Barbarda, J., Benton, J., Bimage, K., Blankenburg, K., Bonton, D., Burnell, K.L., Byrd, N.C., Carron, F., Carter, M., Cavazos, S.R., Chacks, J. Chavez, D., Chen, G., Chen, R., Chen, Z., Coyle, M.D., Dathorne, S.R., David, R., Davila, M., Davila, M., L., Davids, C., Davy-Carroll, L., Dederfich, D., Delancy, K.R., Deladaco, D., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Dubtin, K.J., Banhary, K.R., Deladaco, D., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Dubtin, K.J., Earlbary, K., Ganer, T., Garza, N., Gill, R., Gao, L., Ganer, T., Garza, N., Gill, R., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gao, L., Harris, C., Harris, K., Hart, M., Hale, S., Hamilton, K., Hernandaz, J., Hernandaz, O., Hodgeon, A., Hogues, M., Holloway, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, C., Kureshi, A., Landry, N., Molnson, S., Home, J., Joudsh, S., Karlsson, E., Kaelly, S., Khan, U., King, L., Kure, J., Li, Z., Lichtarge, O., Lieu, C., Liu, H., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Mantinez, E., Massey, E., Markine, R., Massey, E., Markine, M., Massey, E., Markin, R., Massey, E., Morgan, M., Moore, S., Woser, M., Moore, S., Organ, M., Moore, S., Organ, M., Moore, S., Organ, M., Moore, S., Ordago, R., Parkin, M., Moore, S., Ordago, R., Parkin, M., Sparks, A., Sodergen, P., Sodergen, C., Shen, H., Shocsheri, M., Stone, H., Suthon, N., Tansey, J., Taylor, T., Tablfrod, B., Thomas, N., Thomas, S., Ushan, S., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC107307 158066 bp DNA linear PRI 31-JUL-2002
Homo sapiens 3 BAC RP11-657G2 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
                                                                                                                                                                                                                                                                                                                                   42648 CCAAGCTAAAAGGTAGGTTTTTTGAAAAGATCAACAAAACTAACAGACATTTATCTATATG 42589
                                                                                                                                                                                                                                                                                                                                                                                                                                        42708 AGAATAATGAAGATTAGAATTAAAAGCAGTGAAATAGAAATTACAATTTTAAAGAATCAA 42649
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                                                                                                                                                                                                                                                                     678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
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Pred. No. 5.6;
0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC107307.3 GI:19774327
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       Query Match
Best Local Similarity 52.2 Matches 96; Conservative
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AC107307/c
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences:
Genes and Replace of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:389-3402) similarity (expect < id-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-FB2-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 158066) Worley, K.C.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 158066)
                                                                                                                                                                                                                                                                                                                                     Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (31-JUL-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 28, 2002 this sequence version replaced gi:18449849. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (OZ-MAY-2002) Human Genome Sequencing Center, Departmen
Submitted (OZ-MAY-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
(Dases 1 to 158066)
                                                                                                                                                                                                                                                                                                                  Submitted (18-JAN-2002) Human Genome Sequencing Center, Departmen of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (based 1 to 188066)
Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and
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repeat_region
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AUTHORS
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AC025807
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Unpublished
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Birten, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
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Howland, J.C., Iliev, T., Johnson, R., Jones, C., Kann, L.,
Klein, J., LaRocque, K., Lanazares, R., Landers, T., Lehoczky, J.,
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Marphy, T., Naylor, J., Norman, C., Mirada, C., Menga, Y., Morrow, J.,
Murphy, T., Naylor, J., Norman, C., Riee, R., P., Sentos, R., Santos, R., Schauer, S., Severy, P., Sperce, N.,
Pisant, C., Pollara, V., Raymond, C., Rilee, R., Sentos, R., Santos, R., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J.,
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Young, G., Zainoun, J., Zimmer, A. and Zody, M.
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HOMO saplens clone RPll-657G2, WORKING DRAFT SEQUENCE, 15 unordered
pieces.
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                                                                                                                                                                                                Score 42.8; DB 9; Length 158066; Pred. No. 6.8;
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Conservative
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Best Local Similarity
Matches 155; Conserv
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CNSO18P0 186158 bp DNA linear PRI 26-APR-2001 Human chromosome 14 DNA sequence BAC R-603H7 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
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/note="assembly_fragment"
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/note="assembly_fragment"
10516. .14122
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2471. .4141
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16505. .22459
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                           Direct Submission
Submitted (14-MAR-2000) Whitehead Institute/MIT Center for Genome Submitted (14-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON MAT 30, 2000 this sequence Version replaced 9i:7239693.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as tuns of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing vector: M13: M77815; 100% of reads Sequencing vector: M13: M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0, 956731 Consensus quality: 155485 bases at least 040 Consensus quality: 155717 bases at least 020 Consensus quality: 157717 bases at least 020 Insert size: 157700; agarose-fp Insert size: 157000; agarose-fp Coulity coverage: 4.8 in 020 bases; agarose-fp Quality coverage: 4.7 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                 p of 100 bp contig of 44688 bp in length.
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1120 2370: contig of 1251 bp in length
1131 2470: gap of 100 bp
2471 4141: contig of 1671 bp in length
4142 4241: gap of 100 bp
4142 4241: gap of 100 bp
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/note="assembly_fragment"
1120. .2370
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/db_xref="taxon:9606"
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Raturo, Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Adiobrooks, S.L., Amaratunge, H.C., Are, J.R., Bonnin, D., Barbaria, J., Benton, J., Berleva, M., Brown, E., Brown, M., Bryat, N. P., Buoke, S., Burch, P., Burkelt, C., Burrell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, Z., Chen, Z., Chow, Y., Chen, Z., Chow, T. Corte, M.D., Dathorre, S.R., David, R., Devida, M.C., Davy-Carroll, L., Dederloh, B., H., Delaney, K.R., Delade, D., Edwards, C., Elhaj, C., Escotto, M., Earlbart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Earlbart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Earlbart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Earlbart, C., Edgar, D., Edwards, C., Elhaj, C., Escotto, M., Earlbart, C., Edgar, M., Hartis, M., Harris, K., Hart, M., Harlak, S., Hanilton, K., Harris, K., Hart, M., Harlak, S., Hamilton, K., Harris, K., Hart, M., Harlak, S., Hamilton, K., Harris, K., Hart, M., Harlak, S., Hume, J., Jackson, L.E., Jacobson, B., Jay, Y., Odnson, R., Hollyk, S., Hume, J., Jackson, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegd, H., Mareson, E., Kalls, Marthall, A., Landry, M., Matchell, T., Mohabbat, K., Morgan, M., Matchell, T., Mohabbat, K., Morgan, M., Mitchell, T., Mohabbat, K., Morgan, M., Mitchell, T., Mohabbat, K., Morgan, M., Noiderson, E., Mawhiney, E., Mackon, E., Markine, E., Mawhiney, E., Mackon, E., Marthalls, E., Marthall, E., Marthalls, M., Marth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188385 bp DNA linear HTG 13-JUL-2002 settus norvegicus clone CH230-30L4, *** SEQUENCING IN PROGRESS ***, 65 unordered pieces.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                     Db 61470 AAAAGACATATACAGATGACAAATAAGCACATGAAAAATGTTAAAAAATCATTAGTTATT 61529
                                                                                                                                                                                                                                                                                                          678 AAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                                                                                                                                               738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                                                                                                                                                                   798 CAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTGTTAATGACAGAAGATGAA 857
                                                                                                                      Gaps
                                                               Length 186158;
                                                                                                                   Indels
                                                            Score 42.8; DB 9; I
Pred. No. 6.7;
0; Mismatches 102;
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                                                               3.9%;
                                                            Query Match 3.99
Best Local Similarity 50.59
Matches 104; Conservative
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Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                         Submitted (26-APR-2001) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr / On Feb 28, 2001 this sequence version replaced gi:11611112.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 186158)
Hellig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottler,P., Cattolico,L., Barbev,V., Pelletier,E., Artiguenave,F., Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C., Sequenciny of the human chromosome 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The following BAC sequence is oriented from the T7 to the SP6 end. Upstream BAC (overlapping the T7 end): R-66E7 Downstream BAC (overlapping the SP6 end): R-423117 (AC=AL513142)
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/note="matching EMBL:T16335
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146274. .146413
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Location/Qualiflers
1. 186158
/Organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap; version 2.0
Quality coverage: 7.54x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
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/clone_lib="RPCI-11"
146268. 144422
/note="matching EMBL:238793
RHdb:RH53848
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dbSTS:STS25118
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1758
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NOTE: This is a "working draft' sequence. It currently consists of 65 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary, gaps between the configs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                2 'Description of the property                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (13-7012.002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced g1:20303170.
     Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williams,G., Williamson,A., Wieczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
Unpublished
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Center: Daylor College of Medicine
Center: Code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project name: GRAP
Center clone name: GRAP
Center clone name: CH230-304
Center clone hame: 12120-304
Center clone hame: 12130-304
Center clone hame: 12130 by core
Sequencing vector: Plasmid:
Chemistry: De-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 132544 bases at least Q40
Consensus quality: 139955 bases at least Q20
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gap of unknown length
contig of 1123 bp in length
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contig of 1075 bp in length
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Direct Submission
Submitted (01-MRA-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916169.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (20-0CT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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HOMO Sapiens BAC clone RP11-20H7 from 2, complete sequence.
ACC92584 AC015490
HUMO STATES OF SEQUENCE.
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Armstrong, J., Kozlowicz, A., Hawkins, M. and Spalding, L. The sequence of Homo sapiens BAC clone RP11-20H7 Unpublished (2001)
3 (bases 1 to 159035)
Waterston, R.H.
: gap of unknown length

: contig of 255 bp in length

: gap of unknown length

:: contig of 3454 bp in length

: gap of unknown length

:: contig of 3807 bp in length
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Genome Res. 8 (11), 1097-1108 (1998)
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Louis
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                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Data from AC068537, AC073994, and AC016827 was used to finish this clone, AC092584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa. K., woon.p.Y., 2hoo.B., Frengen,E. Tateno.M., Catranese,J.G. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from and coworkers at http://www.resgen.com) or Pieter de Jong WECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RPI1-138Cl3, 2000 bp overlap: the clone sequenced to the right is RPI1-2IL7. Actual start of this clone is at base position 1 of RPI1-2OH7; actual end is at base position 159035 of RPI1-2OH7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. 1840. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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Location/Qualifiers
1. .159035
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/chromosome="2"
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550. 2451
/rpt_family="L1"
2031. 2068
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1. .108
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3780. .4131
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4308. .4401
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/rpt_family="L1"
344. .387
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ILIDEIKSLCFDIIVI"
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1 (bases 1 to 2706)
                                                              /rpt_family="L"
31201. 31310
/rpt_family="T-rich"
32226. 33096
/note="similar to Sus scrofa EST BI184750 (NID:g14659159)"
32227. .32588
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                                                                                                                                                                                                                                                                                      21687 GCCAGACAAAAAAAAGATACAAATAAATAAATAAATCAGAAATGAAATGGAG 21628
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                                                                                                                                                                                                                                                                                                                                                                                                        792 IGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTTTGATAATGACAGAA 851
                                                                                                                                                                                                                                                                                                                                    732 TCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGGGAG 791
                                                                                                                                                                                                                                                                  672 AATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTT 731
                                                                                                                                                                                                                                    1; Gaps
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3.9%; Score 42.4; DB 9; Length 159035;
Best Local Similarity 52.8%; Pred. No. 8.5;
Matches 114; Conservative 0; Mismatches 101; Indels 1;
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                                29568. .29848
/rpt_family="Alu"
29849. .32251
28081. .29567
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29568. .29848
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<1. .184
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frote="similar to Homo sapiens EST BE565142
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10104. 10426
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10574. 10605
/rpt_family="(TTTTA)n"
10601. 11026
/rpt_family="L1"
11062. 11958
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/rpt_family="(GAAA)n"
31727. .21845
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19069. .19154
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3365. .13877
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2799. .13336
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1987. .12289
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6515. .7739
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8684. 1900
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9010
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19830. 107-
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:085. .18013
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.8381. .18406
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3879. .14061
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7582. 76?
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family="L1"
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4072. .14232
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1334. .11362
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Joint Genome Institute and Stanford Human Genome Center.
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41323 a 21680 c 22194 g 40813 t
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/db_xref="taxon:9606"
/chromosome="5"
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Homo sapiens chromosome 5 clone CTD-2015B23, complete sequence.
ACO10342
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(bases to 126010)

DOE Joint Genome Institute.

Direct Submission

Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

(bases to 126010)

DOE Joint Genome Institute and Stanford Human Genome Center.
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (28-APR-2001) DOE Joint Genome Institute, 2800 Mitchell
Dive, Walnut Creek, CA 94598, USA
4 (bases 1 to 120010)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 2706;
                                                                                                                                                  /product="RNA polymerase beta-prime subunit"
/protein_id="AAK55949.1"
/db_xrefe"GI:14193387"
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3.9%; Score 42.2; DB 1; Length 2;
Best Local Similarity 50.2%; Pred. No. 15;
Matches 104; Conservative 0; Mismatches 103; Indels
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                                                                                        /codon_start=1
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Direct Submission
Submitted (01-MAY-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94599, USA
On Apr 28, 2001 this sequence version replaced gi:13699503.
Draft Sequence Produced by DOE Joint Genome Institute
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(bases 1 to 141635)
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                                                                                                                                                                                                                                                                                                                                                                                                               www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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0; Mismatches 243; Indels
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Quality: Phrap Quality >=40 99.9% of Sequence;
Estimated Total Number of Errors is 0.1.
STS Content:
SHGC-104285 G58244
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HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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AUTHORS

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ALB07375 192168 bp DNA linear HTG 17-JUL-2002 Mus musculus chromosome X clone RP23-247H23, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.
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Db 118892 CACAIGGAGGTAITATTACAGCCTAAACCCTICAGAAAAAGTITGAAAATCACTA 118833
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43.6%; Pred. No. 9.6;
1 92004: contig of 92004 bp in length 92005 92105; gap of 100 bp 92105 117227: contig of 25123 bp in length 117228 117327: gap of 100 bp 117328 117327: gap of 100 bp 117328 1262034: contig of 3107 bp in length 120535 126202: contig of 6668 bp in length 120535 126202: contig of 5668 bp in length 126303 1292188: contig of 6668 bp in length 129159 131961: contig of 2703 bp in length 131962 132061: gap of 100 bp 129259 131961: contig of 2703 bp in length 132062 135799: contig of 6708 bp in length 13540 135840 141655: contig of 5796 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 243; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="11"
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42227 a 27391 c 27480 g 43740 t
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/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALBO775.5 GI:21738714
HTG: HTGS_PHASE1.
Mus musculus.
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     885 AAATAGAAATG 895
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Best Local Similarity
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AL807375/c
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alloun, J., Zembek, L., Zimmer, A. and Zody, M.
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission

Submitted (24-JAN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

(Escentch, 320 Charles Street, Cambridge, MA 02141, USA

Escentch, 320 Charles Street, Cambridge, MA 02141, USA

(Escentch, L. Bastien, V., Bloom, T., Boqusiavkiy, L., Boukhgalter, B.,
Barna, N., Bastien, V., Bloom, T., Boqusiavkiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Chepel, Y., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S.,
Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Gardyna, S., Graham, L., Grand-Plerre, N., Hagos, B.,
Horton, L., Hulme, W., Illev, I., Johnson, R., Johes, C.,
McCarthy, M., Meddrim, J., Macdonald, P., Major, J., Matthews, C.,
McCarthy, T., Naylor, J., Naylen, C., Nicol, R., Norbu, C., Norman, C.,
Phunkhang, P., Plerre, N., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Roy, A., Schuber, S., Schupback, R., Semen, S., Severy, P.,
Smith, C., Spencer, B., Stanger Thomann, N., Stojanovic, M., Talmas, J.,
Zembek, L., Zimmer, A. and Zody, M. X., Wyman, D., Young, G., Zainoun, J.,
Zembek, L., Zimmer, A. and Zody, M. X., Wyman, D., Young, G., Zainoun, J.,
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                                                                                                                         unpunished
cycleases 1 to 141635)
Birren,B. Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
Barren,B., Linton,L., Nusbaum,C., Lander,L., Boukhgalter,B.,
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Vola, W., Yo,A., Wilson,B., Wu,X., Waman,D., Ye,W.J., Young,G.,
Zainoun,J., Zambek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (24-AuG-2002) Whitehead Institute/MIT Center for Genome Submitted (24-AuG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2002 this sequence Version replaced gi:20336822.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the finished sequence as soon as it is available and the accession number will be preserved.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                               Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone CTD-3038L12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
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JOURNAL
                                        AUTHORS
TITLE
JOURNAL
REFERENCE
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REFERENCE

COMMENT

0

Gaps

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 192168)
Plumb, B.
                                                                                                                                                                                                                Submitted (14.70L-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 188, UK. E-mail enquiries: hunquery6sanger.ac.uk clone requests: clonerequest6sanger ac.uk on Jul 12, 2002 this sequence version replaced gi:21727570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator: 100% of reads
Consensus quality: 189470 bases at least Q40
Consensus quality: 190260 bases at least Q30
Consensus quality: 190881 bases at least Q30
Insert size: 191468; sum-of-contigs
Insert size: 191468; sum-of-contigs
Quality coverage: 6.94x in Q20 bases; sum-of-contigs Quality
Coverage: 6.89x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55214 55313: qap of 100 bp 66635: contig of 1322 bp in length 66636 66735: qap of 100 bp 666736 73181: qap of 100 bp 73081 contig of 6346 bp in length 73082 73181: qap of 73182 118845: contig of 45664 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55213: contig of 55213 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     % foote="assembly_fragment:00648
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73182. 118845
//note="assembly_fragment:01518
fragment_chain:1"
118946. 130156
//note="assembly_fragment:02035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone_end:SP6
                                                                                                                                                 Plumb, B.
Direct Submission
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                                                                                                                                                                                                                          JOURNAL
                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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202801 bp DNA linear HTG 12-AUG-2002 Mus musculus chromosome X clone RP23-146020, *** SEQUENCING IN AL831718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 202801)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 155143 AATGTTGAAAGCAGAAAATCTCAATAACATTAAAAGCAAGGTCAAAGTCTCGAGAAGAA 155084
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D 155083 CACATAGTTACTTCAGGAAATCAATTTTTTTTTTTTTCATGGAAATAAGGGGATATGCTTTAA 155024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (08-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBLO 185, UK. E-mail enquiries: hunquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk on Aug 13, 2002 this sequence version replaced gi:21953128.
                                                                                                                                                                                                                                                                                                                                                          188 AATTCTAAAGGGAGAACACGTACGTTATCAATGAAAGCGTGTCCAAGTTCCTGAGGAGAA 247
                                                                                                                                                                                                                                                                                                                                                                                                                                   248 CTGATAAGAACGCTCCATATGCTTTTCTTCTTCATGGTTTTCAATAAGTCCGCTTTCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATSTITES OI:22213735
HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                   DB 2; Length 192168;
                                                                                                                                                                                                                               703 others
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                     68;
                 130257. 135973. 7.00ce assembly_fragment:01769 fragment_chain:1" 136074. 138937 7.00ce assembly_fragment:01554 fragment_chain:1" 139038. 192168 7.00ce assembly_fragment:02173 fragment_chain:1 clone_end:77
                                                                                                                                                                                                          vector_side:right"
57525 a 37280 c 37166 g 59494 t
                                                                                                                                                                                                                                                                                   Score 42.2; DI
Pred. No. 9.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 ACAGTAAACCAAAAGCAGCGTACAATAGCGA 338
fragment_chain:1"
130257. .135973
                                                                                                                                                                                                                                                                                   3.98;
55.08;
                                                                                                                                                                                                                                                                                                                     83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clark, S.
                     misc_feature
                                                                             misc_feature
                                                                                                                                   misc_feature
                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
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AL831718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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Kawarabayasi, Y., Tanaka, T., Hino, Y. and Kikuchi, H.

Submitted (2-DEC-1999) Yutaka Kawarabayasi, National Institute of
Submitted (2-DEC-1999) Yutaka Kawarabayasi, National Institute of
Submitted (2-DEC-1999) Yutaka Kawarabayasi, Nishihara 2-49-10,
Technology and Evaluation, Bitechnology Center; Nishihara 2-49-10,
URL: http://www.bio.nite.go.jp/, Tel:81-3-3481-8951,
Fax:81-3-3481-8824,
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21456156
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Sulfolobus tokodaii
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 190083 AATGTTGAAAGCAGAAAATCTCAATAACATTAAAAGCAAGGTCAAAGTCTCGAGAAGAA 190142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 CTGATAAGAACGCTCCATATGCTTTTCTTCCTTCATGGTTTTCAATAAGTCCGCTTTCA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
          runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Pred. No. 9.2;
0; Mismatches
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Best Local Similarity 55.09
Matches 83; Conservative
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KEYWORDS
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EKBALEPRKINMLYSSLENYYNLGFESQALENLKKMIELKDIIGISSHKDKILPLIK
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IVGEORKEKLSYTVQHLTEELVERKRYEDVIQCLKVARKYMTIEDFNNLLSQIKENYK
RKRQLVSLINKYLS"
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/gene="S11859"
/note="Swiss_Prot:046819 percent identity: 32.759 in 58aa.
motif=prokaryotic membrane lipoprotein lipid attachment
site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"PIR:B69172 percent identity: 24.545 in 110aa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                      /gene="ST1858"
2952. AE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ST1859"
4578. 6/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="ST1860"
6481. .7200
                                                                                                                                                                                                                                                                                                                                                                                                                          2952. .4544
/gene="ST1858"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="ST1860"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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8806. 9507

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8806. 9507

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// gene="ST186953"
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// gene="Gene" general protein"
// gene="General protein"
// general gen
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PGVLLDYKRINIISFITSELIVELLELAGAEELGRRLKVESSRPFFFFLELSLILII
SILLLYRKRINLLLYPLAMTSGPLTRLLIDLGISKHKIGLALFYGSVLNETLILI
SILLLYPLAMTSGPLTRLIDLGISKHKIGLALFYGSVLNETVAVVV
FARIFSKFOILDISILLYVLFFFLGGKINKLLELIEGYWKWRRIEFRYIISYTFIG
SPTLLLSLTFFCFGLLRORPYLLERLAFTYGFFEPLFKYIISYTFIG
SPTLLLSLTFFFSSLAFKRGGGKYKKYRRITRAFYKSFFEPLFKYIISYTFKY
NLTPFYGYSFSSLATFSSLVENLEFRKRFGCKYKTORNKTATROPYVNC
YQTLERAIGIINRGYRALVONDENFRLGYVSSGLLETDRNYVELIKAVCDIYKNEV
KILEKKSKYLDVLRYFRETEEPVVVIVDDOGRILSVVYERELLRYTFIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MSLPWNVNEKNIYFSHOEFMSKISVIKPLYENPDQITITIPSI
| LPLITPRINITEVMETILSFRIFFLYISISLELPLSKYLGGELEKNVSSKTVLYIVLLESIL
| FINTRIGLYTLISILIFFYIYFTHKSKYAPAFSAPASNIYFESVKNSSKTVLKSDL
| RLSPYKMYLELISINSGILFHPFITIYAINKGRVGIIIEVEYYVKDMRNKKFKELLNT
| HPDLUNKSFLISKLNKERHILG"
| complement(10828..12117)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC004854 104-JUN-2002 BNA linear PRI 04-JUN-2002 Homo sapiens PAC clone RP4-673M15 from 7p13-p11.2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98697)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         575 GACAAGTATTGATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCT 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635 AATTCGAAGAATTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCT 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    695 TCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.9%; Score 42.2; DB 1; Length 266050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMKISQIMETRNRTS"

complement(10064. .10783)

complement(10064. .10783)

/gence "ST1863"

/gence "ST1863"

/gence "ST1863"

/gence "ST1863"

/gence "ST3863 long hypothetical protein"

/protein_id="RAB6654."

/db_xrefe"GI:15622965"
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:21322205
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Best Local Similarity 51.38
Matches 98; Conservative
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|11935 TAAAGTTAATA 11925
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AC004854.3
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KEYWORDS
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EST AA057332 (NID:g1550170) zf56all.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST AA057332 (NID:g1550170) zf56all.rl"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST AW131540 (NID:g6133147) xf31b08.x1"
                                                                                                                                                                          oę
                                                                                                                                                                             Actual start
                                                                                                                                                                                                                                     Base positions 19689 to 19719 of the submitted sequence is represented by single chemistry only.

Location/Qualifiers
1. 98697
//organism="Homo sapiens"
//db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST BE727822 (NID:910141814)"
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The library is from one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
VECTOR: pcYPAC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST BE075304 (NID:98424032)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST AA216094 (NID:91816041)"
                                                                                                                                                                       The clone sequenced to the right is DJ0647J21. this clone is at base position 1 of DJ0673M15.
                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="7"
/map="7p13-p11.2"
/clone="RP4-673M15"
/clone_lib="RPCI-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            254. 568
/note="similar to i
554. 857
/rpt_emily="Alu"
862. 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1381. .1662
/rpt_family="L1"
1663. .1954
/rpt_family="Alu"
1673. .1727
/note="similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       886. 1075
/note="similar to
886. 922
/note="similar to
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886. 1075
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/note="similar to
254. .568
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177. .568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="Alu"
3239. .3404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu" 3625. .3935
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2468. .2522
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2912. .3207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (04-JUN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
on Jun 4, 2002 this sequence version replaced gi:4827328.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                       Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
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mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, Afforest Park Avenue, St. Louis, Missouri 63108,
7 (bases 1 to 98697)
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Missouri 63108,
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Center code: WUGSC
                                                                                                                           2 (bases 1 to 98697)
Ozanich,A. and Mead,K.
The sequence of Homo sapiens PAC clone RP4-673M15
Unpublished (2001)
3 (bases 1 to 98697)
Waterston,R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (22-OT-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
( Chases 1 to 98697)
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Contact: saplens@watson.wustl.edu
------- Summary Statistics
Center project name: H_DJ0673M15
                   Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 98697)
Waterston, R.H.
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/note="similar to EST AI183467 (NID:g3734105) qd42b07.x1"
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0; Mismatches 160; Indels
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                                                                                                                                                                                                      7052. 7503

7062. 7503

7064. similar to B

8898. 9026

7074. family."L1"

7076. 9334

7027. 9334

9027. 9334

9027. 9066

9027. 9066

9039. 9519
                                                                                                                              /rpt_family="Alu"
6288. 6427
/rpt_family="MaLR"
6723. 7034
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9627. .9933
/rpt_family="Alu"
9971. .10226
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7052. 7503
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10236. 1020.
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11269. .11542
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11903. 19903
3937. .4238
/rpt_family="Alu"
                            1241. .454<u>2</u>
/rpt_family="Alu"
                                                       549. .4662
/rpt_family="MIR"
1929. .5086
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5667. .5976
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11544. .11877
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/rpt_family="Alu"
10346. .10437
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LOCUS AC108637 124767 bp DNA 11near HTG 13-JUL-2002 DEFINITION Rattus norvegicus clone CH230-276G19, *** SEQUENCING IN PROGRESS

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Rayayb.M., Adams.C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alisbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Bartaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Carron, T., Bovie, S., Briteva, M., Caracos, S. K., Chacko, J., Chavez, D., Chen, G., Chen, G., Chowdhry, I., Christopoulos, C., Coylen, G., Day, Carroll, L., Byd, N.C., Chen, G., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davilla, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Davilla, M.L., Dayer, Carroll, L., Ding, Y. Dinh, H. H., Douthwaite, K.J., Draper, H., Dugan Rocha, S., Durbin, K.J., Earnhard, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., Hernandez, J., Gabisi, M., Gao, J., Garcia, A., Garcia, P., Halla, C., Escotto, M., Call, R., Gabisi, M., Gao, J., Garcia, A., Garrer, T., Garza, N., Galli, R., Hernandez, J., Hoyera, M., Gunratne, P., Hala, S., Hamilton, K.J., Harris, C., Harris, K., Hayle, P., Hala, S., Hamilton, K.J., Harris, C., Harris, K., Hayle, S., Hume, J., Jackson, L.E., Loward, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Loxado, R.J., Lu, X., Lucier, A., Lucier, R., Luua, R., Maylon, S., Krattovic, J., Krattovic, J., Krattovic, J., Krattovic, J., Krattovic, J., Lu, X., Lucier, A., Lucier, R., Luua, R., Maylon, N., Mosser, M., Mortis, S., Massey, E., Mawhiney, E., McLeod, M.P., Macador, M., Mei, G., Metzker, M., Massey, E., Mawhiney, E., McLeod, M.P., Macador, M., Mei, G., Metzker, M., Miner, G., Mitchell, T., Mohabat, K., Morgan, M., Morser, M., Nickerson, J., Newtson, J., Sutch, M., Svatek, A., Rojubcker, S., Staner, S., Savery, G., Scherer, S., Soctt, G., Spark, A., Stanley, H., Stono, H., Sutcher, J., War, F.P., Sutcher, J., War, S., Warten, R., Walliams, G., Williams, S., Warfeld, M., Welse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (13-JUL-2002) Human Genome Sequencing Center, Department Submitted (13-JUL-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:18846705.
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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Center clone name: CH230-276G19
AC108637.3 GI:21737753
HTG; HTGS_PHASE1.
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Worley, K.C.
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723 AATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAA 782
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                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/doss/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                  Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 59885 bases at least Q40
Consensus quality: 65135 bases at least Q40
Consensus quality: 65093 bases at least Q20
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ERGREYGSNTGKPRIGHIDLVALKKYAIRVGGIDQLFLTLFDVLDTEEKIKICTAYKL
DNQITHSIPANENDFKDV"
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HOMO sapiens chromosome 1 clone RP11-711C8 map 1, LOW-PASS SEQUENCE
SAMPLING.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 23;
                                                                                                                                                                                                        1 others
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 1, clone RP11-711C8
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HTG; HTGS_PHASE0.
HOMO Sapiens.
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Direct Submission
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                                                                                                                                                                                                                                                                                                  Query Match
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EMBL. Meyerhofstr.1, 69012 Heidelberg, Germany
E-mail borkembl.heidelberg de
More than 870,477 bases have been sequenced by the genomic walking technique and assembled into 372 non-overlapping contigs (Accession numbers 233005 to 233376) covering 214,528 base pairs. The length of the contigs varies from 63 base pairs to 2049 base pairs with an average length of 58 base pairs. The dength of the contigs varies from 63 base pairs. The length of the contigs varies from 63 base pairs at 2049 base pairs with an average length of 58 base pairs. The length of the contigs varies from 63 base pairs at 2049 bases (4%) from one pass fluorescent sequencing and 201,437 bases (4%) from the pass fluorescent sequencing and 120,637 bases (5%) are covered on both strands. There is a total of 968 ambiguous nucleotide assignments in the data set (6%) are compared 8,686 bases of our data with Mycoplasma capricolum sequences already stored in the public databases and note less than 0.7% difference between the two data sets (100,000 pairs) insertions, deletions and mismatches ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [bases 1 to 363]
[cllevet.P., Ally, A., Barton, F., Brenner, S.E., Clark-Whitehead, R., Dolan, M., Douglas, N., Hau, E., Purzcki, M.S., Richter, B., Russo, S., Sartell, J., Smith, S.W., Wang, C., Williams, J. and Gilbert, W. Direct Submission.

Submitted (13-30L-1994) Mycoplasma capricolum Genome Project, Institute for Computational Sciences and Informatics George Mason University, Cambridge, MA 02138 Prokaryotic Genomes Project Institute for Computational Sciences and Informatics George Mason University, Fairfax, Virginia, USA, 22030-4444 B-mail:

[bases 1 to 363]
[bases 1 to 363]
[bases 2 to 363]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Exploring the Mycoplasma capricolum genome: A Parasite reveals it's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bork,P., Ouzounis,C., Casari,G., Schneider,R., Sander,C., Dolan,M.,
Gilbert,W. and Gillevet,P.M.
Exploring the Mycoplasma capricolum genome: a minimal cell reveals
                                                                                                                                                                                                                                   BCT 10-AUG-1994
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/coplement(<1...553)
/note="emptrified by homology to SwissProt entry swiss|P30520|PURA_HUMAN; Probablity 3.8-33"
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Gillevet,P.
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/product="adenylosuccinate synthetase"
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/transl_table=4
                                                                                                                                                                                                                         363 bp
M.capricolum DNA for CONTIG MC445.
233336
                                                   Db 95237 CCCAAAATACAGCTTGCTTTAGTTGA 95212
                    903 GTCGAGCTAAAGCTTGCTTCTTTA 928
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Mycoplasma capricolum.
Mycoplasma capricolum
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us-09-438-185a-1_1199590_1200675.rge

21785: contig 2865: gap of 2266: contig 23543: contig 643: gap of 2426: contig 2529: gap of 126: gap of 126: gap of 126: gap of 2529: contig 2529: contig 2529: contig 2739: gap of 2730: contig	27,007 27,008 300 300 300 300 300 300 300 300 300	2443: 9ap 3323: 332108: 34108: 9ap 34982: 5863: 9ap 5863: 9ap 35716: 6816: 37591: 9ap	37692 38467; contig of 776 bp in length 38468 3857; gap of 100 bp 38568 39336; contig of 769 bp in length 39437 40436; gap of 100 bp 36437 40184; contig of 748 bp in length 40185 40284; gap of 100 bp 4028 41192 41191; gap of 100 bp in length 41092 41191; gap of 100 bp in length 41043 42042; gap of 100 bp in length 42044 42923; gap of 100 bp 42823; contig of 781 bp in length 42824 42923; gap of 100 bp 42824 43708; contig of 785 bp in length 43824 43808; gap of 100 bp 43809 44860; contig of 772 bp in length 43809 44860; contig of 772 bp in length	44881 44680: app of 100 bp 44681 45425: contig of 745 bp in length 45428 45525: app of 100 bp 45526 45525: app of 7784 bp in length 4510 6409: app of 7784 bp in length 4710 47293: app of 784 bp in length 47293: app of 773 bp in length 47293: app of 773 bp in length 47293: app of 773 bp in length 48932 49031: contig of 773 bp in length 48932 49031: contig of 785 bp in length 49032 49812: contig of 781 bp in length 49033 49032: app of 100 bp in length 49033 49032: contig of 782 bp in length 49033 49032: contig of 782 bp in length 50665: 50764: app of 100 bp 50765: 51522: contig of 758 bp in length 51523: contig of 758 bp in length 51523: contig of 758 bp in length 51533 51243: app of 100 bp 51523: contig of 758 bp in length 51533 52483: sap of 100 bp 6752 bp in length 51533 52483: sap of 100 bp 6753 bp in length 51533 51243: app of 100 bp 6753 bp in length 51533 52483: sap of 100 bp 6753 bp in length 51533 52483 52483 5254: contig of 782 bp in length
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Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	is record contains and reads that Runs of N are order in which order in which and clones that relationships it should not sequenced to c rid is updated,	736 835; contig of 7; 736 835; gap of 100 836 835; gap of 100 1596 1695; gap of 100 2462 2561; gap of 100 2462 2561; gap of 100 3465 3464; gap; contig of 7 4550 4349; cap of 100 4350 5141; contig of 7 5142 5241; gap of 100 5142 5241; gap of 100 5142 5241; gap of 100 5141; contig of 7 5142 5241; gap of 100 5141; contig of 7 5142 5241; gap of 100 5141; contig of 7 5142 5241; gap of 100 5142 5241	8 (177 940 of 100 bp 10	* 12249 12348: gap of 100 bp * 13034 13133: gap of 100 bp * 1304 13133: gap of 100 bp * 13890 13899: contig of 756 bp in length * 13891 13989: gap of 100 bp * 13891 13989: gap of 100 bp * 14815 14914: gap of 100 bp * 14815 15682: contig of 758 bp in length * 15683 15782: gap of 100 bp * 15783 16561: gap of 100 bp * 1662 17452: contig of 779 bp in length * 1652 16661: gap of 100 bp * 1652 1661: gap of 100 bp * 1652 1661: gap of 100 bp * 1753 13152: contig of 76 bp in length * 1817 1912: contig of 76 bp in length * 1817 1912: contig of 76 bp in length * 1913 1929: gap of 100 bp * 20055 20155: gap of 100 bp * 20055 20155: contig of 764 bp in length * 20156 2019: gap of 100 bp * 20156 2019: gap of 100 bp * 20156 2019: contig of 764 bp in length * 20156 2019: contig of 764 bp in length

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/note="japonica cultivar-group"
32490 a 24957 c 25425 g 31751 t 1043 others
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/cultivar="Nipponbare"
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00 Apr 25, 2002 this sequence version replaced gi:2015307.
* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 GCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAAT 715
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                                                                                                                                                                                                                                                84 55983: gap of 100 bp in length 1675: contig of 774 bp in length 168 55632: contig of 775 bp in length 188 57832: gap of 100 bp 100 bp 185512: contig of 775 bp in length 188 55812: contig of 780 bp in length 18 59370: contig of 758 bp in length 189 59370: contig of 758 bp in length 16040: gap of 100 bp 100 bp 116040: contig of 770 bp in length 160340: gap of 100 bp 1160340: gap of 100340: gap
53364: gap of 100 bp
54144: contig of 780 bp in length
54244: gap of 100 bp
55007: contig of 763 bp in length
55107: gap of 100 bp
55883: contig of 776 bp in length
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Human DNA sequence from clone RP11-91K11 on chromosome 1, complete
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* are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

18478 20885: contig of 18477 bp in length 18578 20885: contig of 18477 bp in length 20886 20985: contig of 18477 bp in length 20886 20985: contig of 2308 bp in length 25667 25666: contig of 4981 bp in length 49470 49559: gap of unknown length 49500 52659: contig of 3090 bp in length 52660 52659: contig of 3090 bp in length 52660 82861: contig of 3090 bp in length 52660 82861: contig of 3090 bp in length 82862 110436: contig of 27475 bp in length 11037 110536: gap of unknown length 110537 1105
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AC004153 156060 bp DNA linear HTG 12-AUG-2000 plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (18-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 110223 CAAAAAAAAAAAAATAATAATGATGATAATTCAGATATGGAATGGGAAAATTTCAATCCAC 110282
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                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium. (bayea 1 to 15606)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Mao, J., Tamaki, T., Rudl, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Aug 12, 2000 this sequence version replaced gi:8810454.
* NOTE: This is a "working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T. (bases 1 to 156060)
Hyman, R. W. (Oin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission
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0 102369: gap of unknown length
0 156060: contig of 53691 bp in length.
Location/Qualifiers
1 156060
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Plasmodium falciparum.
Plasmodium falciparum
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AC004153
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                                                                                                                                                Direct Submission

Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

Cambridgeshire, CB10 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk (lone requests: Clonerequest@sanger.ac.uk

on Nov 16, 2001 this sequence version replaced gi.15131273.

During sequence assembly date is comperated from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL: Sw:, SMISSROT; T:: TRRMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human was generated from part of bacterial clone contigs of human professor. Purther information can be found at http://www.sanger.ac.uk/MFC/MISSORCHIP HISTORY FILE TREAFFORMER THEIL STANDER FILE TREAFFORME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMPORTANT: This sequence is not the entire insert of clone strength It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RPI1-91KII is at 126371 in this sequence. The true left end of clone RPI1-460G22 is at 31870 in this sequence. The true right end of clone RPI1-460G22 is at 31870 in this sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 126371)
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0; Mismatches 132;
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                       63911: contig of 6774 bp in length 64011: gap of 100 bp
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54822 54921: gap of 100 bp
54922 57037: contig of 2116 bp in length
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Vector_side_left"

Zu47. :5841

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700te* assembly_fragment:01044

fragment_chain:3"

40193 ... 44742

fragment_chain:4"

fragment_chain:4"

fragment_chain:4"

44843 ... 47640
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    .157515
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/clone_lib="RPCI-11.1"
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57038 63913: contil
63912 64011: gap of
64012 69774: contil
6975 69844: gap of
71952 72651: gap of
72652 75671: gap of
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101918 10969
109694 109793:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukarorea, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 157515)
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On Oct 26, 2000 this sequence version replaced gi:10716373.
Center: Sanger Centre
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4742: contig of 4550 bp in length
42: gap of 100 bp
4740: contig of 2798 bp in length
40: gap of 100 bp
52469: contig of 4729 bp in length
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7540: contig of 5795 bp in length
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40092: contig of 2452 bp in length
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Db 110523 ACAAAAATAAAAATATGAATCATACATCTT 110555
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AL391598.3 GI:11023953
HTG; HTGS_PHASE1; HTGS_DRAFT.
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47741 52
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52570 54
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AL391598/c
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Bukamalia; Butherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 194247)
                                                                                                                                                                                                                Direct Submission
Submitted (24-UL-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (24-UL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Jul 26, 2002 this sequence version replaced g1:21748207.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; Version 4.5

Chemistry: Dye-terminator: 0% of reads
Chemistry: Dye-terminator ET-amersham; 1% of reads
Chemistry: Dye-terminator ET-amersham; 3% of reads
Consensus quality: 1942.7 bases at least Q40
Consensus quality: 1942.7 bases at least Q20
Insert size: 1942.47; sum-of-contigs
Insert size: 1873.47; sum-of-contigs
Unsert size: 1873.46; 12.3% error; agarose-fp
Couplity coverage: 10.76x in Q20 bases; sum-of-contigs Quality
Coverage: 12.13 in Q20 bases; agarose-fp
                                                                 HTG; HTGS_PHASE2; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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/db_xref="taxon:9606"
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PROGRESS ***, in ordered pieces. AL358253
AL358253.14 GI:21998163
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/clone="RP11-460G22"
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Matches 121; Conservative
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                                                                                          Homo sapiens.
                                                                                                                   Homo sapiens
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Statistical Control Collins, S. Collymore A. Chararo, B. Butren, B., Lintcon, L. Barian, N. Bastien, V. Boguslawkiy, L. Boukhgalter'B., Anderson, S. Barna, N. Bastien, V. Boguslawkiy, L. Boukhgalter'B., Concept Y. Colangelo, M. Collins, S. Collymore A. Cook A. Cooke P., DeArellano, M. Collins, S. Collymore A. Cook A. Cooke P., DeArellano, M. Collins, S. Collymore A. Cook A. Cooke P., DeArellano, M. Collins, S. Collymore A. Cook A. Cooke P., DeArellano, M. Collins, S. Collymore A. Cooke P., Berreira, P. FitzHugh, W. Cage, D., Galagan, J. Gardopels, Rand. A. Karatas, A. Kells, C. Hand. S. Collymore A. Cooke, D. Berreira, P. FitzHugh, W. Cage, D., Galagan, J. Gardopels, M. Cooke, P., Bonders, T., Lehoczky, J. Lechick, R. Liu, G. MacLean, C. Macdan, P., McKernan, K., Meldrim, J. Menquis, N. Matquis, C. MacQuis, R. Micha, P. Marquis, N. Matquis, C. MacQuis, M. Morman, C. H. O'Connor, T. O'Connoll, P. O'Nell, D. Oliver, J. Peterson, K. Punkhang, P. Piurkhang, P. Piurkhang, P. Piurkhang, P. Piurkhang, P. Piurkhang, P. Sancos, S. Schopbeck, R. Sedman, S. Sereit, M. Roy, A. Sancos, M. Sancos, M. Palama, J. Terders, M. Subraminan, A. Sancos, M. Sancos, M. Sancos, M. Solamon, C. N. Scolamon, C. Senchope, R. Sedmer, M. Sancos, M. Waman, D. Ye, W. J. Young, G. Sereit, M. Sancos, M. Mardis, M. W. Waman, D. Ye, W. J. Young, G. Janner, A. Walley, M. J. Roy, A. Wilson, B. Wu, X. Waman, D. Ye, W. J. Young, G. Janner, A. Wilson, B. Wu, X. Waman, D. Ye, W. J. Young, G. Charles, Street, Cambridge, MA Ollins, S. Collymore, A. Colarge, DeArellano, W. Bloom, Y. Boguslavkly, L. J. Charderson, S. Barran, N. Bastien, V. Bloom, T. Boguslavkly, L. J. Gradeler, B. Brown, A. Bastien, V. Bloom, T. Gardeler, S. Dodge, S. Gooke, P. DeArellano, W. Backer, M. Major, J. Marquis, M. Macdana, C. Reper, P. Macdonald, P. Major, J. Marquis, M. Macdonald, P. Major, J. Marquis, M. Major, J. Wallen, W. Jule, R. Winger, J. Peterson, R. Phunkhang, P. Pitzhigh, W. York, Waman, J. Researth, N. Subramanian, A. Sancos, S. Theodore, J. Col
                                                                                                                                                                                      AC109165 200279 bp DNA linear HTG 25-APR-2002
Mus musculus clone RP23-30B3, WORKING DRAFT SEQUENCE, 16 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammallis Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2002/9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-30B3
                                                                                                                                                                                                                                                                                                      AC109165.3 GI:20303726
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
MUS musculus.
Mus musculus.
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Db 13383 TACACAGTCTTGC 13395
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SOURCE
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DEFINITION
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AC109165/c
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All repeats were identified using Repeatuasker:

Smit, A.F. & Green, P. (1995-199)

Intp://ftp.genome.washington.edu/RW/RepeatWasker.html

Concern: Michaed Institute/ MIT Center for Genome Research

Web Sit Content Sequence.semblastons designed

Content project Information (A. 1997)

Content project name: 10,833

Content project Information (A. 1997)

Content project name: 10,833

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Content project information (A. 1997)

Content project name: 10,833

Content project name: 1,833

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DDLASAVKALKSSDWSIDESSLETYVPKVADDLKNSFGHIFAGIYEKYAANLAKRCA
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (31-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostellum/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostellum/project.shtml
                                                                                          Glockner, G. Eichinger, L., Szafranski, K., Pachebat, J., Dear, P., Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and
                                                                                                                                                                                                                                                                                          Submitted (05-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 27785)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agency:
Agency:
Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                        Sequence and Analysis of Chromosome 2 of Dictyostelium Unpublished
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Dictyostelium discoideum
Dictyostelium discoideum
Eukaryota; Woetozoa; Dictyosteliida; Dictyostelium.
1 (bases 1 to 27785)
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DNLASVKÄLKSSSDWSIDESSLETYVPRVADDLKNSFGHIFAGTYBKVANANTARROM
DNLASVKÄLKSSSDWSIDESSLETYVPRVADDLKNSFGHIFAGTYBKVANANTARROM
DDEMILEAVQBATTNHTIVIKHDANLNAHWSWSFESGNIVITFKSYTNTNDVQTFDFIK
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DNLSAVKRALKSSBWSIDESSLETVPKVADDLKNSFGHIFPGIVEKVANLAKRCA
DEMILEAVQEATHNIYIYIKHDANLANHWSNSFESGAIVIIFKSYTNTNDVQTFDFIK
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DNLSAVKRALKSGSSDWSIDELSLETVYPKVADDLKNSFGHIFAGIVEKVAANLARRCA
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/note="ORE_ID:dd_00708"
/codon_start=1
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complement(join(14916. .15729,15822. .15844))
/note="ORF_ID:dd_00706"
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/note="ORF_ID:dd_00707"
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/LTGATELT OF MIND WAS ARK GOLAKIKKY I PGTKFKV DELDKENRS I LHHAIDG DOLOWYNT LLEGGAN INKLEDKENPELLEGFT LMELKER INAIDKOEDLA LLEVNG ADLDVE SREKKIV PETALA PASPATOVLLAGTAGLP PSREKNVER V POKATA PASSATOVLLAGTAGLP PSREKNVER V POKATA PASSATOVLLAGTAGLP PSREKNVER V POKATA PASSATOVLLAGTAGLP PSREKNVER V POKATA PASSATOVLLAGTAGLP PSREKNVER V POKATA PREMDLILOES LLGDD DKEQDLNII WELST GESTLEG STEN RETOR PROTOKORAN STREAT SER LAGE STEN STEN SETTS FROM STATE PROTOK TRANDEST TEN SETTS FROM STATE PROTOK TRANDEST TREPEDAR KLSDSC PVI SETTS KLMY TRY PROTOK TRANDEST TREPEDAR KLSDSC PVI SETTS KLMY TAV TRY PEDAR KLSDSC PVI SETT SETT TRY TRY TRY TRY PEDAR V GONLSSKEBRELNESANOLR SINNK SDITTTTTTTTN SENNNITOLI
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Ekcrednnkngvlakivereosisniasci.ppegveliefcislfrunillystylek
Elektrednnkngvlakivereosisniasci.ppegveliefcislfrunillystylek
Inenvindosilk (folipwilkivensyrecepisylensiinleyilkcokkivknu)
Pinykslpmyytnenbrinnynkleitheselpselinlevtskomkryknyn
Pinykslpmyytnenbrinnynkleitheselpselinlevtskomkryknyn
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Penliktronillevelkikeinfollertgeligslloglicettsel
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CATDOGEVYSWGLSVFGOLGHGNKSYLHRKYLOQFVELBRIAQVOGSNFTWNRS
VQGLLYAFGHGEVGCQLGSTEETQHLDFGGRDNHFKYSIPTVKSLETKKIKNNACGHI
HTIVVTDENEVYQWGWGSSGALGLGNKRFQLVPQLITSLSGEEIASITAGEKHTIVVR
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YIKEQSDSLSEEFKDQITNAINCSAHFSTQQLFSVSALICHNRITDISQLGYSSRNIA
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HSLAVSREGDVYSWGRSKEGQLGIGQGYGGSDKVMFVAKPTLIKSLQHERIIKVACGN
FHSLALTDMGKVYEWGQLHRLDESQSSLDIQSTNGLIEMPRLSSQRIIEASVSQYLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              646 TTTAATGACTGCTTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  819 AACCTTCCCTTTGATTCTTTGATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAA 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 ATGGGGAGCTACAAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAA 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                706 AAGAAA-----AAATCTTGGACAATAGCTTTTCCATAGAGAAACCGTGAGAAAGGA 758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         759 GTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 41.6; DB 2; Length 27785; 41.7%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(21354 ..23054,23166 ..23375))
/note="ORF_ID:dd_00710"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(24733. 24739,24851. 27393)
/note="ORF_ID:dd_00704"
/codon_start=1
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/db_xref="GI:21281378"
/note="ORF_ID:dd_00709"
/codon_start=1
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/iote="34 copies 2 mer tt 66% conserved"
32814. 32972
/note="LiPal6 repeat: matches 6010. 6152 of consensus"
complement(34432. 34805)
                                                                         /note="2 copies 40 mer 90% conserved"
4468. .4856
hote="LiME1 repeat: matches 5768. .6163 of consensus"
4891. .8809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat: matches 363. .1016 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7412. .7600
7402e-"LiM4 repeat: matches 3928. .4117 of consensus"
9029. .9351
7note="AluJo repeat: matches 1. .312 of consensus"
11294. .11677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P5 repeat: matches 1263. .5781 of consensus"
6796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lips repeat: matches -265. .1263 of consensus" .18819
                                                                                                                                                                 4891. .5809
/note="LIM4 repeat: matches 4494. .5479 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER5A repeat: matches 151. .188 of consensus"
26883. .27175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27691. 28135
/note="L2 repeat: matches 2268. .2744 of consensus"
83160. .28329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29184. .29623
//note="112 repeat: matches 1472. .1940 of consensus"
29945. .30376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="L2 repeat: matches 2271. .2748 of consensus" 31294. .31361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="L2 repeat: matches 1942. .2132 of consensus"
8334. .28945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="12 repeat: matches 2700. .2745 of consensus"
19427. .19450
//note="12 copies 2 mer tt 100% conserved"
19814. .19891
                                                                                                                                                                                                                                                                                                                                                                                   2 repeat: matches 2341. .2736 of consensus"
12171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2 repeat: matches 2699. .2746 of consensus"
12962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 4. .234 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Alusx repeat: matches 1. .289 of consensus" (6797, .18337
                                                                                                                                                                                                                    5894. .6201
/note="AluY repeat: matches 1. .296 of consensus"
                                                                                                                                                                                                                                                               5235. ,7203
/note="LTR5 repeat: matches 1. ,969 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13024 ...te="17 copies 2 mer ta 88% conserved" //note="LIP5 repeat: matot
                                                                                                                                                                                                                                                                                                                                                                                                                                                /notes 32 copies 2 mer ct 68% conserved"
12338. 12384
                    2570. 2989
/note="match: GSS: Em:AQ175736"
2718. 2797
               /note="match: GSS: Em:AQ499128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MER4D rep
  complement(2145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MER4D
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18333. 1881
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12929. 120
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/note="L2 |
12108. .12
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Direct Submission

Direct Submission

Direct Submission

Submitted (15-FEB-2000) Sanger Centre, Hinxton, Cambridgeshire, Submitted (15-FEB-2000)

COBO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Feb 7, 2000 this sequence version replaced gi:678223.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the together within not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                               Human DNA sequence from clone RP1-39M18 on chromosome 6q26-27.

Contains part of the PDE10A gene for phosphodiesterase 10A, ESTS, SISS and GSSs, complete sequence.
AL136130
AL136130, G1:6911361
HTG; PDE10A; phosphodiesterase.
Homo sapiens.
Enkarvaters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The following abbreviations are used to associate primary accession mubers given in the feature table with their source databases:
Em:, EMBL; Sw.; SWISSPOT: Tr:, TREMBL; Wp:, WORMPEP. Information on the WORMPEP database can be found at their source action of the WORMPEP. Information on the WORMPEP database can be found at chromosome from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at the Norwasian is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further works.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMPORANT: This sequence is not the entire insert of clone RP1-38MH8 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone RP1-38MH8 is at 1 in this sequence. The true left end of clone RP1-38MH8 is at 69575 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Laird,G.
                                                /note="MIR repeat: matches 158. .206 of consensus" 1502. .1595
                              879 ATTCTAAAATAGAAAIGCATTTGTGTCGAGCTAAAAGCTTGCTTCTCTTTATTTTCCTTTT
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/note="47 copies 2 mer tt 61% conserved"
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/db_xref="taxon:9606"
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/map="q26-27"
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/clone_lib="RPCI-1"
57. .110
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KEYWORDS
SOURCE
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718 TGGACAATAGCTTTTCCATAGAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCG 777

68183 GCTCTACTACTGTATAAATATATAAAACTTTAATTAGGACAAGCATCTTTTAGAGGCTA 68124

qq

qq

778 ATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTT 837

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AGREE - Coptes to matches 2592. 2665 of consensus"
AGREE - Coptes to matches 2592. 2665 of consensus"
AGREE - TIGGERI repeat: matches 2220. 2414 of consensus"
AGREE - TIGGERI repeat: matches 3.300 of consensus"
AGREE - TIGGERI repeat: matches 1.33 of consensus"
AGREE - TIGGERI repeat: matches 1.371 of consensus"
AGREE - TIGGERI repeat: matches 1.371 of consensus"
AGREE - TIGGERI repeat: matches 5582. 6133 of consensus"
AGREE - TIGGERI repeat: matches 5582. 613 of consensus"
AGREE - TIGGERI repeat: matches 5582. 613 of consensus"
AGREE - TIGGERI repeat: matches 5582. 613 of consensus"
AGREE - TIGGERI repeat: matches 5582. 6916 of consensus"
AGREE - TIGGERI REPEAT - TIGGERI REPEA
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                                                                                                      7000-1.2 repeat: matches 1013. .2076 of consensus."
71782. .37446
71016-1.87B repeat: matches 202. .422 of consensus."
71788. .37867
70016-1.2 copies 40 mer 96% conserved."
88780. .38849
/note-"match: GSS: Em:AQ129042"
34047. .35639
.7note-"L1 repeat: matches 3078. .3788 of consensus"
35657. .36708
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OY 838 T-GATAMCGACGAGGAGGAGAAAACTTTAAAGTTTCAAACT 888

DD 68123 GAGATAAAACCACACAAAAAACAAAAACTTTAAACTTTCAACAT 68072

AC115405

AC115406

AC115407

AC115406

AC115407

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us-09-438-185a-1_1199590_1200675.rge

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contig of 1061 bp in length gap of unknown length gap of unknown length contig of 1570 bp in length gap of unknown length gap of unknown length contig of 1831 bp in length gap of unknown length length gap of unknown length gap of unknown length gap of unknown length gap of unknown length length contig of 1855 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 1855 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 1815 bp in length gap of unknown length contig of 1818 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 2855 bp in length gap of unknown length contig of 3824 bp in length gap of unknown length contig of 3824 bp in length gap of unknown length length length gap of 
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1. .103337
Acroganism="Rattus norvegicus"
Abxref="taxon:10116"
/clone="CH230-74F14"
18325 c 18083 g 29634 t
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60863:
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NOTE: This is a "working draft' sequence. It currently consists of 50 configs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the configs are represented as tuns of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                 Direct Submission
Submitted (19-3/UL-2002) Human Genome Sequencing Center, Department
Submitted (19-3/UL-2002) Human Genome Sequencing Center, Department
Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:19549112.

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Center project Information
Center project Information
Center clone name: CM330-4814
                                                                                                                                     Submitted (13-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 1 (bases 1 to 103337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid;
Sequencing vector: plasmid;
Assembly program: Phrap; version 0.990329
Consensus quality: 50186 bases at least Q40
Consensus quality: 53149 bases at least Q30
Consensus quality: 55140 bases at least Q20
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1168: gap of unknown length
2333: contig of 1165 bp in length
2433: gap of unknown length langth
3443: contig of 1101 bp in length
3543: gap of unknown length
4555: contig of 1012 bp in length
4555: contig of 1012 bp in length
4557: contig of 1012 bp in length
4557: contig of 1012 bp in length
547: contig of 102 bp in length
7509: gap of unknown length
7509: gap of unknown length
7509: gap of unknown length
1509: gap of unknown length
1509: contig of 1102 bp in length
1509: gap of unknown length
1189: contig of 1075 bp in length
1189: contig of 131 bp in length
14555: contig of 1831 bp in length
14555: contig of 1848 bp in length
16163: contig of 1868 bp in length
16163: contig of 1868 bp in length
16163: contig of 1868 bp in length
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                                                           2 (bases 1 to 103337)
Worley, K.C.
Direct Submission
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17519:
19034:
              Direct Submission
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 13 clone RP11-78L16, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.

AL334818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 148549)
                                                                                                       57537 TAAAAGGTCCAGAGGAAATTTCCCAAATTCAGAAAATCAGATATGAAAAGGTAGAGGTAG 57596
                                                                                                                                                                                                                                                              91774 TTAGCCAGACCAAAAAGAGAGAGAGAGACCCAAATAAACAAAAACAGAGATAAAAAAG 91833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91714 ACAAAACATCAATGAAACAAAAATTGGTTTTTTTAGAAGATAAATTATGGACAAACCA 91773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (10-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:9581627.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    729 TTTTCCATAGAGAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAGG 788
                                                                             678 AAAGGAGCCCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGCTTTTCCATA 737
                                                                                                                                                           738 GAGAAAACCGTGAGGAAAGGAGTCGATACCATAAATTCCGATTAAAAAAGGGAGTGCTTA 797
                                                                                                                                                                                                                                         798 CAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTTTTGATAATGACAGAAGATGAA 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         669 AGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCTTGGACAATAGC 728
                                           Gaps
  DB 2; Length 103337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS AL353694 Accession AL353694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41.6; DB 2; Length 110000;
Pred. No. 14;
0; Mismatches 69; Indels 0;
  Score 41.6; DB 2; Length 1
Pred. No. 14;
0; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91834 GAGACATTACAACTGATACCACAGAAATTCAA 91865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  789 GAGTGCTTACAACAGCCATATCAGTGGAGCAA 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL354818.3 GI:10039795
HTG; HTGS_PHASE1; HTGS_CANCELLED.
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310000
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  3.8%;
51.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.8%;
Query Match 3.8%
Best Local Similarity 51.6%
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.89
Best Local Similarity 54.69
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fragment Name
AL353694_0
AL353694_1
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AL353694_1
WPCOMMENT
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AL354818/c
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Insert size: 146149; sum-of-contigs
Insert size: 153445; 5.9% error; agarose-fp
Quality coverage: 2.84x in Q20 bases; sum-of-contigs Quality
coverage: 3.00x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently * consists of 25 contigs. The true order of the places * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the apps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18287: gap of 100 bp 12237: contig of 4040 bp in length 130709: contig of 8282 bp in length 130809: gap of 100 bp 100 bp 13287: contig of 8282 bp in length 132827: contig of 2018 bp in length 13527: gap of 100 bp 135248: contig of 3321 bp in length 135348: gap of 100 bp 135348: gap of 100 bp 100 bp 135348: gap of 100 bp 10
                                                                                                                          Genter project information
Center project information
Center project name: bAPBL16
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; LOB75; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 13724 bases at least Q40
Consensus quality: 139166 bases at least Q30
Consensus quality: 142544 bases at least Q30
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contig of 22568 bp in length
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4895 4994: gap of 100 bp
4995 16378: contig of 11384 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          first gap of 100 bp 10 bp 100 
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3127 bp in length
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18187: contig of 5389 bp in length
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5661 bp in length
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72: contig of 9810 bp in length
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52389: contig of 4017 bp in length
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96: contig of 9907 bp in length
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148549: contig of 4979 bp in length
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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32601: contig of 3
2 32701: gap of 10
2 38362: contig of 5
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FEATURES

URES Source	Location/Qualifiers 1148549 Organism="Homo sapiens"	BAS
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Updaes I to 215896)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Bairen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Bladwin, J., Barna, N., Bastien, V., Beda, F., Boduslavkiy, L., Boukhgaiter, B., Brown, A., Burkett, G., Lander, C., Calangepino, A., Castle, A., Changepino, K., Calangel, Y., Colangel, N., Calangel, N., Colangel, N., Colangel, N., Colangel, N., Colangel, N., Colangel, C., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Hotton, L., Karangen, S., Langers, T., Macdars, T., Marquis, N., McChan, P., McGurk, A., McKennah, R., Merchy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Nellara, V., Raylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Isar, T. M., Oliver, J., Peterson, K., Pierre, N., Pisange, Thomann, N., Schauer, S., Severy, P., Spercer, B., Tealge, Thomann, N., Schauer, S., Severy, P., Spercer, B., Tealge, Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J., Yong, R., Walley, R., Wayman, D., Yong, Yong, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Poline, A., Tangel, M., Waman, D., Wolley, S., Sander, A., Sander,
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Homo sapiens chromosome 15 clone RP11-465J17 map 15, WORKING DRAFT
SEQUENCE, 27 unordered pieces.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 215896)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-465317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   b 30904 GCTCTACTACTGTATAAATATATAAAAACTTTAATTAGGACAAAGCATCTTTAGAGGCTA 30845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    837
                                                                                                                                                                                                                                                                                                                                                                                                                                                   658 TTGATGGTCTAAGAAATCAGAAAGGAGACCGAAAGCTTCTAAGTAATCAAGAAAAATCT 717
                                                                                                                                                                                                                                                                                                   598 AAATCCTGAAACGGGATAATAGGAAAAATGTGTTTCTAATTCGAAGAATTTAATGACTGC 657
                                                                                                                                                                                                                            1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                778 ATTAAAAAAGGGAGTGCTTACAACAGCCATATCAGTGGAGCAACCTTCCCTTTGATTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 b 30844 GAGATAAAAACCACAACTAAAAAACAAGGAAAAACTTTAAAGTTTCAAACAT 30793
                                                                                                                                      Query Match 3.8%; Score 41.6; DB 2; Length 148549; Best Local Similarity 48.6%; Pred. No. 13; Matches 142; Conservative 0; Mismatches 149; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        838 T-GATAATGACAGAAGATGAACAAAGAGTAAGTTTTTGAAAAATTCTAAAAT 888
vector_side:right"
43637 a 27779 c 27991 g 46687 t 2455 others
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
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101520 114909: contig of 13390 bp in length 114910 115009; app of 100 bp 115010 130182: contig of 15173 bp in length 130183 130282: gap of 100 bp 130283 151503: contig of 21213 bp in length 151504 151603: gap of 100 bp 151504 151603: gap of 100 bp 179980 180079; app of 179980 180079; app 
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NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 220000; agarose-fp
Insert size: 213296; sum-of-contigs
Quality coverage: 4.3 in Q20 bases; agarose-fp
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1012 1111: gap of 1011 bp in length
1012 1111: gap of 100 bp
2634 2733: contig of 1522 bp in length
2634 2733: gap of 100 bp
2734 4193: gap of 100 bp
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5299 5398: gap of 100 bp
5399 7188: gap of 100 bp
789 7189: gap of 100 bp
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88567: contig of 11300 bp in length
88667: gap of 100 bp
101419: contig of 12752 bp in length
101519: gap of 100 bp
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77167: contig of 9063 bp in length
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54497: contig of
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Search completed: January 9, 2003, 12:09:21 Job time : 6395 secs THIS PAGE BLANK (USPTO)

81.5 4.3 818 81.5 4.3 1216 81.5 4.3 1216 81.5 4.3 3056	81 4.3 323 1 81 4.3 474 1 81 4.3 823 9	.3 1993 9 .3 736 9 .3 736 9	80.5 4.3 736 9 80.5 4.3 736 9 80.5 4.3 736 9 80.5 4.3 736 9	80.5 4.3 765 1 80 4.2 560 1 80 4.2 897 1	79 4.2 645 1	79 4.2 867 9 79 4.2 867 9	79 4.2 867 9 79 4.2 867 9 79 4.2 867 9	79 4.2 867 9 79 4.2 867 9 79 4.2 867 9	79 4.2 867 1	79 4.2 867 1 79 4.2 867 1	79 4.2 867 1 79 4.2 867 1 79 4 2 867 1	79 4.2 867 1 79 4.2 867 1	79 4.2 867 1	79 4.2 867 1 78.5 4.2 410	78 4.1 185 9 78 4.1 328	78 4.1 328	77.5 4.1 506	77 4.1 639	77 4.1 749	77 4.1 1663	76.5 4.0 311	76.5 4.0 311 76.5 4.0 830	75.5 4.0 745 75.5 4.0 833	75 4.0 342	75 4.0 396 75 4.0 407	75 4.0 771	75 4.0 1155	75 4.0 1659	74.5 3.9 396 74.5 3.9 833	74.5 3.9 1421 74.5 3.9 2167	74 3.9 263 10 US-0
GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	Run on: January 9, 2003, 16:59:59; Search time 41 Seconds (without alignments) 171.297 Million cell updates/sec	Title: US-09-438-185A-1047 Perfect score: 1889 Sequence: 1 VHYCERTLDPKYILKIALKLESIPLYNQEKYLSGFEVLCQ 362	Scoring table: BLOSUW62 Gapop 10.0 , Gapext 0.5	Searched: 118974 segs, 19401057 residues	Total number of hits satisfying chosen parameters: 118974	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 10% Maximum Match 100% Listing first 150 summaries	d Applicati		/cgn2_6/ptodata/	/cgn2_6/ptodata/ /cgn2_6/ptodata/	. /cgn2_6/ptodata/ . /cgn2_6/ptodata/	0: /cgn2_6/ptodata 1: /cgn2_6/ptodata	2: /cgnz_6/prodate 3: /cgn2_6/prodate 4: /cqn2_6/prodate		s greater than or equal to the is derived by analysis of the t	SUMMARIES	Ouery	Score Match Length DB ID Description	216.5 11.5 484 9 US-10-154-674-8	216.5 11.5 486 9 US-10-154-674-4 Sequence 4,	2.06.5 11.9 490 9 05-10-13-07-2 2.06.5 10.9 532 10 US-09-205-658-313 Sequence	95 5.0 1427 10 US-801-368-354 Sequence of 4 4 4 27 10 US-09-817-774-23 Sequence	92 4.9 4563 9 US-09-870-759-128 Sequence	0 88.5 4.7 519 10 US-09-746-491-40 Sequence	1 88.5 4.7 550 10 US-09-746-491-39 sequence 2 87.5 4.6 541 10 US-09-981-421-4	3 87.5 4.6 541 12 US-10-157-447-2 Sequence	14 84 4.4 450 10 US-09-004-701-4220/ OCTUBED 385, APP 15 83.5 4.4 450 10 US-09-014-669-385 Sequence 385, APP 16-09-301-574-22 Sequence 22, APP 16-09-901-574-22	7 82.5 4.4 995 10 US-09-864-761-49017 Sequence	8 82.5 4.4 1202 10 US-09-884-781-43001 Sequence 9 82 4.3 909 10 US-09-815-242-12990 Sequence

Sequence 366, App Sequence 13699, A Sequence 2, Appli Sequence 30, App Sequence 30, App Sequence 22, Appli Sequence 526, App Sequence 84, Appli Sequence 1177, Appli Sequence 1177, Appli Sequence 1177, Appli Sequence 1204, Appli Sequence 1204, Appli Sequence 1204, Appli Sequence 1204, Appli Sequence 1177, Appli Sequence 21, Appli Sequence 21, Appli Sequence 31, Appli Sequence 5, Appli Sequence 5, Appli Sequence 6, Appli Sequence 7, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 6, Appli Sequence 5, Appli

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RESULT 1
US-10-154-674-8
Sequence 8, Application US/10154674
Publication No. US20020192694A1
GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Miranda, Maricar
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
APPLICANT: Hu, Yi
TITLE OF INVENTION: No. US20020192694A1el Human Hydroxylases and Polynucleotides
FILE REFERENCE: LEX-0352-USA
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                                                                                                                                                                                                   Sequence 6373, Apsequence 2, Appli sequence 113, App sequence 1145, App sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 4, Appli sequence 11, Appli sequence 4, Appli sequence 12, Appli sequence 12, Appli sequence 132, App sequence 132, App sequence 133, App sequence 136, Appli sequence 137, Appli sequence 137, Appli sequence 272, Appli sequence 369, Appli sequence 369, App sequence 369, App sequence 115, App sequence 115, App sequence 115, App sequence 117, App sequence 118, Appli sequence 118, Appli sequence 118, Appli sequence 118, Appli sequence 117, App sequence 117, App sequence 118, Appli sequence 117, App sequence 117, Appli seque
                                                                                                                                                                                                   Sequence 5426, Ap
Sequence 12620, A
Sequence 169, App
Sequence 59, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 249, App
Sequence 39, Appl
Sequence 39, Appl
Sequence 37, Appl
Sequence 73, Appl
               Enco
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Publication No. US20020192694A1

GENERAL INFORMATION:
APPLICANT: Yu, Xuanchuan
APPLICANT: Hu, Yi
APPLICANT: No. US20020192694A1el Human Hydroxylases and Polynucleotides
FILE REFERENCE: LEX-0352-USA
CURRENT APPLICATION NUMBER: US/10/154,674

CURRENT APPLICATION NUMBER: US/10/154,674

CURRENT APPLICATION NUMBER: US 60/294,076

PRIOR APPLICATION NUMBER: US 60/29
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; ORGANISM: homo sapiens
US-10-154-674-8
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CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/294,076
PRIOR FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                             Query Match 11.5%; Score 216.5; DB 9; Best Local Similarity 26.2%; Pred. No. 5.4e-13; Matches 67; Conservative 42; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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                                                         169 YLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKV 228
                                                                                          222 LSKLYPTHACREYLKNFPLLTKYCGYREDNVPQLEDVSMFLKERSGFTVRPVAGYLSPRD
                                                                                                                      117 LWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVSGFVAPHQ 168
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FIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE------L
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67; Conservative
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                                                                                                                                                 Indels 43;
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216 EFFINWGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI----- 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
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                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                     / Match
Local Similarity 26.2%; Pred. No. 5.5e-13;
les 67; Conservative 42; Mismatches 104; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCREALION;

APPLICANT: RUNCHALLON;

APPLICANT: RUNCHALLON;

TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC TOOLS FOR

TITLE OF INVENTION: 1997-05.658

CURRENT FILING DATE: 1998-12-03

EARLIER PELLING DATE: 1997-05-15

EARLIER FILING DATE: 1997-07-07

EARLIER FILING DATE: 1997-07-07

EARLIER FILING DATE: 1998-05-15

NUMBER OF SEQ ID NOS: 328

SEQ ID NO 313

LENGTH: 532
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 313, Application US/09205658; Patent No. US20010029617A1; GENERAL INFORMATION:
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Best Local Similarity 25.2%
Matches 70; Conservative
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                                                                                                      TYPE: PRT
CRGANISM: homo sapiens
US-10-154-674-2
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Sequence 2. Application US/10154674
Fublication No. US20020192694A1
GENERAL INFORMATION:
APPLICANT: Wiranda, Maricar
APPLICANT: Miranda, Maricar
APPLICANT: Hu, YI,
TITLE OF INVENTION: NO. US20020192694A1e1 Human Hydroxylases and Polynucleotides Encerning Prince Presence: Las. 0352-0354
CURRENT FILING DATE: 2000-05-23
PRICE APPLICATION NUMBER: US 60/294,076
PRICE APPLICATION UNUMBER: US 60/294,076
NUMBER OF SEQ ID NOS: 8
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APPLICANT: YI, XUANCHUAN
APPLICANT: Wiranda, Maricar
TITLE OF INVENTION: No. US20020192694Alel Human Hydroxylases and Polynucleotides Ence
FILE REPERSENCE: LEX-0352_USA_10/154,674
CURRENT PILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/294,076
PRIOR APPLICATION NUMBER: 2001-05-29
NUMBER OF SEQ ID NOS: 8
SOFWARE: ReatSEQ for Windows Version 4.0
LENGTH: 486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 IEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHA 288
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            336 ---LASLGASDEDVQXLAT-----CYFFTIEFGLCKQEGQLRAYGAGLLSSIGELKHA 385
                                                                            289 FIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE-------- 329
                                                                                                                                                     386 LSDKACVKAFDPKTTCLQECLITTFQEAYFVSESFEEAKEKMRDFAKSITRPFSVYFNPY 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/10154674 Publication No. US20020192694A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       330 TSKLEWMLDQGLLESI 345
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nes 67; Conserve
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US-10-154-674-2
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US-10-154-674-4
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US-09-801-368-354
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; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-354
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APPLICANT: Silva, Jeff
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 10272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 99/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SED ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 354
LENGTH: 1427
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Best Local :
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APPLICANT:
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  264 LIENHEGRK--
                                                                                     208
                                                                                                                                438 DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL 496
                                                                                                                                                                        167 HQYLSLLQDRYFPIASVM------RTLDKDN-----FSLTPDLIHDLLGHVP
                                                                                                                                                                                                                                                                                                        327 YYIVSSSKSMINDENYIINDIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI 386
                                                                                                                                                                                                                                                                                                                                                                                              267 EFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 YILE---KLIFDMTNHYNDSOOL-RTWKROISYFLKLLGNCYSLRLINKE---IFHHWLV 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 SILEFEKNLLF----VHLLSLSKNQREGCSTDMAVVST-----PFF------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 YILKIALKLRQSLSLFFQNSQSLQRAYSTFYSYYRII-----LQKENKEKQALARHKCI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .0%; Score 95; DB 10; Length 1427; Local Similarity 18.8%; Pred. No. 1.1; Local Similarity 65; Mismarches 155; Indels 204;
                                                                                                                                                                                                                                                                                                                                                      -----WKS 120
                                        WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                  WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG 263
                                                                                                                                                                                                                     YKPLLFEIVSNADTNONSDMKKKLELISYRNESLKNNSSIR------NVIMSASNAN
                                                                                                                                                                                                                                                             YCPRFF-----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEEAQQ---KLRMFTNNMKRPFIVRYN--PYTESVEVL 504
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Holtzman, Kevin
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Salama, Sofie
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  ---AYGAV---
  ----LISSP----QELGHAFID--
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TITLE OF INVENTION: Dwf5 MUTANTS
FILE REFERENCE: 2225-0020 / 91020.002
CURRENT APPLICATION NUMBER: US/09/817,774
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/192,202
PRIOR FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 45
SOFTMARE: Patentin Ver. 2.0
SEQ ID NO 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-817-774-23
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  RESULT 8
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Patent No. US20020120111A1
GENERAL INFORMATION:
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN A., Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 GTAVFWDIELYYLYTHFLQFALAAIV-----FSVVLSVYLYARSLKVPRDELSPASSGNA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 WEKYCQ 416
                                                                                                         357 FEVLCQ 362
                                                                                                                                                      351 WWGFVRHPNYLGDLIMALAWSLPCGFNHILPYFYVIYFTALLIHREARDEHQCRRKYGLA 410
                                                                                                                                                                                               320 ----IRHFDELVELTSKLEWMLDQGLLESIPLYN--------QEKYLSG 356
                                                                                                                                                                                                                                         293 DISWPLTSVIJALKLCGYVIFRCANSOKNAFRKNPTDPKLAHLKTIP--TSTWKSLLVSG 350
                                                                                                                                                                                                                                                                                                                                                                                                                    177 VYDFF--IGRELNPRIGAFDLKFFCELRPGLIGWVVINLVMLLAEMKVQERSAPSLAMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146 ----IKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       665 KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       605 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL--------
                                                                                                                                                                                                                                                                                    284 ELGHAFIDNVRVLPL-----
                                                                                                                                                                                                                                                                                                                               235 VNSFQLLYVVDALWF--EEALLTTMDIIHDGFGFMLAFGDLVWVPFTYSLQAFYLVNHPQ
                                                                                                                                                                                                                                                                                                                                                                       248 ----NLIAIVRCFWFTVESGLIEN----HEG---RKAYGAV------LISSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 IHDLLGHVPWLLHPSFS----EFFINM--GRLFTKVIEKVQALPSKKQRIQTLQS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 REGCSTDMAVVSTPFFN-RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAV 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.9%; Score 92; DB 10; Length 427; al Similarity 20.4%; Pred. No. 0.41; 87; Conservative 53; Mismarch-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Mismatches 138; Indels 148;
                                                                                                                                                                                                                                                                                    ------ELDQIIRLPFNTSTPQETLFS- 319
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Gaps

19;

292 283 234 247

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Squence 40, Application US/09746491
Squence 40, Application US/09746491
Sequence 40, Application US/09746491
Sequence 40, Application US/02013720241
GENERAL INFORMATION:
GENERAL INFORMATION:
TILL REPERBURE: 15966-621
CURRENT FILING DATE: 2000-12-20
PRIOR PILING DATE: 1999-12-21
SUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 QEVKFELIVSEASYLRSLNIAVDH-----FQLSTSLR---ATLSNQEHQWLFSRLQDVR 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 FPIASVMRTLDK--DNFSLTPDLLHDLLGH------VPWLLHPSFSE----FFINMGR 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 NFREVLEKTESDPVCQRLSLKSFLILPFQRITRLKLLLQNILK----RTQPGSSEBAEAT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 NOREGCSTD----MAVVSTPFFNRNLWYRLLSSRFSLW------KS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 21.9%; Pred. No. 1.2;
Matches 84; Conservative 59; Mismatches 109; Indels 131; Gaps
                                                                                                                                                                                                                                                                                                                                           272 KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                           9 SKLINSSQLLYQEYSD-----VVLNKEIQSQQRLE------SL 40
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                                                                                              178 FPIASVMRTLDK--DNFSLTPDLIHDLLGH-----VPWLLHPSFSE----FFINMGR 223
                                                                                                                                                                                       224 LFTKVIEKVQALP----SKK-----QRIQTLQSNLIAIVRCFWFTVESGLIENHEGR 271
                                                                                                                                                                                                                                                                                          204 NFREVLEKLESDPVCQRLSLKSFLILPFQRITRLKLLLQNILK----RTQPGSSEEAEAT 259
                                                                121 YCPRFFLDYLEAFGL--LSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYL-SLLQDRY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 SLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVHLLSLSK 84
36 SETPQPSSPRQPRKALVSSESYLQRL---SMASSGSLWQEIPVVRNSTVLLSMTHEDQKL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 KLEWMLDQGLLESIPLYNQEKYL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                            332 KLEWMLDQGLLESIPLYNQEKYL 354
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CORGANISM: Homo sapiens
US-09-746-491-40
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US-09-746-491-40
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FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT PILING DATE: 2000-12-20
RIOR APPLICATION NUMBER: USSN 60/171,329
RIOR APPLICATION NUMBER: USSN 60/171,329
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PARCHELIN VET: 1999-12-21
                                                                                                         APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOFLASTIC DISEASE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOFLASTIC DISEASE
CURRENT APPLICATION NUMBER: 108/09/870,759
CURRENT PILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR PILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4371 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 4430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4211 YTREELCTMFIREVGTVLSQVYSKVHNGSEIL------F8YFQDLVITLPFE-----L 4257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4258 RKHKLIDVISMYREL----LKDLSKEAQEVFKALQSLKTTEVL-RNLQDLLQFIFQLIED 4312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match
Local Similarity 21.9%; Pred. No. 1.1;
les 84; Conservative 59; Mismatches 109; Indels 131; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ARHKCISILEFFKNLLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 -----HOYLSLLQDRYFPIASVMRT----LDKDNFSLTPDLI------ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 SLFPQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVHLLSLSK 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.9%; Score 92; DB 9; Length 4563;
Best Local Similarity 20.7%; Pred. No. 10;
Matches 61; Conservative 48; Mismatches 118; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 YCERTLDPKYILKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4431 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI--IKSQAIA 4483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                Sequence 128, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-09-746-491-37
Sequence 37, Application US/09746491
Patent No. US20020137202A1
GENERAL INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT; ORGANISM: Homo sapiens
US-09-746-491-37
                                                                                                                                                                                                                                                                                                                                                                                           , ORGANISM: Homo sapiens
US-09-870-759-128
                        US-09-870-759-128
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RESULT 12
US-09-981-421-4
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                 APPLICANT: Sims, John E.
APPLICANT: Mohler, Kendall M.
APPLICANT: Mohler, Kendall M.
APPLICANT: BORN, Teresa L.
TITLE OF INVENTION: METHODS FOR TREATING IL-18 MEI
FILE REFERENCE: 3086-A
CURRENT APPLICATION NUMBER: US/09/981,421
CURRENT FILING DATE: 2001-10-17
PRIOR RELING DATE: 2000-10-18
PRIOR FILING DATE: 2000-10-18
NUMBER OF SEQ ID NOS: 5
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US-09-746-491-39
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US-09-746-491-39
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Patent No. US20020137202A1

GENERAL INFORMATION:

APPLICANT: Burgess, Catherine E.

TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 15966-621
CURRENT APPLICATION NUMBER: US/09/746,491
CURRENT FILING DATE: 200-12-20
CURRENT FILING DATE: 200-12-20
                                                                                                                                                                                                                                                                    Sequence 4, Application US/09981421
Patent No. US20020098185A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: USSN 60/171,329
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 72
SOFTMARE: PatentIn Ver. 2.0
SEQ ID NO 39
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query March

4.7%; Score 88.5; DB 10; Length 550;
Best Local Similarity 21.9%; Pred. No. 1.3;

Matches 84; Conservative 59; Mismatches 109; Indels 131;
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           327 KIEFE----CKIFPLISQSRWL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 KLEWMLDQGLLESIPLYNQEKYL 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 NFREVLEKLESDPVCQRLSLKSFLILPFQRITRLKLLLQNILK----RTQPGSSEEAEAT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 FPIASVMRTLDK--DNFSLTPDLIHDLLGH------VPWLLHPSFSE----FFINMGR 223
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296 KIEFE----CKIFPLISQSRWL 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 LFTKVIEKVQALP-----SKK------QRIQTLQSNLIAIVRCFWFTVESGLIENHEGR 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 DVSATFLSDLEENFENNIFSFQVCDVVLNHAPDFRRVYLPYVTNQTYQERTFQSLMNSNS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 YCPRFFLDYLEAFGL--LSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYL-SLLQDRY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 NQREGCSTD----MAVVSTPFFNRNLWYRLLSSRFSLW------KS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 SLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVHLLSLSK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEVKFELIVSEASYLRSLNIAVDH-----FQLSTSLR---ATLSNQEHQWLFSRLQDVR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SETPGPSSPROPRKALVSSESYLORL---SMASSGSLWQEIPVVRNSTVLLSMTHEDOKL 128
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-981-421-4
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US-10-157-447-2
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TENGTH: 541
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Patent No. US20020143155A1
GENERAL INFORMATION:
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Best Local S
  INFORMATION FOR SEQ ID NO: 2:
                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/578,178

FILING DATE: UNLOWN
APPLICATION UNMBER: 09/110,618

FILING DATE: "UNKNOWN
APPLICATION UNMBER: 09/110,618

FILING DATE: "UNKNOWN
ATTORNEY/AGENT INFORMATION:

NAME: Anderson, Kathryn A.
REGISTRATION UNMBER: 32,172

REFERENCE/DOCKET NUMBER: 2619

TELEPHONE: (206) 587-0430

TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   271 TPEGKWHA----SKVLRIE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 CENSYYQTLVNSTSLYKN-CKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 SPQELGHAFIDNVRVLPLE 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 ISILEFF------KNLLFVHLLSLSKNQREGCSTDMAVVS-----TPFFN-- 103
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                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOPTMARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA: Word, Version 5.1a
APPLICATION NUMBER: US/10/157,447
FILING DATE: 28-May-2002
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Receptor Designated 2F1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---YWMFGEENGSDPNIHEEKE----MRIM 270
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us-09-438-185a-1047.rapb

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 HLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

4.4%; Score 84; DB 10; Length 978;
Best Local Similarity 17.9%; Pred. No. 7.4;
Matches 53; Conservative 42; Mismatches 77; Indels 124; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                639 UDQTYKLKAIDPKQRELSFIVNSSVFLEEVISELLCKILYAFSHNMLVTENPDRVKLKLT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 LDPKYILKIALKIRSLSLFFQNSQSLQRAYST-----PYSYYRIILQKENKEKQALA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           826 ITVLPHSLLEDMVYRLLGHVFPSTHTBNELKEKKFPPDDEFVEAASKLTDEIIKEI 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: MAP TO AC008174.1,
OTHER INFORMATION: EXPRESEED IN BRAIN, SIGNAL = 2.6
OTHER INFORMATION: SWISSPROT HIT: Q62209, EVALUE 5.00e-03
US-09-864-761-43207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Forsyth, R. Allyn
APPLICANT: Porsyth, R. Allyn
APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
TITLE OF INVENTION: Genes identified as required for TITLE OF INVENTION: proliferation of E. coli
FILE REFERENCE: ELITRA.009A
CURRENT FILING DATE: 2000-12-19
PRIOR APPLICATION NUMBER: US 60/173005
PRIOR FILING DATE: 1999-12-23
NUMBER OF COLI
                                                 PRIOR APPLICATION UNDRER: PCT/USO1/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION UNDRER: PCT/USO1/0061
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION UNDRER: PCT/USO1/00670
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49177
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 43207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version 4.0
                                 FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
      APPLICATION NUMBER: PCT/US01/00663
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Patent No. US20020022718A1
GENERAL INFORMATION:
APPLICANT: Forsyth, R. Allyn
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; ORGANISM: Escherichia coli
US-09-741-669-385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
SEQ ID NO 385
LENGTH: 450
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Barid R.
APPLICANT: Bank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Great, Wensheng
TITLE OF INVENTION: HUANA GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: WHORER: US/99/864,761
CURRENT APPLICATION NUMBER: US/99/864,761
CURRENT APPLICATION NUMBER: US/99/864,761
CURRENT FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR PLING DATE: 2000-02-04
PRIOR FILING DATE: 2000-08-36
PRIOR PLING DATE: 2000-08-36
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 K---NVRLNCSALLNEEDVI-----YWMFGEENGSDPNIHEEKE----WRIM 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-PTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                    Query Match
4.6%; Score 87.5; DB 12; Length 541;
Best Local Similarity 21.3%; Pred. No. 1.5;
Matches 68; Conservative 50; Mismatches 106; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ISILEFF-----TPFFN-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELFTHFSYYPVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                34 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL--------HDC 81
                                                                                                                                                                                                                                                                                                                                                    9 DPKYI----LKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: Linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-157-447-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parence 43207, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 SPQELGHAFIDNVRVLPLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :|: || :| :| 271 TPEGKWHA----SKVLRIE 285
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APPLICANT: Wang, Peijing Jeremy
APPLICANT: Bage, David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002
CURRENT APPLICATION NUMBER: US/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR PRIOR PRIOR NUMBER: 60/261,557
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 90
SECTIMARE: FASESEQ for Windows Version 4.0
LENGTH: 835
RESULT 17
US-09-864-761-49017
; Sequence 49017, Application US/09864761
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; ORGANISM: Mus musculus
US-09-801-574-22
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US-09-801-574-22
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Ouery March
Best Local Similarity 24.4%; Prod. No. 6.7;
Matches 47; Conservative 26; Mismatches 47; Indels 73
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                       307 İPLFINDLFNQĞF 319
                                                                                                                                                                                                                                                                                                                                                                 324 DELVE-----LTSKLEW------MLDQGL-----LES 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 LHPSFSEFFINMGRLFTKVIEKVQALP--SKKQRIQTLQSVLIAIVRCFWFTVESGL--- 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          321 RHFDELVELTSKLEWMLDQ-GLL 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 LFIGIIRGWIŚLW------MLAAAGVL-----GIVGMFWLALKRYGMNVŚGDEA 257
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                                                                                                                                                                                                                                    IPLYNQEKYLSGF 357
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                                                                                                                                                                                                                                                                                                    NDLITKLFSPVLLETHCIENGLEWHEYMKTYLLYPEKLWQGLPNVGNTCYINVVLQSLCS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                     ISNEKGKERNVREVDISKP---GFGF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IENHEGR-KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLPSSSTFLHNVGLLENQFIKRKRFFSDLAKNEK----QSNLKDSIRDF----EANLVVC 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 4.4%; Score 83.5; DB 10; Length 450; al Similarity 21.7%; Pred. No. 2.9; 57; Conservative 37; Mismatches 102; Indels 67; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PFETNYPEDSGVDVRDL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47; Indels 73;
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TYPE: PRT

ORGANIZM: Homo sapiens

FEATURE:

PEATURE:

OTHER INFORMATION: MAP TO AC007282.2

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.6

OTHER INFORMATION: EST HUMAN HIT: AI023682.1, EVALUE 8.00e-72

OTHER INFORMATION: SWISSPROT HIT: P30622, EVALUE 1.00e-06

US-09-864-761-49017
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PRIOR APPLICATION NUMBER: PCT/USO1/00661
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR APPLING DATE: 2000-01-29
PRIOR APPLING DATE: 2000-01-29
PRIOR APPLING DATE: 2000-01-29
PRIOR PRILING DATE: 2000-01-29
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PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/23,366

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2000-00-27

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

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SEQ ID NO 49017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
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PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR APPLICATION DATE: 2001-05-23
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                     112
   162 GFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINM 221
                                                                                                                                                                                                 110 HLISEVPNSKSGSSGTVHDYIMRQIFTAPIFSELEIEVKEPSETPMNLENQLPTPWKRSL 169
                                                                                                                                                                                                                                                                  78 HLLSLSKNQREGCSTDM-----AVVSTPFFNR------NL-------WYRLL 111
                                                                SSHILFHEENADEIELPQPRSATSQIIQAFPI--DTLLESGIKVIELDKEHHKSSLLGT 227
                                                                                                                             SSRFSLWKSYCPRFFL------DYLEAFGLLSDFLDHQAVIKFFEL--ETHFSYYPVS 161
                                                                                                                                                                                                                                                                                                                                   1 Similarity 70; Conserv
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                           4.4%; Score 82.5; DB 10;
20.9%; Pred. No. 11;
ative 45; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                   Indels 103; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   Length 995;
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15;

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us-09-438-185a-1047.rapb

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222 GRLFTK-----VIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 AVLISSPQELGHAFIDNV------RVLP-LELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 HLLSLSKNOREGCSTDM-----AVVSTPFFNR-------NL------WYRLL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        317 HLISEVPNSKSGSSGTVHDYIMRQIFTAPIFSELEIEVKEPSETPMNLENQLPTPWKRSL 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 SSRFSLWKSYCPRFFL-----DYLEAFGLLSDFLDHQAVIKFFEL--ETHFSYYPVS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      377 SSHILFHEENADEIELPOPRSATSQIIQAFPI--DTLLESGIIKVIELDKEHHKSSLLGT 434
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                                                                                                                                                                                                                                                                                                       4.4%; Score 82.5; DB 10; Length 1202;
20.9%; Pred. No.14; No.14; Indels 103; Gaps
tive 45; Mismatches 117; Indels 103; Gaps
       CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.81
CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.73
CTHER INFORMATION: EXPRESSED IN BTATA, SIGNAL = 0.73
CTHER INFORMATION: EXPRESSED IN BTATA LIVER, SIGNAL = 0.73
CTHER INFORMATION: EST_HUMAN HIT: AI023682.1, EVALUE 1.00e-71
CTHER INFORMATION: ST_HUMAN HIT: A1023682.1, EVALUE 1.00e-71
US-09-864-761-43061
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APPLICANT: Oblsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Will, Daniel
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA, 011A
CURRENT APLICATION NUMBER: US/09/815,242
CURRENT APLICATION NUMBER: 00/09/815,242
PRIOR APPLICANTON NUMBER: 60/191,078
PRIOR PLING DATE: 2000-03-21
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PRIOR PRILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PLILNG DATE: 2000-05-23
PRIOR PLILNG DATE: 2000-05-26
PRIOR PLILNG DATE: 2000-05-26
PRIOR PELLING DATE: 2000-10-23
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
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PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-11-27
PRIOR PELLING DATE: 2000-12-22
PRIOR PELLING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
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APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: Harzel, David R.
APPLICANT: ON THE EXPRESSION ANALYSIS BY HICROARRAY
FILTE OF INVENTION: HORBER: US 60/240,406
PRIOR FILING DATE: 2000-02-4
PRIOR PLING APPLICATION NUMBER: US 60/240,666
PRIOR APPLICATION NUMBER: US 60/240,666
PRIOR APPLICATION NUMBER: US 60/240,666
PRIOR APPLICATION NUMBER: PCT/USO1/00666
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PRIOR PRIOR DATE: 2001-01-30
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                                                                                                                                                                                                                                                                  276 AVLISSPQELGHAFIDNV------RVLP-LELDQIIRLPFNTSTPQETLFSIRH 322
228 GITSPKGNLKDSQEYYSEIRSETEPLSEQSIPIIPKDTTSV------SRAEFIQED 277
                                                                                            222 GRLFTK-----VIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                   323 FDELVE-----LITSKLEWMLDQGLLES 344
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Patent No. US20020048763A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
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APPLICANT: Mohamath, Raodon
APPLICANT: Indirias, Carol Y.
APPLICANT: Ean, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
SOFTWARE: FastSEQ for Windows Version 4.0
SSC) ID NO 366
LENGTH: 818
TYPE: PRT
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US-09-833-790-366
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LENGTH: 909
TYPE: PRT
                                                                                                                                 Query Match 4.3%; Score 81.5; D
Best Local Similarity 19.8%; Pred. No. 10;
Matches 57; Conservative 39; Mismatches
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Best Local :
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APPLICANT: Wans, Tongtong
APPLICANT: Secrist, Heather
APPLICANT: Mohamath, Raodoh
APPLICANT: Indirias, Carol Y.
140 LDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT--LDKDNFSLTPD 197
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                                                          27
                                                                                             95 AVVSTPF-----FURNLWYRLLSSRFSLWKS-YCPRFFLDYLEAFGLLSDF 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.3%; Score 82; DB 10; Length 909;
Local Similarity 22.4%; Pred. No. 10;
les 87; Conservative 66; Mismatches 144; Indels 92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTSKLEWMLDQGLLESIPLYNQEKYLSGF 357
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                                                        AFVTTPMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAF 86
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                                                                                                                                                                          DB 10; Length 818;
                                                                                                                                   93; Indels 99; Gaps
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; ORGANISM: Streptococcus pneumoniae US-09-815-242-13312
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US-09-815-242-13312
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION UNMBER: 60/219,078
PRIOR APPLICATION UNMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION UNMBER: 60/207,727
PRIOR TILING DATE: 2000-05-23
PRIOR APPLICATION UNMBER: 60/207,727
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION UNMBER: 60/242,578
PRIOR APPLICATION UNMBER: 60/253,625
PRIOR APPLICATION UNMBER: 60/257,931
PRIOR APPLICATION UNMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION UNMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11312
LENGTH: 1216
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Best Local
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PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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APPLICANT:
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134 GLLSDFLDHQAVIKFFELETHFSYYFVSGFVAPHQYLSLLQ---DRYFFIASVMRTLDKD 190
                                                                                             676 NAQKWASSQKGLIHTALAEKLKQFMDILASWRLYAKTHSLYDLIWKIYNDRFYYDYV--- 732
                                                                                                                                                                                                                                                                                                                                                             556 TGEMRLVIKEILKLHQEKGVAFKEIALLTSSRSRNDQILLALSEYGIPVKTDGEQNNYLQ 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 NYAPNMDKHWIMQYTGPMLPIHMEFTNILQ------RKRLQTLMSVDDSVERLYNMLV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    137 YFTDLITNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSY 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 LIHDLL----
                                                                                                                                                             85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                             7 TLDPKYILKIALKLRQSLSLFFQ-----NSQSLQRAYSTPYSYYRIILQ----KENKEKQ 57
                                                                                                                                                                                                                             SLEVQVMLDTLRVIHNPLQDYALVALMKSPMFGFDEDELARLSLQKAEDKVHENLYEKLV 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÉTGELÉN----TYIIYTADHGYHIGQFGLVKGKSMPYDFD--ÍRVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF 308
                                                                                                                                                             NQREGCSTDMAVVST-----PFFNRNLWYRLLSSRFSL----WKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FG-----KYLN-EYNGSYIP-PGW---REWLGLIKNSRFYNYTVCRNGIKEKHGFDYAKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 4.3%; Score 81.5; DB 10; Il Similarity 21.6%; Pred. No. 17; 69; Conservative 46; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wall, Danier
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zyskind, Judith W. Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Mismatches 123; Indels 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----GHVPWLLHPSFSEFFINMGR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136
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APPLICANT: Swift, Michael R.
APPLICANT: Athma, Prasanna
APPLICANT: Athma, Prasanna
APPLICANT: L. Alrong
TITLE OF INVENTION: Predisposition to Breast Cancer by
TITLE OF INVENTION: Mutations at the Ataxia-Telangiectasia Genetic Locus
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1475 YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 1532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1382 PSHVIKATFAYISNCHKTKLKSILBILSK-----SPDSYQKILLAICEQAAETNN 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV------- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLMYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.3%; Score 81.5; DB 8; Length 3056;
Best Local Similarity 18.5%; Pred. No. 60;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 PKYILKIAL------KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
791 AVELM--TIHKSKGLEFPYV-----FILNMDQDFNKQDSMSEVILSRQ---NGLGVKY 838
                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Rothwell, Figg, Ernst & Kurz, P.C.
P: 555 Thirteenth Street, N.W., Suite 701-B
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,090 FILING DATE: 03-DEC-1997 CLASSIFCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSITICATION DATA:

PRIOR APPLICATION DATA:

PELING DATE:

03-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Inhun, USFIFEY, 1897

REGISTRATION NUMBER: 28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2323-103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         Sequence 2, Application US/08984090
Patent No. US20010021502A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 28,957
REFERENCE/DOCKST NUMBER: 233
TELECOMMUNICATION INFORMATION:
TELEPHOME: 202-783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 202-183-602-
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
1.ENGTH: 3056 mino acids
                                                     250 IAIVRCFWFTVESGLIENH 268
                                                                                                 839 IA-----KMETGAVEDH 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein US-08-984-090-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                             RESULT 23
US-08-984-090-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 GLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQ---DRYFPIASVMRTLDKD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 NFSLTPDLIHDLIG-HVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         616 SLEVOVMLDTLRVIHNPLQDYALVALMKSPMFGFDEDELARLSLQKAEDKVHENLYEKLV 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
4.3%; Score 81.5; DB 10; Length 1216;
Best Local Similarity 21.6%; Pred. No. 17;
Matches 69; Conservative 46; Mismatches 123; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 ILDPKYILKIALKIRQSLSLFFQ-----NSOSLQRAYSTPYSYYRIILQ---KENKEKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 GALPNGPARQA--NLYALALRADQFEKSNFKGLSRFIRMIDQVLEAQHDLASVAVAPPKD 790
                                                          191 NFSLTPDLIHDLLG-HVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL 249
                                                                                               791 AVELM--TIHKSKGLEFPYV-----FILNMDQDFNKQDSMSEVILSRQ---NGLGVKY 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ITAWALCA, SOUR D.
APPLICANT: ATMANCO, ROBERT T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Robert T.
APPLICANT: W. H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TILE REPERBNCE: ELITRA.011A
CURRENT PELING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR PELICATION NUMBER: 60/206,848
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-216
NUMBER OF SEQ ID NOS: 14110
SECOFTWARE PRESED FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                           Sequence 13698, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT;
CRGANISM: Streptococcus pneumoniae
US-09-815-242-13698
                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
                                                                                                                                                               250 IAIVRCFWFTVESGLIENH 268
                                                                                                                                                                                              APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W
                                                                                                                                                                                                                                                                                                           US-09-815-242-13698
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RESULT 25
US-09-765-272-60
US-09-765-272-60
; Sequence 60, Application US/09765272
; Patent No. US20020061545A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 24
US-09-801-368-352
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TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR PELING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO 352
LENGTH: 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 CPOYIRTLVSEARTLWPEFIPPDPTKVTEFEFYLLEELESY----LIVHHPYOSLKO-- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 CPRFFLDYL-EAFGLLSDFL--DHQAV--IKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                     300 WDKY 303
                                                                                                                                                                                                                                                                                                                                                                              231 KVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFI 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 4.3%; Score 81; DB 10; Length 323; Local Similarity 23.0%; Pred. No. 3.2; Indels 56; Conservative 31; Mismatches 71; Indels
                                                                                                                                                                                                           -EKY
    APPLICANT: Choi et. al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                       ---IVQVLKQPPFQITLSSDDLQNCWSLINDSYINDVHLLYPPH---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----AYGAVL 278
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Holtzman, bel
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Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. US20020128250Alman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0128250A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Peter
man, Doug
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                                                                                                                                                                                                                                                      -AIRDPKNSSSPVQIAFNRFMAESLVD----LEEVMDT-IQEQITLYDH 299
                                                                                                                                                                                                                                                                                                                                        ----IIAVACLFITI-----SIHGKPTKGSSLASAASE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secondary Metabolite Production in Fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                        256
Sequence 244, Application US/09895913A
Patent No. US20020160456A1
GENERAL INFORMATION:
APPLICANT: Kleanthous, Harold
APPLICANT: Al-Garawi, Amal
APPLICANT: Miller, Charles
APPLICANT: Tomb, Jean Francois
APPLICANT: Oomen, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-765-272-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (301) 309-8:
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                    286 YOKLKEAVKYLTDLIEETKATILYLESVETVLNQAGLEEIAEIREELIQTGF
                                                                                                                                                                                                                                                                                             314 -QETLFSIRHFDELVELT-----SKLEWMLDQGLLESIPLYNQEKYLSGF 357
                                                                                                                                                                                                                                                                                                                                   226 ATDNAEEFROKGELLTTFLHQVPNDQDQVILDNYYTNQPIMIALDKALTPNQNAQRYFKR 285
                                                                                                                                                                                                                                                                                                                                                                                                                       173 EPFANLSDLLDTYYKDKAERDRVKQQASELIR-----RVENELQKNRHKLKKQEKELL 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 LTAKNLQSLFQGLGRDTANELERILVSEKLSAFRNFFNQETKPCLTETSFSPVPFANQVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 LLSDFLDHQ--AVIKF--FELETHFSYYPVSGFVAPHQYLSL-----LQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                223 RLFTKVIEKVQAL---PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 LLVDKSSHKILEVIKHVGFSQNSYRTLLPGSTYIAPPSTKSLNPFTIKDEKLFEILQTQE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
PILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Uan-2001
FILING DATE: 21-Uan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Brookes, A. Anders REGISTRATION NUMBER: 36,373 REFERENCE/DOCKET NUMBER: PB TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 SSP----QELGHAFIDNVRVLPLELDQIIRLPFNTSTP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 474 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.3%; SCORE 81; DB 10; Length 474; llarity 20.2%; Pred. No. 5.4; Conservative 44; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309-8512
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172

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313

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1264 RENRT---DSACSLKQMVHE--GNQRW-------DNLQKRVTSILRRLKHFIGGREE 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1364 AQGBQLIEKSEPLDAAIIEE-----ELDELRRY-----CQEVFGRVERYHKKLIRL-- 1409
                                1154 DAČATDABCDŠIOQATRNLDRRWRNICAMSMERRLKIEETWRLWQKFLDDYSRFEDWLKS 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1309 FETARDSILV-----WLTEMDLQLTNIEHFSECDVQAKIKQLKAFQQEISLNHNKIEQII 1363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 RIQTLQSNLIAIVRCFWFTVESGLI------ENHEGRKAYGAVLISSPQELGHA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 DLIHDLLGHVPWLLHP-----SFSEFFINMGRLF---TKVI-EKVQALPSKKQ 240
                                                                                                                                                                                                                                                                                                     182 SVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQR 241
                                                                                                                                                                                                                                                                                                                                                                                                     242 IQTLQSNLIAIVRCFWFT-----BGRK 272
                                                                                                   88 EGCSTDMAVVSTPFFNRNL---WYRL-----LSSRFSLWKSYCPRF--FLDYLEA 132
                                                                                                                                                                                                    133 FGLLSDFLDHQAVI-----KF--FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 AYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSI-RHFDELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Indels 33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 DAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLKKPPSRDQ 69
  30 NSQSLQRAYSTPYSYYRIILQKENKEKQALARHK--CISILEFFKNLLFVHLLSLSKNQR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.3%; Score 80.5; DB 10; Length 197; 23.8%; Pred. No. 1.8; tive 22; Mismatches 41; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION UNMBER: US/09/764,853
CURRENT APPLICATION DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 KLEWMLDQGLLESIPLYNQEKYLSGFEV 359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 836, Application US/09764853
Patent No. US2002009672A1
GENERAL INFORMATION:
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 23.8
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-853-836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 FIDNVR 294
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TITLE OF INVENTION: Identification of Polynucleotides
TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in the
FILE OF INVENTION: Genome
FILE REFRENCE: 06132/043002
CURRENT APPLICATION NUMBER: US/09/895,913A
CURRENT PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 08/881,227
PRIOR FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 368
SOFTWARE: FastSEQ for Mindows Version 4.0
LENGTH: 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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4.3%; Score 81; DB 9; Length 1993;
Best Local Similarity 18.0%; Pred. No. 38;
Matches 70; Conservative 61; Mismatches 121; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              , Match
Local Similarity 20.7%; Pred. No. 11;
les 59; Conservative 44; Mismatches 116; Indels 66; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F--LDYLEAFGLLSDFLDHQ------AVIKFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LODRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     723 IQKEVLSPFKIASFLDRDDVYLTPNMTYK-----PRILKKE-KGYVVNGS--VAILIPKN 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 KNLLFVHLLSLSKNORE----GCSTDMAVVSTP--FFNRNLWYRLLSSRFSLWKSYCPRF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       618 KGVLVETIAIVTQKSKEVLARSLPLNLSIKQKPSYIFDKQLPY------WVIYRNAF 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDKVFHSMOFGLFEVFRDROITNSVLVKNGIRVIKSRNIDEN-----GKIISIENYDSY 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 ALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCI-SILEF----F 71
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APPLICANT: MYGNATION:
APPLICANT: SUGJECAN:
APPLICANT: SUGJECAN:
APPLICANT: SUGJECAN:
APPLICANT: SUGJECAN:
TITLE OF INVENTION: TSG101-INTERACTING PROTEINS AND USE THEREOF
FILE REFERENCE: 1907.06
CURRENT APPLICATION NUMBER: US/10/098,979
CURRENT APPLICATION NUMBER: US 60/276,259
PRIOR FILING DATE: 2002-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-07-07
PRIOR PLING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: US 60/304,101
PRIOR PLING DATE: 2001-07-07
PRIOR PLING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: to be assigned
PRIOR PLING DATE: 2001-07-07
PRIOR PLING DATE: 2001-07-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233 QALPSKKQ-----RIQTLQSNLIAIVRCFWFTV 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/10098979
Patent No. US20020177207A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                        ORGANISM: Helicobacter pylori
US-09-895-913A-244
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Mapier Napier Napier Pan, J Pan, J Shelto Stewar Willia	APPLICANT: Desnoyers, Luc APPLICANT: Eaton, Dan APPLICANT: Ferrara, Napoleon APPLICANT: Filvaroff, Ellen APPLICANT: Filvaroff, Ellen APPLICANT: Gao, Wei-Qiang APPLICANT: Gao, Wei-Qiang APPLICANT: Gerber, Hanspeter APPLICANT: Goddard, Audrey APPLICANT: Goddwski, Paul J. APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Grimaldi, J. Christopher APPLICANT: Hillan, Kenneth J APPLICANT: Kljavin, Ivar J.
PRIOR APPLICATION NUMBER: 60/080328 PRIOR APPLICATION NUMBER: 60/08033 PRIOR PILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/08033 PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PILING DATE: 1998-04-09 PRIOR PRIOR PRIOR NUMBER: 60/081229 PRIOR PRIOR PRIOR DATE: 1998-04-09 PRIOR PRIOR PRIOR DATE: 1998-04-09 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-15 PRIOR PRIOR PRIOR DATE: 1998-04-27 PRIOR PRIOR PRIOR DATE: 1998-04-27 PRIOR PRIOR PRIOR DATE: 1998-04-27 PRIOR PRIOR PRIOR DATE: 1998-04-27 PRIOR PRIOR PRIOR DATE: 1998-04-27 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-22 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR DATE: 1998-04-29 PRIOR PRIOR	PRIOR APPLICATION NUMBER: 60/079920 PRIOR FILLING DATE: 1998-03-30 PRIOR APPLICATION NUMBER: 60/079923 PRIOR APPLICATION NUMBER: 60/079923 PRIOR FILLING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080105 PRIOR APPLICATION NUMBER: 60/080107 PRIOR APPLICATION NUMBER: 60/080167 PRIOR PILLING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080169 PRIOR PILLING DATE: 1998-03-31 PRIOR PILLING DATE: 1998-03-31 PRIOR PILLING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080194 PRIOR APPLICATION NUMBER: 60/080197 PRIOR APPLICATION NUMBER: 60/080197 PRIOR APPLICATION NUMBER: 60/080327

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APPLICANT: WILLIAMS; F. HILASAY
APPLICANT: WOOD, WIlliam; F. HILASAY
APPLICANT: WOOD, WILLIAM: F. HILASAY
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
PRIOR PLING DATE: 2001-07-30
PRIOR PLING DATE: 1997-10-15
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-11-03
PRIOR PLING DATE: 1997-01-11
PRIOR PLING DATE: 1999-03-11
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PRIOR PLING DATE: 1999-03-14
PRIOR PLING DATE: 1999-03-15
PRIOR PLING DATE: 1999-03-15
PRIOR PLING DATE: 1999-03-16
PRIOR PLING DATE: 1999-03-19
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Grimaldi, J. Christopher
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Garritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Botstein, David
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4.3%; Score 80.5; DB 9; Length 736;
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PRIOR APPLICATION NUMBER: 60/079728 PRIOR FILING DATE: 1998-03-27 PRIOR APPLICATION NUMBER: 60/079786

Sequence 526, Application US/09978697 Patent No. US20020169284A1 GENERAL INFORMATION:

RESULT 30 US-09-978-697-526

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APPLICANT: Ashkenazi, Avi APPLICANT: Baker Kevin P.

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Pred. No. 11;
22; Mismatches
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RESULT 31
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; APPLICANT: Ashkenazi, Avi
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
                                                                                                                         Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Baker Kevin P.
Botstein, David
Desnoyers, Luc
Eaton, Dan
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RESULT 32
US-09-999-832A-526
; Sequence 526, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
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DR APPLICATION NUMBER: 60/085580
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DR APPLICATION NUMBER: 60/085573
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OR APPLICATION NUMBER: 60/084640
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OR APPLICATION NUMBER: 60/084598
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
FILING DATE: 1998-05-13
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FILING DATE: 1998-05-
APPLICATION NUMBER: 6
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FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085323
FILING DATE: 1998-05-13
APPLICATION NUMBER: 60/085582
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APPLICATION NUMBER: 60/0
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FILING DATE: 1998-05-05
APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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FILING DATE: 1998-04-30
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APPLICATION NUMBER: 60/
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larity 23.8%;
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Pred. No. 11;
22; Mismatches
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CCURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/91895
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PRIOR APPLICATION NUMBER: 60/077641
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PRIOR PILING DATE: 1998-03-12
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PRIOR APPLICATION NUMBER: 60/078986
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APPLICANT: Tumas, Daniel I.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: P2630P1C63
FILE REPERENCE: P2630P1C63
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OR APPLICATION NUMBER: 60/078910
OR FILLING DATE: 1998-03-20
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OR FILLING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/079294
OR FILLING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079656
OR FILLING DATE: 1998-03-25
OR APPLICATION NUMBER: 60/079664
OR FILLING DATE: 1998-03-27
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Filvaroff,
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Stewart, Timothy A.
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Grimaldi, J. C
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Gerritsen, Mary E.
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ni, Nicholas F.
, Margaret Ann
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ff, Ellen
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Sequence 526, Application US/09978189 Publication No. US20030004102A1

| APPLICANT: Pan, James; APPLICANT: Roy, Margaret Ann APPLICANT: Roy, Margaret Ann APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Williams; p. 10.14 ickey APPLICANT: Williams; p. 10.14 ickey APPLICANT: Williams; p. 10.14 ickey APPLICANT: Williams; p. 2001.107.30 CURRENT PERENCE: P65091C78 Encoding the Same EILE REPERENCE: SHKEN Baker Baker Baker Botat Desno Eacon Ferra Fong, Gao, Geri- |
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| PRIOR PILLING DATE: 1998-04-01 PRIOR PILLING DATE: 1998-04-01 PRIOR PILLING DATE: 1998-04-01 PRIOR PILLING DATE: 1998-04-01 PRIOR PILLING DATE: 1998-04-08 PRIOR PILLING DATE: 1998-04-08 PRIOR PILLING DATE: 1998-04-08 PRIOR PILLING DATE: 1998-04-08 PRIOR PILLING DATE: 1998-04-08 PRIOR PILLING DATE: 1998-04-08 PRIOR PILLING DATE: 1998-04-09 PRIOR PILLING DATE: 1998-04-09 PRIOR PILLING DATE: 1998-04-09 PRIOR PILLING DATE: 1998-04-09 PRIOR PILLING DATE: 1998-04-09 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-15 PRIOR PILLING DATE: 1998-04-21 PRIOR PILLING DATE: 1998-04-21 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-22 PRIOR PILLING DATE: 1998-04-23 PRIOR PILLING DATE: 1998-04-29 | NEOENE NE |

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CURRENT APPLICANTON WOMER: US/11/052,586

PRIOR APPLICANTON WOMER: US/11/052,586

PRIOR APPLICANTON WOMER: CO/05263

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PRIOR PLING DATE: 1997-10-10

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Wood, William I.
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Gurney, Austin L.
                                                          Baker, Kevin P.
Chen, Jian
Patent No. US20020127584A1
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1 Similarity 23.8%; Pred. No. 11;
30; Conservative 22; Mismatches 41; Indels
                                                                                                                                     PRIOR FILING DATE: 1998-04-29
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PRIOR PAPLICATION NUMBER: 60/08463
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OR FILING DATE: 1998-03-27

OR APPLICATION NUMBER: 60/06

OR APPLICATION NUMBER: 60/06

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OR FILING DATE: 1998-03-31

OR APPLICATION NUMBER: 60/06

OR FILING DATE: 1998-04-01

60/080107

APPLICATION NUMBER: FILING DATE: 1998-0

APPLICATION NUMBER: FILING DATE: 1998-0

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PR APPLICATION NUMBER: 60/088212

PR FILLING DATE: 1998-06-05

PR APPLICATION NUMBER: 60/088217

PR APPLICATION NUMBER: 60/088326

PR APPLICATION NUMBER: 60/088326
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088029
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R FILING DATE: 1998-06-04
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                                                                                                                            RIQTLOSNLIAIVRCFWFTVESGLI --
                                                                                                                                                                    DAIYDMIGFPDFILEPKELDDVYDGYEISEDSFFQNMLNLYNFSAKVMADQLRKPPSRDQ 523
                                                                                                                                                                                                              DLIHDLLGHVPWLLHP------SFSEFFINMGRLF---TKVI-EKVQALPSKKQ
                                          FIDNVR
FDDQGR
                                                                                                                                                                                                                                                      g 4.3%; Sc
Similarity 23.8%; Pr
584
                                          294
                                                                                    VNAYYLPTKNEIVFPAGILOAPFYARNHPKALNFGGIGVVMGHELTHA 578
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Pred. No. 11;
22; Mismatches
                                                                                                                         ---ENHEGRKAYGAVLISSPOELGHA 288
                                                                                                                                                                                                                                                                                                   DB 12;
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OR FILING DATE: 1998-04-27
OR APPLICATION NUMBER: 60/082569
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60/082568

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60/081195 60/081070 60/081049 60/080333 60/080327 60/080194

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OR APPLICATION NUMBER: 60/08463
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OR APPLICATION NUMBER: 60/085573

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60/085579

RESULT 35 US-09-888-615-80

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R FILING DATE: 1998-06-0
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NUMBER: 60/087827 1998-06-03

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OR FILING DATE: 1998-05-28
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Query Match
4.2%; Score 80; DB 10; Length 560;
Best Local Similarity 20.3%; Pred. No. 8.4;
Matches 60; Conservative 43; Mismatches 109; Indels 84; Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 RELLATDNAEEFRQKGELLTTFLHQVPNDQDQVILDNYYTNQPIMIALDKALTPNQNAQR 367
                                                                                                                                                                                                                                                                                                                              135 LLSDFLDHQ--AVIKP--FELETHFSYYPVSGFVAPHOYLSL----LQDRYFPIASVMR 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 LTAKNLOSLFQGLGRDTANELERILVSEKLSAFRNFFNOETKPCLTETSFSPVPFANQAG 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 BFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
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APPLICANT: TASELDECK, KOUSTL
APPLICANT: Tyskind, Judith W.
APPLICANT: Tyskind, Judith W.
APPLICANT: Tavack, John D.
APPLICANT: Taxack, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Taxamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILLE REPERRECE: ELITERA, 011A
CURRENT APPLICATION NUMBER: 05/191,078
FRIOR FILING DATE: 2000-03-21
PRIOR PELICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-226
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
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PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
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PRIOR APPLICATION NUMBER: 60/253,089
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SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13304
LENGTH: 560
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Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                   ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13304
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US-09-815-242-11609
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23.8%; Pred. No. 11;
tive 22; Mismatches 41; Indels 33; Gaps
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APPLICANT: Onlsen, Nail D.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, Sobert T.
APPLICANT: Yamannco, Robert T.
APPLICANT: Yamannco, Robert T.
APPLICANT: Yamannco, Robert T.
APPLICANT: Will H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Dentary
TITLE OF INVENTION: Prokaryotes
FILE REPERBENCE ELITRA. 0.11A
CURRENT FILING DATE: 2001-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PUBLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-23
PRIOR PUBLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-23
PRIOR PUBLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
                                                                                                                                      APPLICANT: WHYTE, DAVID
APPLICANT: CAENEREEL, SEAN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: CHARYDCZAK, GLEN
APPLICANT: BUDARSANAM, SUCHA
APPLICANT: SUDARSANAM, SUCHA
TITLE OF INVENTION: NOVEL PROTEASES
FILE REFERRNCE: 038622/1214
CURRENT APPLICATION NUMBER: 06/26
PRIOR APPLICATION NUMBER: 60/214,047
PRIOR PILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PATENTING DATE: 2000-06-26
SEQ ID NO 80
LENGTH: 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13304, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
              Sequence 80, Application US/0988615
Patent No. US20020064856A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 23.8%
Matches 30; Conservative
                                                                                                             APPLICANT: PLOWMAN, GREGORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-80
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RESULT 38
US-09-731-231A-2
US-09-731-231A-2
; Sequence 2, Application US/09731231A
PATENT NO. US20020082189A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
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CURRENT APPLICATION NUMBER: US/09/731,231A
CURRENT FILING DATE: 2000-12-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASTSBQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 645
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TYPE: PRT
ORGANISM: Human
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                                                                                                -----FTKVIEKVQAL-PSKKQRIQTLQS 247
                                                                                                                                             YPKELNAIMESMLNKNPSLRPSAIEIL--KIPYLDEQLQNLMCRYSEMTLEDKNLDCQKE 313
                                                                                                                                                                                          Y-FPIASVMRTLDKDNFSLTPDLIHDLLGHVPWL-----LHPSFSEFFINMGRL-----
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19.7%; Pred. No. 13;
1tive 47; Mismatches 107; Indels 70; Gaps
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4; Mismatches
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CURRENT APPLICATION NUMBER: 60/049787
PRIOR APPLICATION NUMBER: 60/04250
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/083322
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087106
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PRIOR PRILING DATE: 1998-06-02
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US-09-992-598-84
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OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/08021
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OR APPLICATION NUMBER: 60/08026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/08026
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OR APPLICATION NUMBER: 60/08039
OR APPLICATION NUMBER: 60/08039
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Gerritsen, Mary E.
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Kljavin, Ivar J.
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art, Timothy A.
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RESULT 40
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PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PPLICATION NUMBER: 60/065311
PRIOR PPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-24
PRIOR PRILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR PPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
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OR APPLICATION NUMBER: 60/088021
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Gerber, Hanspeter
Gerber, Mary E.
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Kljavin, Ivar J.
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art, Timothy A.
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OR APPLICATION NUMBER: 60/089599
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APPLICANT: Zhang Zemin 1.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730PLG1
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11.
139 FLDHQAVIKFFELETHFSYYP-----VSGFVAPH------QYLSLLQDRXFPIASVMR 185
                                          195 LITNDSV-SFF--RTSKKMYPHRPVLMVISHAAPHGPEDSAPQY-----SRLFPNAS-QH 245
                                                                                             186 TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKORIOTL 245
                                                                                                                                                 246 ITPSYNYAPNPD------KHWIMRYIGPMKPIHME--FTNMLQ------RKRLQTL 287
                                                                                                                                                                                                    246 QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305
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PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PLING DATE: 1997-11-12
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065710
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PRIOR PRILING DATE: 1998-02-25
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R APPLICATION WINBER: 60/087507
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Gerber, Hanspeter
Gerten, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Publication No. US20020193299A1
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-03-29
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PRIOR PELLING DATE: 1998-06-03
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089598
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C19
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                                                                                                                                                                                                                                                                                                                                         195 LITNDSV-SFF--RİSKKMYPHRPVLMVISHAAPHGPEDSAPQY----SKLFPNAS-QH 245
                                                                                                                                                                                                                                                                                                                                                                                               186 TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTL 245
                                                                                                                                                                               99 TPFFNRNL------WYRLL-SSRFSLWKSYC----PRFFLDYLEAFGLLSD 138
                                                                                                                                                                                                                                                                                       139 FLDHQAVIKEFELETHFSYYP-----VSGFVAPH-----QYLSLLQDRXFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                              246 ITPSYNYAPNPD-----RHWIMRYTGPMKPIHME--FTNMLQ------RKRLQTL 287
                                                                                                                                                                                                                        70; Gaps
                                                                     Query Match

4.2%; Score 79; DB 9; Length 867;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 59; Conservative 34; Mismatches 85; Indels
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CURRENT FILING DATE: 2001-11-14
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Fong, Sherman
Gerber, Hanspeter
Godderd, Andrey
Goddard, Audrey
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                     , PRIOR FILING DATE: 1998-07-09
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Napier, Mary A.
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Botstein, David
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Eaton, Dan L.
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341 VPFYVRGP 348
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FILING DATE R FILING DATE: R APPLICATION N R FILING DATE:

60/089600 60/089599

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APPLICANT: Paoni Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Walliams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Acids Encoding the Same
FILE OF INVENTION: Acids Encoding the Same
FULE REFERENCE: P2730P1669
CURRENT APPLICATION NUMBER: US/09/989,730
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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Best Local S
Matches 59
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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OR FILING DATE: 1998-07-02
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OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR APPLICATION NUMBER: 60/092182
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OR FILING DATE: 1998-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITPSYNYAPNPD-----KHWIMRYTGPMKPIHME--FTNMLQ------RKRLQTL
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Gerber, Hanspeter
Gerritsen, Mary E.
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Eaton, Dan L.
Ferrara, Napoleone
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Pan, James
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ilarity 23.8%;
Conservative 3
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Publication No. US20020198148A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
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                                                                                           Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Gerber, Hanspeter
Gerritsen, Mary E.
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Godowski, Paul J.
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   Watanabe, Colin K. Williams, P. Mickey Wood, William I.
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR PLICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/06226
PRIOR APPLICATION NUMBER: 60/06316
PRIOR APPLICATION NUMBER: 60/06516
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PRIOR PILING DATE: 1997-11-24
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Matches 59; Conservative 34; Mismatches 85; Indels
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PRIOR FILING DATE: 1998-06-25
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Sequence 84, Application US/09991181
Publication No. US20020197615A1
SENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Kljavin, Ivar J.
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Baker, Kevin P.
Bottetin, David
Desnoyers, Luc
Eaton, Dan L.
Perrara, Napoleone
Pong, Sherman
Gerber, Hanspeter
Gertitsen, Mary E.
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Betterin, David; APPLICANT: Eston, Dan L.
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OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091478
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PR FILING DATE: 1998-06-24
PR APPLICATION NUMBER: 60/090472
PR FILING DATE: 1998-06-24
PR APPLICATION NUMBER: 60/090535
PR FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090557
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APPLICATION NUMBER: 60/090676
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APPLICATION NUMBER:
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;; Pred. No. 19;
34; Mismatches
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DR APPLICATION NUMBER: 60/089532

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APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876

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1998-06-

APPLICATION NUMBER: 60/089512

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APPLICATION NUMBER: 60/088858

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APPLICATION NUMBER: 60/088826

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OR APPLICATION NUMBER: 60/090444

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
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A PPLICATION NUMBER: 60/088028
R FILING DATE: 1998-06-04
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PRIOR PLING DATE: 1997-10-11-19
PRIOR PLING DATE: 1997-10-12
PRIOR PLING DATE: 1997-10-13
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Sequence 84, Application US/09989734 Publication No. US20030003531A1 GENERAL INFORMATION:
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
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                                                              APPLICANT: Sakkenazi, Avi J. APPLICANT: Baker, Kevin P. APPLICANT: Botstein north
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Eaton, Dan L.
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PRIOR APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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OR FILING DATE: 1998-07-02
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R FILING DATE: 1998-06-25

DR APPLICATION NUMBER: 60/090690

R FILING DATE: 1998-06-25

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R FILING DATE: 1998-06-25
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NR APPLICATION NUMBER: 60/090429

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NR APPLICATION NUMBER: 60/090435
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R FILING DATE: 1998-06
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090535
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APPLICATION NUMBER: 60/090540
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FILING DATE: 1998-06-
APPLICATION NUMBER: 6
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Pred. No. 19;
34; Mismatches 85; Indels
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PRIOR FILLING DATE: 1997-06-18
PRIOR PELICATION NUMBER: 60/056974
PRIOR PELICATION NUMBER: 60/056974
PRIOR PELICATION NUMBER: 60/059113
PRIOR PELLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059115
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Publication No. US20030004311A1
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CURRENT APPLICATION NUMBER: US/10/028,072
CURRENT FILING DATE: 2001-12-19
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                  OR APPLICATION NUMBER: 60/059122
OR FILING DATE: 1997-09-17
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Godowski, Paul J.
Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
Stewart, Timothy A.
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Watanabe, Colin K
Wood, William
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Gerritsen, Mary E.
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DeForge, Laura
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PRIOR APPLICATION NUMBER: 60/08332 PRIOR APPLICATION NUMBER: 60/08345 PRIOR APPLICATION NUMBER: 60/084600 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/084627 PRIOR FILING DATE: 1998-05-07 PRIOR PELLING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR PELLING DATE: 1998-05-07 PRIOR PELLING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/08533 PRIOR APPLICATION NUMBER: 60/08533 PRIOR FILING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-13 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-15 PRIOR PELLING DATE: 1998-05-16 PRIOR PELLING DATE: 1998-05-16 PRIOR PELLING DATE: 1998-05-16 PRIOR PELLING DATE: 1998-05-16 PRIOR PELLING DATE: 1998-05-16 PRIOR PELLING DATE: 1998-05-17 PRIOR PELLICATION NUMBER: 60/090345 PRIOR PELLING DATE: 1998-05-17 PRIOR

16; 4.2%; Score 79; DB 9; Length 867; 23.8%; Pred. No. 19; tive 34; Mismatches 85; Indels Query Match Best Local Similarity 23.8% Matches 59; Conservative

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Sequence 64, Application US/09989722 Sequence 64, Application US/09989722 Patent No. US20022007267A1 GREEAL INFORMATION APPLICANT: Back-Kovin', APPLICANT: Back-Kovin', APPLICANT: Back-Kovin', APPLICANT: Back-Kovin', APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Gerber Hanspeter APPLICANT: Milliam I. APPLICANT: Watenabe, Colin K. APPLICANT: Watenabe, Colin K. APPLICANT: Watenabe, Colin K. APPLICANT: Watenabe, Colin K. APPLICANT: Watenabe, Colin K. APPLICANT: Wood, William I. APPLICANT: Wood, Wil	QY 139 FLDHQAVIKFFELETHFSYYPVGGFVAPHQYLSLLQDRYEPIASVMR 185 Db 195 LITNDSV-SFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLEPNAS-QH 245 QY 186 TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTL 245 Db 246 ITDSYNYAPNDPKHWIMRYTGPMKPIHMEFTNMLQRKRLQTL 287 QY 246 QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAPIDVRVLFLELDQIR 305 Db 36 MSVDDSMETIYNMLVETGELDNTYIVYTADHGYHIGQFGLVKGKSMFYEFDIR 340 QY 306 LPFNTSTP 313 Db 341 VPFYVRGP 348
PRIOR APPLICATION NUMBER: 60/08030 PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/08033 PRIOR FILING DATE: 1998-06-04 PRIOR APPLICATION NUMBER: 60/080326 PRIOR APPLICATION NUMBER: 60/080326 PRIOR APPLICATION NUMBER: 60/080326 PRIOR APPLICATION NUMBER: 60/080202 PRIOR FILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/080217 PRIOR PILING DATE: 1998-06-05 PRIOR APPLICATION NUMBER: 60/080217 PRIOR APPLICATION NUMBER: 60/080217 PRIOR APPLICATION NUMBER: 60/080217 PRIOR APPLICATION NUMBER: 60/080734 PRIOR APPLICATION NUMBER: 60/080734 PRIOR APPLICATION NUMBER: 60/080734 PRIOR APPLICATION NUMBER: 60/080734 PRIOR APPLICATION NUMBER: 60/080734 PRIOR APPLICATION NUMBER: 60/080874 PRIOR APPLICATION NUMBER: 60/080874 PRIOR APPLICATION NUMBER: 60/080824 PRIOR APPLICATION NUMBER: 60/080824 PRIOR APPLICATION NUMBER: 60/080824 PRIOR APPLICATION NUMBER: 60/080826 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NUMBER: 60/080829 PRIOR APPLICATION NU	

16; APPLICANT: Zhang, Zemin Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same 246 OSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305 288 MSVDDSMETIYNMLVETGELDN----TYIVYTADHGYHIGQFGLVKGKSMPYEFD--IR 340 186 TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTL 245 246 ITPSYNYAPNPD------KHWIMEXTGPMKPIHME--FTNMLQ-------RKRLQTL 287 99 TPFFNRNL------WYRLL-SSRFSLWKSYC----PRFFLDYLEAFGLLSD 138 139 FLDHQAVIKFFELETHFSYYP-----VSGFVAPH-----QYLSLLQDRYFPIASVMR 185 Gaps 70; Query Match
4.2%; Score 79; DB 10; Length 867;
Best Local Similarity 23.8%; Pred. No. 19;
Matches 59; Conservative 34; Mismatches 85; Indels ' ICATION NUMBER: US/09/989,723 CURRENT APPLICATION NUMBER: US/09/989, CURRENT FILTON DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787 PRIOR PILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/06250 PRIOR FILING DATE: 1997-11-12 PRIOR APPLICATION NUMBER: 60/065186 PRIOR APPLICATION NUMBER: 60/065181 PRIOR APPLICATION NUMBER: 60/06511 PRIOR FILING DATE: 1997-11-13 PRIOR FILING DATE: 1997-11-24 PRIOR FILING DATE: 1997-11-24 PRIOR FILING DATE: 1997-11-24 PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/06570 PRIOR APPLICATION NUMBER: 60/05945 PRIOR APPLICATION NUMBER: 60/07945 PRIOR FILING DATE: 1998-02-25 PRIOR APPLICATION NUMBER: 60/078910 Gerber, Hanspeter
Gerritsen, Mary E.
Gerritsen, Mary E.
Godowski, Paul J.
Grimaldi, J. Christopher
Grimaldi, J. Christopher
Kljavin, Ivar J.
Napier, Mary A.
Pan, James
Paon, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel Sequence 34, Application US/09989723 Sequence No. US20020072092A1 GENERAL INFORMATION: Watanabe, Colin K. Williams, P. Mickey Wood, William I. Ferrara, Napoleone APPLICANT: Ashkenazi, Avi J. Baker, Kevin P. Botstein, David FILE REFERENCE: P2730P1C62 Fong, Sherman :|| | | 341 VPFYVRGP 348 306 LPFNTSTP 313 RESULT 50 US-09-989-723-84 APPLICANT: APPLICANT: 엄 ð 8 g ð g ò

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     January 9, 2003, 14:46:38 ; Search time 26 Seconds (without alignments) 409.658 Million cell updates/sec
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'GGDZ 6/ptodata1/jaa/PCTUS COMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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RESULT 1
US-08-009-075-5
                                                                                                                                                                                                                                          Sequence 5, Application Patent No. 5300436 GENERAL INFORMATION:
                                                   APPLICANT: GOLDSTEIN, Menek
APPLICANT: WI, Jing
APPLICANT: FILER, David
APPLICANT: FILER, David
APPLICANT: FRIEDHOFF, Arnold J.
TITLE OF INVENTION: GENETICALLY MODIFIED TYROSINE
TITLE OF INVENTION: HYDROXYLASE AND USES THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY and NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
  STREET: 419 Seven CITY: Washington STATE: D.C. COUNTRY: U.S.A.
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5, 5300436
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                                                                                                                       Sequence 4, Application US/08009075

Patent No. 5300436

GENERAL INFORMATION:

APPLICANT: GOLDSTEIN, Menek

APPLICANT: WIL, Jing

APPLICANT: FILER, David

APPLICANT: FILER, David

APPLICANT: FILER, GENETICALLY

TITLE OF INVENTION: GENETICALLY

TITLE OF INVENTION: HYDROXYLASE AND US

TOTHER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY and NEIMARK

STREET: 419 Seventh Street, N.W., Su
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING NETE: PS-DOS/MS-DOS
OPERATION SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/08/009,075
FILLING DATE: 199310126
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, GUY K.
NAME: TOWNSEND, GUY K.
NAME: TOWNSEND, GUY K.
NAME: TOWNSEND, GUY K.
NAME: TOWNSEND, GUY K.
NAME: TOWNSEND, GUY K.
OLDSTEIN-IA
INFORMATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-78-3528
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 498 amino acids
TYPE: AMINO ACID
STRANDEDNESS: Single
TOPOLOGY: 11near
MCLECULE TYPE: protein
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COMPUTER READABLE FORM:
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COMPUTER: IBM PC compatible
                                                     ADDRESSEE: BROWDY
STREET: 419 Seveni
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
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AND USES THEREOF
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5.2%; Score 98.5; DB 4; Length 1024;
Best Local Similarity 19.9%; Pred. No. 0.13
Matches 68; Conservative 41; Mismatches 134; Indels 99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193 SLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFT-----KVIEKVQALPSKKQRIQT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 QOTDSLKNLFSV----IGDILSETNVNKITLHÄVKNNELLSLVETASTLKIKHL----- 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 QREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   614 -----ELLNFFPDTKDITPT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 IK--FFELETH------FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     648 İKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAİ------DKT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Young, Richard A.
APPLICANT: Young, Richard A.
APPLICANT: Young, Richard M.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 591966e1 Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
CITY: Lexington
CITY: Lexington
CITY: Lexington
CONNERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 ----HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD 324
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/540,804
                           APPLICATION NUMBER: AU PN7127
FILING DATE: 13-DEC-1995
ATTORNEY/AGENT INPORMATION:
NAME: WINNER, Ellen P.
TELECOMMUTICATION INPORMATION:
TELECHONE: +1 303 499 8080
INPORMATION FOR ERG ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1024 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Mycoplasma genitalium
US-09-091-117-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/08540804
Patent No. 5919666
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein ORIGINAL SOURCE:
         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                      TOPOLOGY: 14-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 SSRFSLWKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 AEEIATWKEVYTTLKGLYATHACGEHLEAFALLERFSGYREDNIPQLEDVSRFLKERTGF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 SYYPYSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346 QFSQDIG-----LASLGASDEEIEKLSTLS------WFTVEFGLCKONGEVKAYG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 AGLLSSYGELLHCLSEEPEIRAFDPEAAAVQPYQDQTYQSVYFVSESFSDAKDKLRSYAS 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
11.6%; Score 220; DB 1; Length 497;
Best Local Similarity 26.7%; Pred. No. 3e-15;
Matches 65; Conservative 38; Mismatches 104; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The University of Melbourne TITLE OF INVENTION: Wycoplasma Recombinant Polypeptides and TITLE OF INVENTION: Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STRATE: Colorado
COUNTRY: United States of America
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/009,075
FILING DATE: 1930126
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: TOWNSEND, GUY K.
REGISTRATION NUMBER: 34,033
FERENGNEY/DOCKET WUMBER: GLESCHMINICATION INFORMATION:
TELECHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S: GREENLEE, WINNER and SULLIVAN P.C. 5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00803
FILING DATE: 13-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/09/091,117
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US-09-1117-5
US-09-091-117-5
; Sequence 5, Application US/09091117
; Patent No. 6171589
; Patent INFORMATION:
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FILING DATE: 12 JUNE 1998
                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 497 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  TELEPHONE: 202-628-31-31-3528
TELEPHAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear;
MOLECULE TYPE: protein US-08-009-075-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREENLEE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                332 KLE 334
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FILING DATE: 11-OCT-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/521,877
FILING DATE: 21-AUG-1995
PRIOR APPLICATION UNBER: US 08/218,26
FILING DATE: 25-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Grannhan, Patricia
REGISTRATION UNBER: W1194
TRIECOMMUNICATION INFORMATION:
TELEPHONE: 617-661-6540
TELEPHONE: 617-661-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-540-804-12
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                                                                                                    Sequence 12, Application US/08218265 Patent No. 5922585
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GENERAL INFORMATION:
APPLICANT: Young, Richard A.
APPLICANT: Koleske, Anthony J.
APPLICANT: Thompson, Craig M.
TITLE OF INVENTION: No. 5922585el Factors Which Modify Gene
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                                                                                                                                                                                                                                                              -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                   LAKNIFSAQKRVVSYMMPSLYRLLNILITYĞIIKVPTYIRKLISSGLLYLQDSNDKEVHVQ 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCPRFF-----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SILEFFKNLLF----VHLLSLSKNQREGCSTDMAVVST-----PFF------ 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----WKS 120
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ATTORNEY/AGENT INFORMATION:
NAMES Granahan, Patricia
REGISTRATION UNMERR: 32,227
REGISTRATION UNMERR: 32,227
REFERENCE/DOCKET NUMBER: WHI9-
FELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
FELEPAX: 617-861-6240
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: TYPE: protein
US-08-218-265-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                              344
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                                                                                                                                                       292 ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL-------
                                                                                                     404 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS 463
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CITY: Lexington
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 EFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 SILEFFKNLLF----VHLLSLSKNQREGCSTDMAVVST------PFF------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 YILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
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ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
                                                    -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                           LAKNFSAOKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLODSNDKFVHVO 403
                                                                                                                                                                                                                                                                                                                    WSIHPSROFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                                                                                                                                                                                                                                                                                                      WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG
                                                                                                                                                                                                                                                                                                                                                                                                                             DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YKPLLFEIVSNADTNONSDMKKKLELISYRNESLKNNSSIR-----NVIMSASNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 5.0%; Score 95; I
Similarity 18.8%; Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NRNLWYRLLSSRFSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 204;
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Query Match
Best Local Similarity 18.8%; Pred. No. 0.4;
Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps
                                                                                                                                                                                           404 ILINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVBITEQIKMRILSNDITNLQLS 463
                                                      ------AYGAV----LISSP----QELGHAFID-- 291
                                                                                                   344 LAKNFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLQDSNDKFVHVQ 403
                                                                                                                                                         292 ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL------ 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 YILKIALKLROSLSLPPQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
296 WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ- 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Young, Richard A.
APPLICANT: Young, Richard M.
APPLICANT: Young, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 6214588el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS: 39
ADDRESSED: Hamilton, Brock, Smith & Reynolds, P.C.
STREET: Two Milltia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PAINE: PLORM:
MEDIUM TYPE: PLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PAINE PC-DOS/MS-DOS
SOFTWARE: PAINE NO NOTE:
APPLICATION NUMBER: US 08/540,804
FILING DATE: 11-CCT-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/521,872
FILING DATE: 31-AUG-1995
PRIOR APPLICATION NUMBER: US 08/521,872
FILING DATE: 31-AUG-1995
PRIOR APPLICATION NUMBER: US 08/218,265
FILING DATE: 25-MAR-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                             334 ------EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                             464 KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,227
RR: WHI94-03A3
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08590399
Patent No. 6214588
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1226 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Lexington
STATE: Massachusetts
                                                            264 LIENHEGRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            186 YKPLLFEIVSNADTNQNSDMKKKLELISYRNESLKNNSSIR------NVIMSASNAN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 HQYLSLLQDRYFPIASVM-----RTLDKDN-----FSLTPDLIHDLLGHVP 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
5.0%; Score 95; DB 3; Length 1226;
Best Local Similarity 18.8%; Pred. No. 0.4;
Matches 98; Conservative 65; Mismatches 155; Indels 204; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66 SILEFFKNILF----VHLLSLSKNOREGCSTDMAVVST------PFF------ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 BFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 YYIVSSSKSMINDENYIINDIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 YILKIALKURQSLSLFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 YILE---KLIFDMINHYNDSQQL-RIWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV 65
                                                                                                                                    APPLICANT: Young, Richard A.
APPLICANT: Young, Anthony J.
APPLICANT: Thompson, Craig M.
APPLICANT: Thompson, Craig M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 6015682el Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
CORRESPONDENCE 37
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----NRNLWYRLLSSRFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/521,872
FILING DATE: 31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Granahan, Patricia
REGISTRATION NUMBER: 32.227
REFERENCE/DOCKET NUMBER: WH194-03A
TELECOMOUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIP TATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,265
FILING DATE: 25-WAR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          Sequence 12, Application US/08521872
Patent No. 6015682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-861-9520 12:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1226 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-08-521-872-12
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ZIP: 02173
                                                                                                                                             GENERAL
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US-09-180-4228-27
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Patent No. 6444644
GENERAL INFORMATION:
                                                          TELEFAX: 7038164100 INFORMATION FOR SEQ ID NO: 27: SEQUENCE CHARACTERISTICS:
                                                                                                                       COMPUTER READNELE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: CURKNOWN:
ATTORISY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION INFORMATION:
TELEPLONE: 7038164000
TELEPHONE: 7038164000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETTELAIE, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLIPOPROTEIN B-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BRUCKDORFER, KARL R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKPLLFEIVSNADTNONSDMKKKLELISYRNESLKNNSSIR-----NVIMSASNAN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ARLINGTON
                      LENGTH: 4536 amino acids TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------NRNLWYRLLSSRFSL-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----WKS 120
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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                              APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
BEFFFERENT/ADCOUNT NUMBER: 32,321/1
                                                                                   REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4404 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI -- IKSQAIA 4456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4344 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 4403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4286 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4231 RKHKLIDVISMYREL----LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED 4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4184 YTREELCTMFTREVGTVLSQVYSKVHNGSETL-----FSYFQDLVTTLPFE-----L 4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Lyon & Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Davis, MAPPLICANT: Sha, Dan TITLE OF INVENTION: NUMBER OF SEQUENCES:
  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 633 West F1:
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ARHKCISILEFFKNLLFVHLLSISKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                             TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A. ZIP: 90071-2066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----HQYLSLLQDRYFPIASVMRT----LDKDNFSLTPDLI------- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 Similarity 20.7%; Pred. No. 6.2; 61; Conservative 48; Mismatches 118; Indels 68;
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633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mamone, oc-
                         SEQ ID NO:
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                                                                                                                                    223/104
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57 QALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 SKKORIOTLOSNLIA------IVRCFWFTVESG----LIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             275 GAVLISSPQELGHAFIDNVRVLP--LELDQIIRLPFNTSTPQE-------- 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             316 -----TLFSIRHFDELVELTSKLEWM---LDQGLL-------ESIPLY-- 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 LWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 EWDSVYPKEFLRYDPPKGTGS-----RRLVDVFLNDSSFDPYDVIMYVVSGAY---LHDP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BGLTHEQCVDNWKSFAGVKF------GCFMPLSLDSD--LTMYLKDKALAALQR 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.8%; Score 91; DB 3; Length 535;
20.6%; Pred. No. 0.31;
tive 46; Mismatches 119; Indels 136;
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STREET: 865 South Figueroa Street, 29th Floor
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CTURCHAIL, MATGARET A. (Ph.D.)
REGISTRATION NUMBER: 39, 944
REPERBUNCE/DOCKET NUMBER: 1279-194XX
TELECOMMULICATION INFORMATION:
TELECHONE: 213/680-4518
INFORMATION FOR SEQ ID NO: 24;
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: anino acids
TYPE: peptide

WOLECULE TYPE: peptide
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nes 78; Conservative
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CITY: Los Angeles
STATE: California
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ZIP: 900
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Matches
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Sequence 24, Application US/08369822C
Patent No. 6015660
GENERAL INFORMATION:
APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Schneider, Patrick A.
APPLICANT: Stinz, Lothar
APPLICANT: Stinz, Lothar
APPLICANT: Stinz, Lothar
APPLICANT: Schneeman, Anette
APPLICANT: Schneeman, Anette
TITLE OF INVENTION: Diagnostics and Therapeutics for Central Nervous
TITLE OF INVENTION: System Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR----LPFN 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 KVIEKVQALPS------KKQRIQTLQSNLIA---IVRCFW-------- 257
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                                                                                                                                                                                                                                      Query Match
Best Local Similarity 17.5%; Pred. No. 0.57;
Matches 74; Conservative 70; Mismatches 141; Indels 139; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                           :| :: : |:: : :::|
224 IKENIENNKELAIMSKRLATIKRDIPIEIDFEEYKVKKFNEEK-------LLELFNK 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 LLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 LEFFSLIDNIKKE----SSIEIVD-----NHKVEKWSK-----VDIKELV 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPHQYLSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 TLLOD-----DL-STRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFOTE----DL 351
                                                                                                                                                                                                                                                                                                                                                                          14 LKIALKURQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NT-WORDPERFECT 8.0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS NT-WORDPE
SOFTWARE: ASCII (DOS) TEXT
CURRENT APPLICATION NOMBER: US/08/369,822C
FILING DATE: 06-JAN-1995
                                 LENGTH: 872 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                   MOLECULE TYPE: peptide
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California
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COUNTRY: USA
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US-08-369-822C-24
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-582-776C-39
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US-08-434-831B-36
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/892-9200
TELEPAX: 213/804-4518
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
                                                                            Sequence 36, Application US/08434831B Patent No. 6113905 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,831
FILING DATE: 04-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A.
REGISTRATION NUMBER: 39,944
REGISTRATION NUMBER: 39,944
APPLICANT: Lipkin, W. I.
APPLICANT: Briese, Thomas
APPLICANT: Kliche, Stefanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: WINDOWS
SOFTWARE: ASCII DOS TEXT
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 SKKQRIQTLQSNLIA-------IVRCFWFTVESG----LIENHEGRKAY 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.8%; Score 91; DB 3; Length 535;
Local Similarity 20.6%; Pred. No. 0.31;
Less 78; Conservative 46; Mismatches 119; Indels 136; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EGLTHEQCVDNWKSFAGVKF-------GCFMPLSLDSD--LTMYLKDKALAALQR 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFNL-----SYSLQEKEIKE-------TGRLFAKMTYKMRA-- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALP 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EWDSVYPKEFLRYDPPKGTGS-----RRLVDVFLNDSSFDPYDVIMYVVSGAY---LHDP
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IBM PC compatible
SYSTEM: WINDOWS NT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/369,822
PILING DATE: 06-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Churchill, Margaret A. (Ph.D.)
REGISTRATION NUMBER: 39,944
REFERENCE/DOCKET NUMBER: 1279-194C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 213/892-9200
TELEPAX: 213/680-4518
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 amino acids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartble
OPERATING SYSTEM: WINDOWS NT-WORDPERFECT
SOFTWARE: ASCII (DOS) TEXT
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APPLICANT: Stitz, Lothar
APPLICANT: Schneemann, Anette
TITLE OF INVERTION: Borna Disease Viral Sequences,
TITLE OF INVERTION: Dispostics and Therapeutics for Central Nervous
TITLE OF INVERTION: System Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA APPLICATION NUMBER: UFFILING DATE: 04-MAY-1
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CTATE: California
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  349 -NQE---KY-LSGFEVLCQ 362
                                                                                                                         316 -----TLFSIRHFDELVELTSKLEWM---LDQGLL----
                                                                                                                                                                            179 GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 238
                                                                            239 YCLNWRYETISLFAQR-LNEIYGLPSFFQWLHKRLETSVLYVSDPHCPPDLDAHIPLYKV 297
                                                                                                                                                                                                                      275 GAVLISSPQELGHAFIDNVRVLP--LELDQIIRLPFNTSTPQE-------
                                                                                                                                                                                                                                                                            128 -----CQVIAENLISNGIGKYFKDNGMAKDEQDLTKALHTLAVSGVPKDLKESHRG---- 178
                                                                                                                                                                                                                                                                                                                      237 SKKQRIQTLQSNLIA------IVRCFWFTVESG----LIENHEGRKAY 274
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                                                                                                                                                                                                                                                                                                                                                                                                                         177 YFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALP 236
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                                                                                                                                                                                                                                                                                                                                                                            EFNL-----SYSLQEKEIKE----
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865 South Figueroa Street, 29th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%; Score 91; DB 3; Length 535; illarity 20.6%; Pred. No. 0.31; Conservative 46; Mismatches 119; Indels 136; Gaps
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4.8%; Score 91, DB 2; Length 2183;
20.6%; Pred. No. 2.6;
tive 46; Mismatches 119; Indels 136; Gaps
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                                                                                                                       607 GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 666
                                                                                        316 -----TLFSIRHFDELVELTSKLEWM---LDQGLL------ESIPLY-- 348
275 GAVLISSPQELGHAFIDNVRVLP--LELDQIIRLPFNTSTPQE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,817
FILING DATE: 04-AUG-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/348,891
FILING DATE: 25-MOV-1994
PRIOR APPLICATION NUMBER: US 08/348,400
FILING DATE: 10-MOMER: US 07/848,400
FILING DATE: 10-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: UP 3-293625
FILING DATE: 14-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Addrew J.
REGISTRATION NUMBER: KP-7501A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 703-521-2997
TELEFRAN: 703-656-0573
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Patent No. 5824777
GENERAL INFORMATION:
                                                                                                                                                                                         349 -NQE---KY-LSGFEVLCQ 362
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2183 amino acids
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Matches 78; Conserve
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US-08-905-817-7
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                                                                                                                                                                                            APPLICANT: SASAKI, Keiko
APPLICANT: MORI, Takayuki
APPLICANT: MORINO, Satoshi
TITLE OF INVENTION: ATTENDATED MEASLES VIRUS VACCINE,
TITLE OF INVENTION: CONTAINING SPECIFIC NUCLEOTIDE SEQUENCE AND A METHOD FOR
TITLE OF INVENTION: ITS ABSOLUTE IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 YFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALP 236
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4.8%; Score 91; DB 1; Length 2183;
Best Local Similarity 20.6%; Pred. No. 2.6;
Matches 78; Conservative 46; Mismatches 119; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING STGTEM: PC-LOS/MS-DOS OPERATING STGTEM: PC-LOS/MS-DOS OFFWARE: Perentin Release #1.30 CURRENT APPLICATION NUMBER: US/08/348,891A FILING DATE: 25-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA: PRILING DATE: 10-MAR-1992
PRIOR APPLICATION NUMBER: US 07/848,400
FILING DATE: 10-MAR-1992
PRIOR APPLICATION NUMBER: 33-293625
FILING DATE: 14-OCT-1991
ATTONEY AGENT INFORMATION: NAME: PATCH, AND AMATONEY AGENT INFORMATION: REGISTATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: XP-7501
TELECHOMUNICATION INPORMATION:
TELECHOMUNICATION INPORMATION:
TELECHOMUNICATION INPORMATION:
TELECHOMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         Sequence 7, Application US/08348891A
Patent No. 5654136
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2183 amino acids
TYPE: amino acid
        298 PNDQIFIKYPMGGIEGYCQ 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein US-08-348-891A-7
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                      -08-348-891A-7
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US-08-484-105-6

APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:

APPLICANT: TITLE OF APPLICANT:

COUNTRY:

USA

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667

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ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard Aron
REGISTRATION UNUMBER: 36.627
REFERENCE/DOCKET NUMBER: A-59032/I
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEFAX: (415) 494-8771
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,105
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           349 -NQE---KY-LSGFEVLCQ 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 GAVLISSPQELGHAFIDNVRVLP--LELDQIIRLPFNTSTPQE--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YCLNWRYETISLFAQR-LNEIYGLPSFFQWLHKRLETSVLYVSDPHCPPDLDAHIPLYKV 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPVLKTYSRSPVHTSTRNVRAAKGFIGFPQVIRQDQDTDHPENMEAYETVSAFITTDLKK 666
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BELL, Stephen P
KOBAYASHI, Ryuji
linear
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PENTION: ORIGIN OF REPLICATION COMPLEX GENES
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HERSKOWITZ, Ira
LI, Joachim J
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Patent No. 5614618
GENERAL INFORMATION:
APPLICANT: STILLMAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 20.7 Matches 64; Conservative
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                                                                                                                                                                                                                                        ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PROPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, VC
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAURENSÓN APPLICANT: HERSKOWITI' APPLICANT: LI, Joach APPLICANT: LI, JOACH APPLICANT: GAVIN, KITILE OF INVENTION: ON UNMBER OF SEQUENCES:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ogman Ph.D., Richard Aron
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-59032/DJB/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELEPHORE: (415) 494-8771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 -QYLSLLQDRYFPIASYMRTLDKDNF-SLTPDL---IHDLLGHVPWLLHP-----SFSEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 QHAPADEILSLLTNKNRGLEEFFVEFLVRENPINGHAKFVARFLEEELNITNFNLIELY- 428
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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5614618
          910 277299
                                                                                                                                                                                                                                                                                                                                                                                                                                                              California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAVIN, Kimberly
VENTION: ORIGIN OF REPLICATION COMPLEX GENES
EQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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HERSKOWITZ, Ira
LI, Joachim J
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FOSS, Margit
McNALLY, Francis J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KOBAYASHI, Ry
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                                                                                                                                                                                                                                                                                            Version
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Sequence 3261, Application US/09134001C

Sequence 3261, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 654
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::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: | ::: 
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4.8%; Score 90; DB 4; Length 654;
Best Local Similarity 20.1%; Pred. No. 0.53;
Matches 83; Conservative 61; Mismatches 152; Indels 116; Gaps
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306 LKDNMNVHFSRTYLRLMSHVYLNNPLTSQIKRLYPFVFNTLYDSIRQLSQDTNIQLSEDE 365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 LDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD-----QGLLES----- 344
                                                                                                                                                                           147 KFFELETHFS--YYPVSGFVAPHQYLSLLQDRYFP----IASVMRTLDKD-NFSLTPDL 198
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; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3261
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US-09-134-001C-3261
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Patent No. 6380370
EBUSTALI INFORMATION:
APPLICANT: Lynn DOUCETE-Stamm et al
TITLE OF INVENTION: BEDDERMIDES FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: GTC-007
CURRENT APPLICATION WORBER: US/09/134,001C
CURRENT FILLING DATE: 1998-08-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.8%; Score 90.5; DB 1; Length 615;
Best Local Similarity 20.7%; Pred. No. 0.43;
Matches 64; Conservative 54; Mismatches 110; Indels 81; Gaps
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1 Similarity 20.5%; Pred. No. 0.5;
91; Conservative 71; Mismatches 172; Indels 110; Gaps
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PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LEWATH.
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                     INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 615 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-106-6
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US-09-134-001C-4504
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US-08-911-853-35; Sequence 35; Applicat; Patent No. 6048710; GENERAL INFORMATION:
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Query Match
Similarity 22.4%; Pred. No. 0.31;
Matches 71; Conservative 40; Mismatches 104; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/699,09
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gerritse, Gijsbert
APPLICANT: Quax, Wilhelmus J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                    306 GAVLSFEVKGGKÉAAWRFÍDATRVISITTNLGDTKTTÍAHPATTSHGRLSÞQÉRASAGÍR 365
                                                                                                            248 WMFLKGLETLRIRMQAQSASALELAR--WLETQPGIDRVYYAGLPSHPQHELAKRQQSAF 305
                                                                                                                                                                                                                                                                                         146 ------PNTKLLFVESPSNPLAELVDIGALAEIAHARGALLAVDNCFCT 188
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                                                           275 GAVL---ISSPQELGHAFIDNVRVLPL----ELDQIIRLPFNTS----TPQETLFS-IR 321
                                                                                                                                                     233 ----QALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE-----NHEGRK----AY 274
                                                                                                                                                                                                 189 PALQQPLALGADMVMH-SATKFIDGQGRGLGGVVAGRRAQMEQVVGFLRTAGPTLSPFNA 247
                                                                                                                                                                                                                                             196 PDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVI----EKV------
                                                                                                                                                                                                                                                                                                                                  149 FELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM------RTLDKDNFSLT 195
                                                                                                                                                                                                                                                                                                                                                                                                                       90 CST-DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
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CITY: Palo Alto
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INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 392 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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US-09-479-409-35
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Patent No. 6
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APPLICANT: Gerrit
APPLICANT: Quax, 1
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REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: GC:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
TELEFAX: 650-845-6504
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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CITY: Palo Alto
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                                           306 GAVLSFEVKGGKEAAWRFIDATRVISITTNLGDTKTTIAHPATTSHGRLSPQERASAGIR
                                                                                                                                                                                                                           189 PALQQPLALGADMVMH-SATKFIDGQGRGLGGVVAGRRAQMEQVVGFLRTAGPTLSPFNA 247
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  322 HFDELVELTSKLEWMLD 338
                                                                                       275 GAVL---ISSPQELGHAFIDNVRVLPL----ELDQIIRLPFNTS----TPQETLFS-IR 321
                                                                                                                                   248 WMFLKGLETLRIRMQAQSASALELAR--WLETQPGIDRVYYAGLPSHPQHELAKRQQSAF 305
                                                                                                                                                                          233 ----QALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE------NHEGRK----AY 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 90 CST-DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKF 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 4.7%; Score 89; DB 4; Length 392;
Similarity 22.4%; Pred. No. 0.31;
71; Conservative 40; Mismatches 104; Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Genencor International
925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gerritse, Gijsbert
Quax, Wilhelmus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION SYSTEM FOR ALTERED EXPRESSION LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/911,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GC361-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-996-338-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ωp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
4.7%; Score 89; DB 4; Length 392;
Best Local Similarity 22.4%; Pred. No. 0.31;
Matches 71; Conservative 40; Mismatches 104; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | ::| | ::| | ::| | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 1.1 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 CSAGDHVLVSRSVF------GSTISLFEKYLKRFGIEV--DYPPLADLDAWQAAFK- 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 PDLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVI-----EKV------ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 ----QALPSKKORIQTLQSNLIAIVRCFWFTVESGLIE------NHEGRK----AY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 WMFLKGLETLRIRMQAQSASALELAR--WLETQPGIDRVYYAGLPSHPOHELAKRQQSAF 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 GAVL---ISSPQELGHAFIDNVRVLPL----ELDQIIRLPFNTS----TPQETLFS-IR 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 GAVLSFEVKGGKEAAWRFIDATRVISITTNLGDTKTTİAHPATTSHGRLSPQERASAGİR 365
                                                                                                                          GENERAL INFORMATION:
APPLICANT: Gerritce, Gijsbert
APPLICANT: Gerritce, Gijsbert
APPLICANT: Gerritce, Gijsbert
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEB: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/479,453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GC361-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/911,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  US-09-479-453-35
; Sequence 35, Application US/09479453
; Patent No. 6313283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 35: SEQUENCE CHARACTERISTICS: LENGTH: 392 amino acids TYPE: amino acid STRANDENNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Glaister, Debra J
REGISTRATION NUMBER: 3698
REFERENCE/DOCKET NUMBER: GCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-846-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               322 HFDELVELTSKLEWMLD 338
366 --DNLVRVAVGLEDVVD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
TOPOLOGY:
US-09-479-453-35
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63 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 FL--HH-----NGKLFNITK------TFNIT--IVEDRSNIVPVLLGPKINHVAVELG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 -RNLWYRLLSSRFSIWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 CENSYYOTLVNSTSLYKN-CKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ISILBFF-----TPFFN-- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 DPKYI----LKIALKLRQSLSLFFONSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.6%; Score 87.5; DB 3; Length 309;
21.3%; Pred. No. 0.32;
tive 50; Mismatches 106; Indels 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FLORPY GIBE
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/996,338
FILING DATE: 22-DE-1997
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 12-MAR-197
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: UP 215,488/1997
FILING DATE: 38-JUL-1997
FILING DATE: 09-OCT-1997
FILING DATE: 09-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                   AUDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
STATE: D.C.
                                                                                                                                                                                            APPLICANT: TORIGOE, Kakuji
APPLICANT: OKURA, TAKANIOATI
APPLICANT: KURINOTO, MUSSSHI
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                      RESULT 22
US-08-96-338-22
; Sequence 22, Application US/08996338
; Patent No. 6087116
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TOF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 21.3*
Matches 68; Conservative
366 -- DNLVRVAVGLEDVVD 380
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RESULT 23
US-08-996-338-20
                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: US-08-996-338-20
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 291,83
FILING DATE: 09-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIORIZATION: INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                             Matches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TOKIOUE,
APPLICANT: OKURA, Takanori
APPLICANT: KURIMOTO, Musashi
TITLE OF INVENTION: POLYPEPTIDES
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 28-JUL-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 74,697/1997
FILING DATE: 12-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 215,488/1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
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                                        104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 SPQELGHAFIDNVRVLPLE 299
                                                                                63 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 120
                                                                                                                        65 ISILEFF----
                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0
FILING DATE: 22-DEC-1997
                                                                                                                                                                15 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL------HDC 62
                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                     9 DPKYI----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC 64
CENSYYQTLVNSTSLYKN-CKKLLLENNK---
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                                                                                                                                                                                                                                           4.6%; Score 87.5; DB 3; Length 521; llarity 21.3%; Pred. No. 0.7; Conservative 50; Mismatches 106; Indels 95;
                                                                                                                                                                                                                                                                                                                                                peptide
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09-OCT-1997
                                                                                                                        -----KNLLFVHLLSLSKNQREGCSTDMAVVS-----TPFFN-- 103
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-NPTIKKNAEFEDQ-GYYSCVH 168
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US-08-604-333-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 756822
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26.
TELECOMMUNICATION INFORMATION
TELEPHONE: (265) 597-0430
TELEPHONE: (206) 233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 51
CITY: Seattle
CITY: WA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 TPEGKWHA----SKVLRIE 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 FL--HH-----NGKLFNITK-----TFNIT--IVEDRSNIVPVLLGPKLNHVAVELG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
    188 FL--HH-----NGKLFNITK---
                                     163 FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
                                                                                140 CENSYYQTLVNSTSLYKN-CKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 187
                                                                                                                        104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
                                                                                                                                                                82 --VLEFWPVELNDTGSYFFQMKNYTQKWKLNVIRRNKHSCFTERQVTSKIVEVKKFFQIT 139
                                                                                                                                                                                                        65 ISILEFP-----TPFPN-- 103
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                             34 EPFYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL-------HDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 21-FE: CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 98101
                                                                                                                                                                                                                                                                                     9 DPKYI----LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kathryn A. Anderson, Immunex Corporation STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LICANT: Parnet, Patricia et al.
LE OF INVENTION: Receptor Designated 2F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2, Application US/08604333
5. 5776731
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                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                              h 4.6%; Score 87.5; DB Similarity 21.3%; Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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  ---TÉNIT--IVEDRSNIVPVLLGPKLNHVAVELG
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APPLICANT: Timans, Jacqueline C.
APPLICANT: Theores, Johannes Eduard Maria
APPLICANT: Antonius
APPLICANT: Sana, Theodore R.
APPLICANT: Sana, Theodore R.
APPLICANT: Ratelein, Robert A.
APPLICANT: Ratelein, Robert A.
APPLICANT: Human Receptor Proteins; Related Reagents and Methods NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
  Query Match 4.6%; Score 87.5; DB 4; Length 541; Best Local Similarity 21.3%; Pred. No. 0.75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOSG/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PELLICATION NUMBER: US/09/173,151A
FILING DATE: 14-OCT 1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/05,776
FILING DATE: 17-MAR-1998
FILING DATE: 12-MAR-1998
FILING DATE: 12-MAR-1998
FILING DATE: 12-MAR-1998
PRIOR APPLICATION NUMBER: US 60/081,883
FILING DATE: 15-APR-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 10-AUG-1998
PRIOR APPLICATION NUMBER: US 60/095,987
FILING DATE: 110-AUG-1998
PRIOR APPLICATION NUMBER: US 60/078,416
FILING DATE: 118-MAR-1998
PRIOR APPLICATION NUMBER: US 60/078,416
FILING DATE: 118-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Lazz
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: PLODS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
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FILING DATE: 15-OCT-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 Sequence 28, Application US/09173151A Patent No. 6326472 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34,090
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        not relevant
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231 K---NVRLNCSALLNEEDVI---
                                                                              281 SPQELGHAFIDNVRVLPLE 299
                                                                                                                         271 TPEGKWHA----SKVLRIE 285
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TYPE: amino acid
STRANDEDNESS: not releva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ching, Edwin P. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-09-173-151A-28
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                                  231 K---NVRLNCSALLNEEDVI------YMMFGEENGSDPNIHEEKE----MRIM 270
223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 RLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW-FTVESGLIEN-HEGRKAYGAVLIS 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 FVAPHQYLSLLQDRYFPIASVMRTLDKONFSLTPDLIHDLLGHVPWLLHPSFSEFFINMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
4.6%; Score 87.5; DB 3; Length 541;
Best Local Similarity 21.3%; Pred. No. 0.75;
Matches 68; Conservative 50; Mismatches 106; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 EPPYLKHCSCSLAHEIETTTKSWYKSSGSQEHVELNPRSSSRIAL-------HDC 81
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Parnet, Patricia et al.
TITLE OF INVENTION: Receptor Designated 2F1
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/110,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/604,333
FILING DATE: 21-FEB-1996
ATTORNEY AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2619
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
                                                                                                                                                                                                                                        5-09-110-618-2
Sequence 2, Application US/09110618
Patent No. 6090918
GENERAL INFORMATION:
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INPORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acide
                                                                                                  281 SPQELGHAFIDNVRVLPLE 299
                                                                                                                                        271 TPEGKWHA----SKVLRIE 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 541 amino acids
rYPB: amino acid
TYPB: amino acid
TOPOLGGY: linear
MOLECULE TYPE: protein
US-09-110-618-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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ZIP: 98101
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US-09-578-178-2
; Sequence 2, Application US/09578178
; Patent No. 6451760
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  Ouery Match

4.6%; Score 87.5; DB 4; Length 541;
Best Local Similarity 21.3%; Pred. No. 0.75;
Matches 68; Conservative 50; Mismatches 106; Indels 9
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/578,178
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/110,618
APPLICATION NUMBER: 09/110,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Parnet,
                                                                                                                                            TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 541 amino acids
                                                                                            TYPE: amino acids
TYPE: amino acid
TOPOLOGY: 14--
TOLECTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Receptor Design
                                                                                                                                                                                                                                    NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A
                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 51 University Street
CITY: Seattle
STATE: WA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 CEŃSYYQTLVNSTŚLYKN-ĆKKLLLENNK------NPTIKKNAEFEDQ-GYYSCVH 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 -RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG 162
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                                                                                                                                                                                                                     (206) 233-0644
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  95;
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  Gaps
  19;
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US-08-392-625-20
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Patent No.
                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
PILING DATE: 30-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REFERENCE/DOCKET NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.09800
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
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TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                     COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392.675
FILING DATE:
CLASSTET
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APPLICANT:
APPLICANT:
TITLE OF INT
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                    Washington
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T: Jung, G nther
T: Kellner, Roland
INVENTION: Biosynthetic Process For The Preparation
INVENTION: Of Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Application US/08392625
5837485
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1100 New York Avenue
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Wieland, bc.
Thomas
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Kaletta, cu
Kaletta, cu
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Schnell, No. 5837485bert
Augustin, Johannes
Engelke, Germar
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Kaletta, Cortina
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                                                                       0652.0980002
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldstein & Fox
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us-09-438-185a-1047.rai

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4.6%; Score 86.5; DB 2; Length 990; 23.1%; Pred. No. 2.4; tive 38; Mismatches 79; Indels 7:
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Patent No. 596223
GENERAL INFORMATION:
APPLICANT: Kupke, Thomas
APPLICANT: Kempter, Christoph
APPLICANT: Jung, Gunther
TITLE OF INVENTION:
TITLE OF INVENTION: Catalyzed by Flavoprotein EpiD
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DADRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
                                                                                                                                0652.0980004
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,234
FILING DATE: 31-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bemond, RODET W.
REGISTRATION NUMBER: 32,893
REGISTRANION NUMBER: 0652.09800C
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISIS:
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NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
                                                                                                                                                                                                                    Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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US-08-645-193B-15
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STATE:
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                                                                                                                           Query Match
4.6%; Score 86.5; DB 2; Length 990;
Best Local Similarity 23.1%; Pred. No. 2.4;
Matches 57; Conservative 38; Mismatches 79; Indels 73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Klein, Cortina
APPLICANT: Klein, Cortina
APPLICANT: Wieland, Bernd
APPLICANT: Wieland, Bernd
APPLICANT: Wieland, Bernd
APPLICANT: Walner, Thomas
APPLICANT: Walner, Roland
TITLE OF INVENTION: Biosynthetic Process for the Preparation of
TITLE OF INVENTION: Chanical Compounds
NUMBER OF SEQUENCES:
ADDRESSE: Sterne, Kessier, Goldstein & Fox
STREET: 1100 New York Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                        764 FYIKFKEDEDFIK------LRLLREDEDYSQIYSFIKNW-KDYCLLNSELYDY 809
                                                                                                                                                                                                                                                                                             50 QKENKE----KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFF-- 102
                                                                                                                                                                                                                                                                                                                        658 NLLNDKHLIILKKELKKHGRIRILESF-----INESNNER-----MLEIVTPLYKK 703
                                                                                                                                                                                                                                                                                                                                                                               103 ------NRNLWYRLLSSRFSLW----KSYCPRFFLDYLEAFGL---LSDFLDHQ 143
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                                                                                                                                                                                                                3 YCERTLDPKYILKIAL-KLRQSLSLFFQNSQSLQRAYSTPYSYY-----RIIL 49
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APPLICATION NUMBER: US/08/466,961A
FILING DATE: 06-UN-1995
RIOR APPLICATION: 435
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G tz, Friedrich
Schnell, No. 5843709bert
Augustin, Johannes
Rogenkerein, Ralf
Kaletta, Cortina
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APPLICATION NUMBER: US 08/392,625
PLING DATE: 22-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/876,791
FILING DATE: 30-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-08-466-961A-20
Sequence 20, Application US/08466961A
                        LENGTH: 990 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-392-625-20
    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                   50 QKENKE----KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFF-- 102
                                                                                                                                                                                                                                                                                                          658 NLLNDKHLIILKKELKKHGRIRILESF-----INESNNER-----MLEIVTPLYKK 703
                                                                                                                                                                                                                                                                                                                                                                                      103 ------NRNLWYRLLSSRFSLW----KSYCPRFFLDYLEAFGL---LSDFLDHQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                             704 TSLKEQSFIIPKNRHFNNLKDWFSIHLSIPKTYQDNFIQDYLLPFITELKVNNFINKF 763
                                                                           3 YCERTLDPKYILKIAL-KLRQSLSLFFQNSQSLQRAYSTPYSYY-----RIIL 49
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REFERENCE/DOCKET NUMBER: 0652
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 990 amino acids
TYPE: amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-645-193B-15
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TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4322
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US-09-134-001C-4322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4322, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn DOUCETTE-Stamm et al
APPLICANT: Lynn DOUCETTE-Stamm et al
TITLE OF INVENTION: EDIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                            Query Match 4.6%; Score 86; DB 4; Length 656; Best Local Similarity 22.5%; Pred. No. 1.5; Matches 51; Conservative 28; Mismatches 78; Indels 70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery March

4.6%; Score 86.5; DB 2; Length 990;
Best Local Similarity 21.7%; Pred. No. 2.4;
Matches 62; Conservative 43; Mismatches 100; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        810 YSIVDYVPEVYRYGGPHVIEDIENFFMYDSLLSINIIQSEFKIPKE 855
101 FFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV 160
                                                                                                                                                                   369 CFQTVNPNNPAELLAEEKEVMDKLLLSFQQSEKLRRHMSFLMRKGKLYLPYNGNLLIHGC 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 HDLLGHVPWLLH------PSFSEFFINMGRLFTKVIEKVQALPSK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 FFYIKFKEDEDFIK------LRLLREDEDYSQIYSFIKNW-KDYCLLNSELYD 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQ--DRYFPIASVMRTLDKDNFSLTPDLI- 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   704 KTSLKEQSFIIPKNRNKHFNNLKDWFSIHLSIPKTYQDNFIQDYLLPFITELKVNNFINK 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    658 LNLLNDKHLIILKKELKKHGRIRILESF-----INESNNER-----MLEIVTPLYK 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              601 FĆPRIIYKNIILKPÄTWKINSEM---FSETENWLNRFATIREKWHIPKDVIIAFGDNRLL 657
                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 LQKENKE-----KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFF- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YCERTLDPKYILKIAL-KLROSLSLFFONSOSLORAYST------PYSYYRII 48
                                                                                                                                                                                                                       4 CERTLDPK---YILKIALKLRQSLSLFFQNSQSLQRAYS-----TPYS----YYRI 47
                                                       IPVDENGEMESFEIEGERLSGRELLDVFEYHVRRAFDH----KESTEDISTDL----- 477
                                                                                                           ILQKENKEKQA-----LARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0652.1540000
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Db 478											
161 GGFVAPHQUISLLOPEXPETASUMETISCOMPESITEDLINGLIGHTP 548 162	S Ω Φ S ι S	유 성	용 성	B &	용 성	B 8	B 8	Z 111 10	US- S GPS	B 8	DЬ
70	33 810-347-2 ence 2, Application US/09810347 nt No. 6461847 nt No. 6461847 LE OF INVERNION: ESOLATED HUMAN ENZYME PROTEINS, NUCLEIC LE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND LE OF INVENTION: THEREOF E REFERENCE: CLOOL169 E REFERENCE: CLOOL169 E REFERENCE: CLOOL3-19 BER OF SEQ ID NOMER: US/09/810,347 RENT APPLICATION NUMBER: US/09/810,347 RENT FILING DATE: 2001-03-19 BER OF SEQ ID NOS: 6 BER OF SEQ ID NOS: 6 ID NO 2 NGTH: 372	NHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF	4	TNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSYNYAPNM	IKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLL :	FPNRNLMYRLLSSRFSLMKS-YCPRFFLDYLEAFGLLSDFLDHQAV	5 YRIILQKENKEKQALARHKCISILEPFKNILFVHLLSLSKNQREGCSTDMAVVSTP	Match 4.5%; Score 84.5; DB 4; Length 360; Local Similarity, 19.6%; Pred. No. 0.85; 95 67; Conservative 51; Mismatches 117; Indels 107; Gaps 14	ion US/09810347 et al. ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, AND US THEREOF 01169 (NUMBER: US/09/810,347 is: 2001-03-19 Or Windows Version 4.0	61 SGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVP 20 	78VWYLWT

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106 -----SASSRAGSKKEIQEAKAPSPSINR------QTSIETDRVTKEFIDFLKT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 F-----HKIGQEVYK--QTRMPLEAMPYKRDLSIEEQSECTQDFYQNVAERMQT---- 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 LEVHLLSLSKNOREGCSTDM--AVVSTPFFNRNLMYRLLSSRFSLWKSYCPRFFLDYLEA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         190 DNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15 KIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNL 74
                                     ---LLPFSSD 505
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18.4%; Pred. No. 2;
tive 48; Mismatches 110; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILITON, BROOK, SMITH & REYNOLDS, P.C. STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                       RESULT 35
US-08-942-819-2
US-08-942-819-2
Sequence 2, Application US/08942819
SEQUENCE 2, Application US/08942819
SEQUENCE 3, Application US/08942819
SEPLICANT: Tam, Sec-Ying
APPLICANT: Tam, Mindy
APPLICANT: Tam, Mindy
TITLE OF INVENTION: RISA
TITLE OF INVENTION: RAS-MEDIATED SIGNALING
TITLE OF INVENTION: RAS-MEDIATED SIGNALING
WUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Fratten Corwindows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,819
FILING DATE: 02-007-1997
:: :|: |: || :: | 3.4 || :: | 3.4 || :- || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3.4 || 3
                                                                                                                              312 TPQETLFSIRHF----DELVELTSKLEWML 337
                                                                                                                                                                                                                   506 SDKSVVNKİYELKNSTDNLTELKSFLETML 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIH96-13pA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/058,520
ATTORNEY/AGENT 11-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: GERBARAIN, PARTIGOS
REFERENCE/DOCKET NUMBER: BIH96-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
TELEFAX: 781-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 491 amino acid TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 18.49
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-942-819-2
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                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
4.5%; Score 84.5; DB 4; Length 372;
Best Local Similarity 19.6%; Pred. No. 0.89;
Matches 67; Conservative 51; Mismatches 117; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.4%; Score 83.5; DB 6; Length 1365;
19.0%; Pred. No. 8.3;
tive 49; Mismatches 100; Indels 167; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 -----YLEAFGLLSDFLDH--- 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         228 NGSRMSSIPQLKKILYTVPKEILVGADNKKQLHDLEPEELRELKLRVTSLISEFYQYKKD 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 -----QAVIKFF----- 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            164 --VAPHQYLSLLQDRYFPIASVWRTLDK-----DNFSLTPDLIHDLLGHVPWL--- 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348 TSLTPYNLLTALKTEYOSLLKITNLLQELEPSKCILDSKFLLNKFSQFSLGKLQNLQPIK 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 TNESINYFKMSKRMYPHRPVMMVISHAAPHGPEDSAPQFSKLYPNASQHITPSYNYAPNM 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 YRIILQKENKEKQALARHKCISILEPPKNLLFVHLLSLSKNQR----EGCSTDMAVVSTP 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 F------FNRNLWYRLLSSRFSLWKS-YCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 MCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRTFAVYLNNTGYRTAFFG---- 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                      146 IKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT--LDKDNFSLTPDLIHDLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 NHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF 308
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Best Local Similarity 19.0%;
Matches 74; Conservative
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                          ; TYPE: PRT
; ORGANISM: Human
US-09-810-347-2
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-913-159-2
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US-09-022-875-2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179
APPLICATION NUMBER: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
                                                                                                                 Sequence 2, Application US/09022875
Patent No. 6071894
GENERAL INFORMATION:
APPLICANT: Wallis, Nicola G.
TITLE OF INVENTION: No. 6071894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
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-4.3%; Score 82; DB 4; Length 284;
Best Local Similarity 26.1%; Pred. No. 1.1;
Matches 53; Conservative 29; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Plasmid-derived of INVENTION: restriction-modi number of Sequences: 14

COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: Dechert,
                                                                                                                                                                                                                                                                                                                                                                                           340 GLLESIPLY---NOEKYLSG-FE 358
                                                                                                                                                                                                                                                                                                                                                                                                                                         111 KMS----EVERAARI------MYMLRVDFNGLYRVNSKNQFNVPYGRYKNPKIVDK 156
                                                                                                                                                                                                                                                                                                                                              157 ELIESISEYLNNNSIKIMSGDFE 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 NVRVLPLELDQIIRLPFNTSTPQETLFSIR-HFDELVELTSKLEW------MLDQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 PSKKQRIQTLQSNLIAIVRCFWFTVES--GLIENH--EGRKAYGAVLISSPQELGHAFID 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          184 MRTLDKDNFSLTPDL-----IHDLLGHVPWLLHPSFSEF---FINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 PVNEEIPEVSDMVVKAITDIIEMDSK 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 APQKAVINDFNSELINCYROMKDNPEQLIELLTNHQRENSKEYYLDLRSSDRD---GRID 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
  CITY: Philadelphia
                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNLLQKNKINLRPFTKWTGGKRQLLPHIQYLMPEKYNHFFEPFIGGGALFFE-----L 53
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                      E: Dechert, Price & Rhoads
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                                                                                                                         No. 6071894el Compounds
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                            1717 Arch Stre
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Sequence 5, Application US/09810347
Patent No. 6461847
GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PF.
TITLE OF INVENTION: THEREOP
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US-09-810-347-5
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SEQUENCE CHARACTERISTICS:
LENGTH: 861 amino acids
TPAPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.3%; Score 82; DB 3; Length 861; Best Local Similarity 22.4%; Pred. No. 6; Matches 87; Conservative 66; Mismatches 144; Indels 92;
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ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
REFERENCE/DOCKET NUMBER: GM5(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION NDYA:
APPLICATION NUMBER: US/09/022,875
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                                                                                                                                                                                                                                                                                                                          329 LTSKLEWMLDQGLLESIPLYNQEKYLSGF 357
                                                                                                                                                                                                                                                                                                                                                                        745 RRHLKKRITVSSSVNLQFIHIDSKLILQALFNLIENAVKHTSTDTKINLSIRYASYEQIE
                                                                                                                                                                                                                                                                                                                                                                                                                  270 GRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD-ELVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     686 -MSIIEKEOLLVHSFQESQYLYLLVTNILSLTKLQSSNVQIKLQPYLVSELVEEIDMILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     225 FTKVIEKVQALP---SKKQRIQTLQSNLIAIVRCFWFTVE-----SGLIEN----HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 LSLLQDRYFPIASVMRTLDKDNF--SLTPDL---IHDLLGHVPWLLHPSFSEFFINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 TSPIK------GILA--IDYQSSQVINPYDASILESMLNELSLA-----VEN 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 FSLWKSYCPRFFLDYLEAFGLLSDFLDHQA--VIKFFE---LETHFSYYPVSGFVAPHQY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 ----KTIPLQNHIDNTTQQHEQALSWVIKNERQAGATTD-----TFPGINKW--LIPIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 LARHKCISILEFFKNLLFVHLLSLS---KNQRE-GCSTDMAVVSTPFFNRNLWYRLLSSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 KYILKIALKLRQSLSLFFQNSQSLQRAYSTP----YSYYRI--ILQKE-----NKEKQA 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                               PROTEINS, AND USES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                195 MNFIEEMDMKKLLLBIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 IR---LPFNTSTPQE-TLFSIRHFDELVELTSKLEWMLDQGLLESIPLYN------ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 YKEAGYQFNVNSPKQLSEFLFEKINLPVIKKTKTGYSTDSEVLEQLVPYNDIVSDIIEYR 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 ISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 FFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPHQYLSLLQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 DRYFPIASVMRTLDKDNFSLTPDLJHDLL-------GHVPWLJHPSFSEF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 FINMGRLFTKVIEKVQALPS------KKQRIQTLQSNLIA---IVRCFW----- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             139 --DLDRVLKKYL-KVD-VPSYEGIFGKGRDKKKIEEIDENILADYICSRCVYLFDLKEKL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKLLELPNKLEFFSLIDNIKKE-----SSIEIVD------38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 --VDIKELVTLLQD-----NRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 4.3%; Score 81.5; DB 1; Length 608;
1l Similarity 18.0%; Pred. No. 4;
67; Conservative 57; Mismatches 120; Indels 129;
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Sequence 2, Application US/08493092;
SEREAL INFORMATION;
APPLICANT: Shiloh, Yosef
APPLICANT: Tagle, Danilo A.
TITLE OF INVENTION: Ataxia-Telangiectasia Gene
WUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard & Perry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALDLE
CONFUTER: IBM PC COMPALDLE
CONFUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
US/DELAGATION NUMBER: US/08/493,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Reising, Ethington, Barnard & Perry
P.O. Box 4390
                                 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 608 amino acids
TYPE: amino acids
TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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ZIP: 48099
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-766-014-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 -----QEKYLSGF 357
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                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O
CITY: Troy
STATE: Mich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 NYAPNMDKHWIMQYTGPMLPIHMEFTNILQ------RKRLQTLMSVDDSVERLYNMLV 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 AVVSTPF-----FNRNLWYRLLSSRFSLWKS-YCPRFFLDYLEAFGLLSDF 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 LDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRT--LDKDNFSLTPD 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 LIHDLL----- 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224 ------CSTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93; Indels 99; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 AFVITEMCCPSRSSMLTGKYVHNHNVYTNNENCSSPSWQAMHEPRIFAVYLNNTGYRTAF 86
                                                                                                                                                                                                                                                                                                                                                                                                          4.3%; Score 81.5; DB 4; Length 307;
19.8%; Pred. No. 1.4;
tive 39; Mismatches 93; Indels 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 ESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPF 308
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APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
APPLICANT: Davis, Maria
APPLICANT: Sai, Dan
APPLICANT: Sai, Dan
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 60/008,688
FILING DATE: December 15, 1995
FILING DATE: December 15, 1995
REGISTATION NUMBER: 32,327
REGISTATION NUMBER: 32,327
                                              CURRENT APPLICATION NUMBER: US/09/810,347
CURRENT FILING DATE: 2001-03-19
NUMBER OF SEG ID NOS: 6
SOFTWARE: PASESEQ for Windows Version 4.0
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM PC. DOS 5.0
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
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FILING DATE: Herewith
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STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08766014 Patent No. 5744312 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 19.89
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
            FILE REFERENCE: CL001169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: HE CLASSIFICATION:
                                                                                                                                                                                                                                                                      TYPE: PRT
, ORGANISM: Human
US-09-810-347-5
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US-08-766-014-3
                                                                                                                                                                                              SEQ ID NO 5
LENGTH: 307
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RESULT 41
US-08-508-836A-2
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TOPOLOGY:
US-08-493-092-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08508836A Patent No. 5777093 GENERAL INFORMATION:
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Query Match
Similarity 18:5%; Pred, No. 19;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/508,836A
FILING DATE:
APPLICATION: 536
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
REGISTRATION: MUMBER: J0,955
REFERENCE/DOCKET NUMBER: P-313 (TAU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1708 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Shiloh, Yosef
APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: Ataxia-Telangiectasia Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 9-5
REFERENCE/DOCKET NUMBER: 9-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 689-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Troy
STATE: Mich
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV------ 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFSLLEEINH-FLSVSVYDALPLTRLEGLKDLRRQLELHKDQMVDIMRASQDNPQDGIMV 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSHVIKATFAYISNCHKTKLKSILEILSK------SPDSYQKILLAICEQAAETNN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Reising, Ethington, Barnard & Perry P.O. Box 4390
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linear
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689-4071
NO: 2:
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US-08-508-836A-8
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APPLICATION: 536
FILING DATE:
CLASSIFICATION: 536
ATTORNEY AGENT INFORMATION:
NAME: KOHN, Kenneth I.
REGISTRATION NUMBER: 9-313 (TAU)
REFERENCE/DOCKET NUMBER: P-313 (TAU)
FILECOMMUNICATION:
TELEPHONE: (810) 689-4071

TELEPHONE: (810) 689-4071
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TOPOLOGY:
US-08-508-836A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08508836A Patent No. 5777093
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Best Local S
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APPLICANT: Shiloh, Yosef
APPLICANT: Tsjle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: Acaxia-Telangiectasia Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (810) 689-4071
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                     SOPTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/508,836A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (810) 689-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 EVOKOVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS COPTWARD PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES PARTIES 
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TYPE: amino acid
STRANDEDNESS: sin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ALARHKCISILEFFKNILFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 PSHVIKATFAYISNCHKTKLKSILEILSK-----SPDSYQKILLAICEQAAETNN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFSLLEEINH-FLSVSVYDALFLTRLEGLKDLRRQLELHKDQMVDIMRASQDNPQDGIMV 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 4.3%; Score 81.5; DB 1; Length 1708;
Similarity 18.5%; Pred. No. 19;
61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michigan
Y: US
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P.O. Box 4390
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linear
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1587 PFSLLEBINH-FLSVSVYDALPLTRLEGLKDLRRQLELHKDQMVDIMRASQDNPQDGIMV 1645
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                                                                                                                                                                              Query Match
4.3%; Score 81.5; DB 2; Length 3056;
Best Local Similarity 18.5%; Pred. No. 47;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
                                                                                                                                                                                                                                                                                                                                       1382 PSHVIKATFAYISNCHKTKLKSILEILSK------SPDSYQKILLAICEQAAETNN 1431
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Sequence 2, Application US/08874266
GENERAL INFORMATION:
APPLICANT: Gatti, Richard A.
APPLICANT: Gatti, Richard A.
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA:MUTATIONS IN THE ATM GENE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSS:
ADDRESSBE: Khobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
CHAPTER OF SECURATIONS IN THE ATM GENE
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                                                                                                                                                                                                                                                                                                                                                                                       58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                           10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
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SOFTWARE: FastESG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,266
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TELECOMUNICATION INFORMATION: 619-235-8550
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Diskette
IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ways Vensko, Nancy
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                  ; ORGANISM: Homo sapiens
US-08-629-001A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Con
OPERATING SYSTEM:
                      linear
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STRANDEDNESS:
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US-08-874-266-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1533 EVQKQVLDLL---YYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 1586
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                                                                                                                                                                                                                                                                                                                                                                       Query Match

4.3%; Score 81.5; DB 1; Length 3056;
Best Local Similarity 18.5%; Pred. No. 47;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP---- 166
                                                                                                                                                                                                                                                                                                                              10 PKYILKIAL-----KURQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08629001A
Sequence 3, Application US/08629001A
Sequence 3, Application US/08629001A
GENERAL INCORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSES
STREET: 30500 No. 5858661thwestern Hwy.
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: IBM PC comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/629,001A
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TLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955

REFERENCE/DOCKET NUMBER: 2290.00032

TELECOMMUNICATION INFORMATION:
TELEPAK: (810) 539-5050

TELEPAK: (810) 539-5050

INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3056 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1646 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 1675
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 3056 amino acids TYPE: amino acid STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                        linear
                                                                                                                                        , TOPOLOGY:
US-08-508-836A-8
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APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: MUTATED FORMS OF THE ATAXIA-TELANGIECTASIA GENE AND METHOD TO
TITLE OF INVENTION: SCREEN FOR A PARTIAL A-T PHENOTYPE
FILE REFERENCE: 22900003
CURRENT APPLICATION NUMBER: US/08/642,274D
CURRENT FILING DATE: 196-05-03
NUMBER OF SEQ ID NOS: 220
SOFTWARE: PATENTIN Ver: 2.1
SEQ ID NO 3
LENGTH: 3056
TYPE: PRT
ORGANISM: Homo sapiens
US-08-642-274D-3
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US-08-642-274D-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08642274D Patent No. 6200749
GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
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Matches 61; Conservative
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Best Local Similarity
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                1382 PSHVIKATFAYISNCHKTKLKSILEILSK-----SPDSYQKILLAICEQAAETNN 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1646 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 1675
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                                                                                                                                                 1432 VYKKHRILKİYHLFVSLLL-----KDIKSGLGGAWA-----FVLRDVIYTLIH----- 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1533 EVQKQVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 1586
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                                                                                              118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                               58 ALARHKCISILEFFKNILFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                                                                                                10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
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---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV--
                                                   YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 1532
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18.5%; Pred. No. 47;
ative 58; Mismatches 114; Indels 97; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 810-539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3056 amino acids
TYPE: amino acid
                                                                                                                                                                       1382 PSHVIKATFAYISNCHKTKLKSILEILSK-----SPDSYQKILLAICEQAAETNN 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERENCE/DOCKET NUMBER: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1533 EVQKQVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 1586
                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION TELEPHONE: 810-539-5050
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1475 YINQRPSCIMDVSLRSFSLCCDLLSQVCQTAVTYCKDALENHL--HVIVGTLIPLVYEQV 1532
                                                                                     1432 VYKKHRILKIYHLFVSLLL------KDIKSGLGGAWA-----FVLRDVIYTLIH----- 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Tagle, Danilo A.
APPLICANT: Collins, Francis S.
TITLE OF INVENTION: ATAXIA-TELANGIECTASIA GENE
NUMBER OF SEQUENCES: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1646 KLVVNLLQLSKMAINHTGEKEVLEÁVGSCL 1675
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APPLICANT: Tagle, Danilo A.
                                          118 WKSYCPRFFLDY-LEAFGLLSDFLDH--QAVIKFFE--LETHFSYYPVSGFVAP----- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267 ------NHEGRK----AYGAVL 278
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                                                                                                                             58 ALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSL 117
                                                                                                                                                                                                                  10 PKYILKIAL-----KLRQSLSLFFQNSQSLQRAYSTPYSYYRIIL---QKENKEKQ 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRRESEE: Kohn & Associates
STREET: 30500 No. 6211336thwestern Hwy., Suite
CITY: Farmington Hills
STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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18.5%; Pred. No. 47;
1tive 58; Mismatches 114; Indels 97; Gaps
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167 --- HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV----

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1533 EVQKQVLDLL--KYL----VIDNKDNENLYITIKLLDPFPDHVVFKDLRITQQKIKYSRG 1586
                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:

APPLICANT: Richard A. Gatti
TILE OF INVENTION: METHODS FOR DETECTION OF ATAXIA
TITLE OF INVENTION: TELANGIECTASIA MUTATIONS
FILE REFERENCE: 510015-223
CURRENT APPLICATION NUMBER: US/09/360,416
CURRENT FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 143
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO
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US-08-540-804-18
; Sequence 18, Application US/08540804
; Setent No. 591966
; Patent NO. 591966

CENERAL INFORMATION:
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US-00-360-416-3
'Sequence 3, Application US/09360416
; Patent No. 6458536
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Best Local Similarity
Matches 61; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 3057
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1382 PSHVIKATFAYISNCHKTKLKSILEILSK------SPDSYQKILLAICEQAAETNN 1431
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4.3%; Score 81.5; DB 4; Length 3056;,
Best Local Similarity 18.5%; Pred. NO.47;
Matches 61; Conservative 58; Mismatches 114; Indels 97; Gaps
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                                                            207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
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                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Shiloh, Yosef
TITLE OF INVENTION: GENOMIC ORGANIZATION
TITLE OF INVENTION: GENOMIC ORGANIZATION
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOLD & Associates
ADDRESSEE: KOLD & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Kohn & Associates
STREET: 30500 No. 6,565158thwestern Hwy., Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 ---HQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,014C
                                                                                                                                                                          1646 KLVVNLLQLSKMAINHTGEKEVLEAVGSCL 1675
                                                                                                                                           267 ----AYGAVL 278
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                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08952014C Patent No. 6265158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: KODH, Kenneth I.
REGISTRATION NUMBER: 30,995
REFERRICE/DOCKET NUMBER: 225
TELECOMMUNICATION INFORMATION:
TELEPHONE: 810-539-5050
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: si
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MOLECULE TYPE: I
ORIGINAL SOURCE:
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ORGANISM:
US-08-952-014C-3
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207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
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                    APPLICANT: Young, Richard A.
APPLICANT: Young, Anthony J.
APPLICANT: Thompson, Crain M.
APPLICANT: Thompson, Crain M.
APPLICANT: Thompson, Crain M.
APPLICANT: Chao, David M.
TITLE OF INVENTION: No. 591966e1 Factors Which Modify Gene
TITLE OF INVENTION: Transcription and Methods of Use Therefor
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEB: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 3057;
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18.5%; Pred. No. 47;
live 58; Mismatches 114; Indels
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEPAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 323 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: protein
US-08-218-265-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match Similarity 23.0%; Pred, No. 1.7;
Matches 56; Conservative 31; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: PLOPBY disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/218,265
FILING DATE: 25-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI94-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Mili
CITY: Lexington
STATE: MA
COUNTRY: US
300 WDKY 303
                                              351 -EKY 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                134 CPQYIRTLVSEARTLWPEFIPPDPTKVTEFEFYLLEELESY-----LIVHHPYQSLKQ-- 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 CPRFFLDYL-EAFGLLSDFL--DHQAV--IKFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                      291 DNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                   231 KVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFI 290
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Page 1

Q99cz3 arabidopsis Q9gf63 arabis alpi Q42428 lates calca Q9gf55 cardamine a Q9gf31 cardamine p Q9gf30 cardamine p Q95f30 whlenbergi Q95f39 wnonnthochl Q95f39 monanthochl Q99f41 aubriera de	OFFIDE bouteloua c Q95160 buchloe dac Q95510 buchloe dac Q95510 schedonnard Q9518 rederochlo Q9718 advosophila Q9723 drosophila Q972m5 sulfolobus Q972m5 sulfolobus Q97517 phodopus su Q964197 sporosophila P97517 phodopus Q91197 sporosophila Q91517 sporosophila Q91517 sporosophila Q91517 sporosophila Q91517 sporosophila Q91517 sporosophila Q91517 sporosophila Q91517 sporosophila Q91517 sporosophila Q91518 adsoppogon Q95411 rattus norv Q8tph6 methanosarc	Ogpilo zeugylobact Ogpilo zeugylobact Ogydz7 oryza sativ Ogydz7 oryza sativ Ogydz8 caenorhabdi Ogyng3 lymnaea sta Ogymy3 lymnaea sta Ogymy3 lymnaea sta Ogymy3 oryza alta; Ogymy3 oryza alta; Ogymy3 oryza gand Ogydc0 oryza sativ Ogyf53 arabis proc Ogyf53 arabis proc Ogyf53 arabis proc Ogyf53 arabis proc Ogyf53 arabis proc Ogyf53 arabis proc Ogyf53 arabis proc Ogyf53 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf63 arabis proc Ogyf64 arabis proc Ogyf64 arabis proc Ogyf64 arabis proc Ogyf64 arabis proc Ogyf64 arabis proc Ogyf64 arabis proce Ogy	Oggims mestiaurus Oggims sassafras t Degrid bacillus su Oggar6 pleurotus o Oge948 apple stem Oggid o arabis blep Oggid o arabis blep Oggid o arabis blep Ogmat lambourissa Ogimt lumpv kin Ogimt lumpv kin Ogimt lumpvissa Ogi
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n 5.1.3 Compugen Ltd. Search time 81 Seconds (without alignments) 920.853 Million cell updates/sec	BSIPLYNQEKYLSGFEVLCQ 362		Tesulis Predicted by Canade to thave a compared by the core of the result being printed, to the score of the result being printed, to the score of the result being printed, to the score of the result being printed, to the score of the result being printed, to the compared by the co
re versic 93 - 2003 8w model 14:44:28	18-09-438-185A-1047 18-89-9438-185A-1047 18-89-95-18-18-18-18-18-18-18-18-18-18-18-18-18-	SPTREMBL 21:* 1	tived by analysis Query Query Match Length DB 12.6 497 591 11.9 497 591 11.4 453 11 11.3 452 4 10.9 524 5 10.9 532 5 9.4 456 55 9.4 456 55 9.4 72 250 6
OM protein - Run on:	Title: Perfect score: 1 Sequence: Scoring table: E Searched: Total number of P Minimum DB seq 16 Maximum DB seq 16 Post-processing:	Database :	Result No. Score 1 237.5 2 244.5 3 219.7 4 219.5 5 213.5 6 213.5 6 213.5 10 206.5 11 1181.5 113 178.5 114 177 115 178.5

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RESULT
Q9PU40
ID QS
AC QS
DT 01
DT 01
DT 01
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STRAIN=PUERTO RICAN;
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MEDLINE=99348305; PubMed=10419488;
Hamdan F.F., Ribeiro P.;
"Characterization of a stable form of thuman parasite Schistosoma mansoni ";
J. Biol. Chem. 274.21746-21754(1999).
EMBL; AF031034, AAD01923.1;
HSSP; P04177; 1TOH.
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MEDLINE=96076133; PubMed=7577670;
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Ernsberger U., Patzke H., Tissier-Seta J.P., Reh T., Goriqis U.,
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"The expression of tyrosine hydroxylase and the transcription factors
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Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
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O96370;
O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
O1-UN-2002 (TrEMBLrel. 21, Last annotation update)
Tryptophan hydroxylase (EC 1.14.16.4).
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EMBL, AJ251387; CAB62388.1; -.

HSSP, P04177; ITOH.

HSSP, P04177; ITOH.

InterPro; IPR001273; Asa_hydroxylase.

Pfam; PF00351; biopterin H; 1.

PRINTS; PR00372; FYWHYDRXLASE

PROSTTE; PS00367; BIOPTERIN HYDROXYL; 1.

PROSTTE; PS00367; BIOPTERIN HYDROXYL; 1.

PROSTTE; PS00367; BIOPTERIN HYDROXYL; 1.

SEQUENCE 491 AA; 56016 MW; 6322F2D58E746930 CRC64;
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSSYGELIHSLSDEFEVRDFDPDAAAVQPYQDQNYQPVYFVSESFSD 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDE 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDIG-----YWFTVEFGLCRQNGIVKAYGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADKTFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
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66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                           tryptophan hydroxylase from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98; Indels
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PRT; 579 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 28.69 es 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuron 2:1167-1175(1989).
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Q8SY95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Q8SY95
DD Q8SY95
AC Q8SY1
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DT 01-JT
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Adams M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutron G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.K.,
Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
April J.F., Agbayani A., An H.-J., Andrews Pfanncon C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., Barman B.P., Bhandari D., Belashev B.M.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Bolshakov S. M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S. M.,
Ballew R.M., Basu D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Burtis K.D., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Bernard S., Pleischmann W.,
Cherry J.M., Cawley S., Dahlke C., Bernard S., Pleischmann M.,
Cherry J.M., Cawley S., Dahlke C., Bernard S., Pleischmann M.,
Charles B., Delcher A., Deng S., Mays A.D., Dew I., Dietz S.M.,
Adoden K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
Alalin M., Kalush P., Karpen G.H., Kravitz S., Kully D., Lai Z.,
Alalin M., Malush P., Leivitsky A.A., Howland T.J., Wei M., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Nelskop P., Lei Y. Levitsky A., Howley B., Murphy U., Marzhern D.H., Palason D.L.,
Nelskop D., Lei Y., Levitsky A., Niskern D.R., Paleson D.L.,
Nelskop D., Pei Y., Pavitsky S., Murphy L., Marzhern D.M., Paleson D.L.,
Nelskop D., Pei Y. Wei Y., Pavitsky S., Paus S., Pollard J., Purit V., Pacese M.G.,
Palazzolo M., Pithman G.S., Pan S., Pollard J., Purit V.
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Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                        96 VVSTPFFNRNLWYRLLSSRFSLWK-SYCPRFFLDYLEAFGLLSDFLDH-----QAVI 146
                                                                                                                                                                                                                                                               201 IVEYTEIEKTTWGRIYRELTRLYKTSACHEF----QKNLGLLQDKAGYNEFDLPQLQVVS 256
                                                                                                                                                                                                                                                                                                    147 KFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206
                                                                                                                                                                                                                                                                                                                              257 DFLKARTGFCLRPVAGYLSARDFLSGLAFRVFYCTQYIRHQADPFYTPEPDCCHELLGHV 316
                                                                                                                                                                                                                                                                                                                                                                                 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                           317 PMLADPKFARFSQEIG-----LASLGTSDEEIKKLAT-----CYFFTIEFGLCR 360
                                                                                                                                                                                29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 QDNQLKAYGAGLLSSVAELQHALSDKAVIKPFIPMKVINEECLVTTFQNGYFETSSFED 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 NHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDE 325
                                                                                                                                           DB 5; Length 497;
                                                                                                                                    Match 11.9%; Score 224.5; DB 5; Length Local Similarity 28.5%; Pred. No. 5.6e-11; Les 68; Conservative 34; Mismatches 108; Indels
                                                                                                 497 AA; 57598 MW; F8964E4E4B2C361D CRC64;
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Last annotation update)
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Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; PYMPTKLABS.
TIGREAMS; TIGR01270; Trp 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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NCBI_TaxID=7227;
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PLE OR CG10118.
                                                                                 Oxidoreductase.
SEQUENCE 497
                                                                                                                                             Query Match
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shuge B.C., Sladen-Klamos I., Singboon M., Skupski M.P., Smith T., Spier E., Sladen-Klamos I., Stapleton M., Strong R., Sun E., Syradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.F. F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A., Zheng K.H., Zhong F.N., Zhong W., Zhou K., Zhu S., Zhu M., Wers E.W., Rubin G.M., Venter J.C.; Smith H.O., Science 287:2185-2195(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 EYRAAFQKLQDEQIFVETRLPQLQEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQ 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389 STQYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIG------LASLGASD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --NVRVLPLE-------LDQIIRLPFNTSTPQETLFSIRHFD--ELVELT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          493 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CANTON S;
STRAIN=CANTON S;
BIDLINES-26014502; PubMed=7929381;
Birman S., Morgan B., Anzivino M., Hirsh J.;
"A novel and major isoform of tyrosine hydroxylase in Drosophila is
generated by alternative RNA processing.";
J. Biol. Chem. 269:26559-26567(1994).
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Neckameyer W.S., Quinn W.G.;
"Isolation and characterization of the gene for Drosophila tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
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InterPro: IPR001273; Aga hydroxylase.
InterPro: IPR001273; Aga hydroxylase.
PR003751; bropterin H; 1.
PRINTS; PR00372; FYMHYDRXLASE.
TIGREMS; TIGR01269; TYr 3 monox; 1.
PROSTIE; PS00367; BIOPTERIM; HYDROXYL; 1.
SEQUENCE 579 AA; 65995 MW; 416CF26E04087E85 CRC64;
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RESULT
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                      Query Match
Best Local S
Matches 64
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Best Local
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Q91WV1;
01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                        TIGRFAMS;
PROSITE;
                                                                                                                                                       Pfam; PF01842; ACT; 1.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC013458; AAH13458.1; -.
InterPro; IPR001273; Aaa hydroxylase.
InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Phenylalanine hydroxylase.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE=KIDNEY;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEIEKLST------VYWFTVEFGLCKEHGQIKAYGAGLLSSYGELLHAISDKCEHRAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STOYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYRAAFQKLQDEQIFVETRLPQLQEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQ 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --NVRVLPLE-----ELVELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY071698;
                    Similarity 64; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 28.
                                                                                                                     ; TIGR01268;
PS00367; BIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         579 AA;
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                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                 Α
                                                                                                                     68; Phe4hydrox_tetr; BIOPTERIN_HYDROXYL;
                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66012 MW; 7700F94E436479E2 CRC64;
                                                                                                 51899 MW;
                                      11.4%; Score 215.5;
27.8%; Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.6%; Score 219; DB 5
28.6%; Pred. No. 2e-10;
:ive 37; Mismatches
                      40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                 x_tetr; 1.
DROXYL; UNKNOWN_1.
551F181FA59DEA5B CRC64;
                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       453
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                                        9e-10;
                                                          DB 11; Length 453;
                        105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
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                      Indels
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                      21;
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                      Gaps
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                      5
RESULT
QBTC14
ID QR
AC QR
AC QR
DT 01
DT 01
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DT 01
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OC MC
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Best Local
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                                                                                                                                                                              Q8TC14;
Q8TC14;
01-JUN-2002
                                                        Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Konecki D.S., Lichter-Konecki U., "Completion of the sequence of PAH, a model disease gene."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF404777; AAL78816.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
    SEQUENCE FROM N.A
                               NCBI_TaxID=9606;
                                                                                                                   Phenylalanine hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                  345
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                                                                                                                                                                                                                                                           7
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                                                                                                                                                                                                                                                                                                                                                                                                                        EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPQPDICHELLGHVPLFSDRSFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKTWGTVFKTLKSLYKTHA----CYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQTCTGF
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                                                                                                                                                                                                                                                                                                                  AGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEFQPLYYVAESFNDAKE
                                                                                                                                                                                                                                                                                                                                                      AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRHFDELVE
                                                                                                                                                                                                                                                                                                                                                                                            QFSQEIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSSFGELQYCLSDKPKLLPLELEKTACQEYTVTEFQPLYYVAESFNDAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              452 AA;
                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LASLGAPDEYIEKLAT-----IYWFTVEFGLCKEGDSIKAYGAGL
                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51861 MW; DEF9DB9D6B8C800C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            -LASLGAPDEYIEKLAT-----IYWFTVEFGLCKQGDSIKAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.3%; Score 213.5; DB 4
26.6%; Pred. No. 4.4e-10;
tive 44; Mismatches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
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Catarrhini; Hominidae; Homo.
                                                          Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                     452
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                                                                             Vertebrata;
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                                                          Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100;
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Length 452; Indels

27;

Gaps 155

275 300 215 240 Euteleostomi;

328

303 218 243 158

Euteleostomi;

Homo

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Hypothetical 59.8 kDa protein.
                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
     . 235 DALVTDG 241
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                                                                                                                                                 023438
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09XZD1
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U., Sanchez C., Chen M., Edwards D.J., Shen B.,
A locus encodaing nouribosomal peptide synthetase and polyketide
"A locus encodaing nouribosomal peptide synthetase and polyketide
synthase functions in the bleomycin producer Streptomyces verticillus
                                                                                                                                                                                                                                                                                                                                                                            301 QFSQEIG------LASLGAPDEYIEKLAT-----IYWFTVEFGLCKQGDSIKAYG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                              184 KKTWGTVFKTLKŚLYKTHA -- - CYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQTCTGF 240
                                                                                                                                                                                                                                                                                                                                                  156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 LGGAILSSADEIRQCLDPACPVEPFDPEVVRFATYDILRLQSRYFAVEDLEEIESALADL 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 VSTPF--FNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFL-DHQAVIKFFELET 153
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                                                                                                                                                                                                   27; Gaps
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Best Local Similarity 13.9%; Score 206.5; DB 2; Length 244;
Best Local Similarity 23.9%; Pred. NO. 8.2e-10;
Matches 59; Conservative 48; Mismatches 123; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 VQEPYGPVDQEVWRHLYRQQAELVPAAAPPLYLEGLALLGLPTDHVPDLGQVNERLSAVS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. (CDI_TaxID=29309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 AGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYIVTEFQPLYYVAESFNDAKE 397
                                                                                                                                            Match 11.3%; Score 213.5; DB 4; Length 452; Local Similarity 26.6%; Pred. No. 4.4e-10; les 62; Conservative 44; Mismatches 100; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF340166; AAK27411.1; -.
InterPro; IPRO01273; Asa hydroxylase.
Pfam; PF00351; biopterin H; 1.
SEQUENCE 244 AA; 27012 MW; 31962679A28916C7 CRC64;
                    Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO26251; AAH26251.1; -.
SEQUENCE 452 AA; 51790 MW; 018E9629BBDD640D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001
                                                                                                                                                 Query Match
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Matches
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298 RVRPVAGYLSARDFLAGLAYRVFFCTQYVRHHADPFYTPEPDTVHELMGHMALFADPDFA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 RKTWGIIYRKLR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI------ 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 QFSQEIG-----LASLGASEEDLKKLATL------YFFSIEFGLSSDDAADSPVK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 ---ENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      402 ENGSNHERFKVYGAGLLSSAGELQHAVEGSATIIRFDPDRVVEQECLITTFQSAYFYTRN 461
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                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
"Direct Submission.";
"Direct Submission.";
submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; UZ1308; AABB3319.2; -...
HSSP; P04176; 1PHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The sequence of C. elegans cosmid ZK1290.";
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypochetical protein. -- SEQUENCE 522 AA; 59781 MW; B6205C4E932C21FA CRC64;
                                                                                                    Last sequence update)
Last annotation update)
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522 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Incept Production 1. 1. PRINTS; PR00351; PYWHYDRXLASE.
TIGREAMS; TIGR01270; TFP_5_monoox; 1.
                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001273; Aaa_hydroxylase.
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MEDLINE=99069613; PubMed=9851916;
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8;

Gaps

15;

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RESULT 11
Q9XYG
ID Q9XYG
D7 01-NG
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Best Local S
Matches 70
STRAIN.BRISTOL N2;
Loer C.M., Davidson B., McKerrow J.;
La phenylalanine hydroxylase gene from th
elegans is expressed in the hypodermis.";
J. Neurogenet. 0.0-0(199).
EMBL; AF11938; AAD31643.1; -.
HSSP, P00439; 4PAH.
InterPro; IPR001273; Aaa_hydroxylase.
InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine hydroxylase (EC 1.14.16.1).
K08F8.4.
                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
[1]
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Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXIASE.
TIGRRAMs; TIGR01270; Trp 5 monoox; 1.
SEQUENCE 532 AA; 60863 MW; BAC6A5
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"tph-1 encodes a C. elegans tryptophan hydroxylase.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF135186; AAD30115.1; -.
HSSP; P04176; 1PHZ.
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2002 (TrEMBLrel. 21,
Tryptophan hydroxylase.
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Sze J.Y., Ruvkun (
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Eukaryota; Metazoa; Nem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKTWGIIYRKLR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QFSQEIG-----LASLGASEEDLKKLATL-----YFFSIEFGLSSDDAADSPVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity 25.: 70; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.9%; Score 206.5; DB 5; Length 532; 25.2%; Pred. No. 2.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47;
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Last sequence update)
Last annotation updat
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Mismatches 116; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8AC6A51C7DD0121F CRC64;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine hydroxylase.
Geodia cydonium (Sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Tetracti
Astrophorida; Geodiidae; Geodia.
NCBI TaxID=6047;
[1]
                   Pfam; PF01842; ACT; 1.
Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
TIGRRAMS; TIGR01268; Phe4hydro:
SEQUENCE 450 AA; 51204 MW;
                                                                                                                                                             hydroxylases.",

Dev. Comp. Immunol. 22:469-478(1998).

EMBL; Y16353; CAA76.84.1; -.

EMSL; P00439; 2PAH.

HSSP; P00439; 2PAH.

InterPro; IPR001273; Aaa hydroxylase.

InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                   MEDLINE=99093257; PubMede=9877430; Wiens M., Koziol C., Batel R., Mueller W., "Phenylalanine hydroxylase from the sponge Implication for allorecognition and evolut
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Pfam; PF01842; ACT; 1.

Pfam; PF01842; ACT; 1.

Pfam; PF00351; biopterin H; 1.

PRINTS; PR00372; FYWHYDRXLASE.

TIGRAD48; TIGR01268; Phe4Hydrox tetr; 1.

PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

PROSITE; PS00192; CYTOCHROME_B_HEME; UNKNOWN_1.

Oxidoreductase.

Oxidoreductase.

SEQUENCE 457 AA; 52189 MW; 7A573B884B9EF6FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 9.6%; Score 181.5; DB 5; Length 457; Local Similarity 21.8%; Pred. No. 2.4e-07; es 83; Conservative 66; Mismatches 137; Indels 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSSFGELQYALSDKPEVVDFDPAVCCVTKYPITEYQPKYFLAESFASAKNKLKSWAATI
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                          ; Phe4hydrox_tetr; 1.
51204 MW; 691880218BB9725D
                                                                                                                                                                                                                                                                                                                                       sponge Geodia cydonium:
evolution of aromatic a
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Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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-----YFFTVEF 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                 143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284 QDVSVYLKRKTGFQLRPVAGYLSPRDFLSGLAFRVFHCTQYIRHSSDPFYTPEPDCCHEL 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 LGHVPWLLHPSFSEPFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVES 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 STDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 LETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 HPSFSEFFINMGRLFTKVIEKV--QAL-------PSKKQRIQTLQSNLIA--- 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 SRDQAV------WRNILGSLRGHLADKAHPVYLEGLEATGIGSECIPSLDEMNEKL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

When the state of mrp, a Locus Essential for Cellular Aggregation of Mycococcus xanthus.",

"Genetic Studies of mrp, a Locus Essential for Cellular Aggregation of Studiation of Mycococcus xanthus.",

"Bacteriol. 183:4786-4795 (2001).

EMBL, AF285263, AAF99327.1;

TherPro. IRROULY3, Aaa hydroxylase.

Pfam: PF00351; biopterin.H; ut. CB22E52F8A613AEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46;
                                                                                                                                                                                                                                                                                                                                                         Query Match 9.4%; Score 178.5; DB 5; Length 555; Best Local Similarity 32.0%; Pred. No. 5.6e-07; Matches 47; Conservative 28; Mismatches 55; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.4%; Score 177; DB 2; Length 495; 23.8%; Pred. No. 6.5e-07; Ive 47; Mismatches 128; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myxococcus xanthus.

Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaces; Myxococcus.
                                                                                                                                                                                               Prem: PF001842; ACT; 1.
Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXIASE.
TIGREAMS; TIGRO1270; TYPE 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
SEQUENCE 555 AA; 61530 MW; 60D527EFB1FA791C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OFFDC3;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                344 LGHMPLLANSSFAQFSQEIG-----LASLGASDADIEKLATL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495 AA.
                                                                                                                                   Flyase; FBGn0035187; CG9122.
InterPro; IPR001273; Aaa hydroxylase.
InterPro; IPR002912; ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 GLIENHEGR-KAYGAVLISSPQELGHA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        388 GLCKQADSTFKVYGAGLLSSVAELQHA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                               EMBL; AE003470; AAF47444.1; -.
HSSP; P04176; 1PHZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 23.8%;
Conservative 4
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es 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
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Q9FDC3
ID Q9FDC
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RAM Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAM Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAM Addams M.D., Celniker S.E., Holt R.A., Eshburner M., Henderson S.N.,
RAM G.G., Wordman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RAM Satton G.G., Wordman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Ramantides P.G., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RAM R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RAM R.K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RAMIN K.M., Basu A., Baxendalb J., Bayraktaroglu L., Beasley B.M.,
Ralleson K.Y., Bernan B.P., Barnadari D., Bolshakov S.,
Ramortis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Ramortis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Ramortis K.J., Doyle C., Davenport L.B., Davies P.,
Ramortis K.J., Evangelista C.C., Perraz C., Ferriera S., Fleischmann W.,
Ramortis K.J., Barnell J.H., Quez., Guan P., Harris M.,
Raturis K.J., Brangelista C.C., Perraz C., Ferriera S., Fleischmann W.,
Raturis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Ramell B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.M., Ketchum K.A.,
Ralus K., Matush F., Karpen G.H., Ke Z., Kennison J.M., Moyn, M., Murphy L., Murphy L., Murphy L., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Spier E., Spradling A.C., Steleler F., Shen H.,
Rainer K., Remington K., Sanders R., Venter E., Wang A.H., Wang Z.,
Ranger E., Spradling A.C., Steleler E., Spradling A.C., Stapeleron M., Strong R., Yao Q., X,
Rang R., Welson K., Welson M., Wenter E., Wang A.H., Wang Z., Rhan M., Zhang G., Zhan M., Zhang G., Zhan M., Zhang G., Zhan M., Zhang G., Zhan W., Zhang G., Zhan M., Zhang G., Zhan G., Zhang G., Zhan G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang G., Zhang 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                              186 WRTIFTNLVDLFPTHACK---EHNHVFPLLQENCGYREDNIPQLEEVSQYLQSCTGFRLR 242
                                                                                                                                                                                                                                                                                               302 QEIG------LASLGAPEEYVQQLAT------LYWFTIEFGLCKQDGQTKAYGAGL 345
                                                                                          107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHFSYY 158
                                                                                                                                                                                159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                      243 PVAGLLSSRDFLAGLAFRVFHSTQYIRHYSQPNYTPEPDVCHELIGHVRCSV-ILFAQFS 301
                                                                                                                                                                                                                                                                   219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                       Gaps
                                                    80; Indels 35;
       9.4%; Score 178.5; DB 5; Length 450; 25.8%; Pred. No. 4.3e-07; Live 43; Mismatches 80; Indels 35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                555 AA
                                                                                                                                                                                                                                                                                                                                                         279 ISSPOELGHAFIDNVRVLPLELDQIIRLPFNTS 311
                                                                                                                                                                                                                                                                                                                                                                                               346 ISSFGELOYCLSDKPEVRPLD-----PFKTS 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
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Query Match
Best Local Similarity 25.8%
Matches 55, Conservative
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RESULT 16
Q95LQ6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 64
Q95LQ6;
Q95LQ6;
01-DEC-2001
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O17498;
O1-JAN-1998
O1-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOI. Biol. Evol. 15:1373-1380(1998).
EMBL; AJ001677; CAA04917.1; -.
HSSP; P04176; 1PHZ.
InterPro; IPR001273; ABA hydroxylase.
InterPro; IPR0022119; Histone_H2A.
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01-JAN-1998 (TrEMBLrel. 05, Last Sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Phenylalanine hydroxylase (EC 1.14.16.1) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01842; ACT; 1.
Pfam; PF00351; biopterin_H; 1.
TIGRPAMS; TIGR01268; Phe4hydrox tetr; 1
PROSITE; PS0046; HISTONE_H2A; ÜNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Patton S.J., Luke G.N., Holland P.W.H.;

"Complex history of a chromosomal paralogy region: :
amphioxus aromatic amino acid hydroxylase genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Branchiostoma floridae (Florida lancelet) (Amphioxus).
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase.
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                                                                                                                                                                                                                                                                                                                  340
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                                                                                                                                                                                                                                                                                                                                                                                 HRSESCRYCLTDKPDIRPFEPEKISVTKYPITEYOPIYFVADSFODAKEKVR--TWS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIG-----LASLGAPDDFVMKLATL------YWFTVEFGLCRQDGEVKAYGRDCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAGLLSSRDFLAGLAFPVFHSTQYIRHHSKPLYTPEPDVCHELLGHAPLFADPSFAQFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSGFVAPHQYLSLLQDRYFPIASVMRTLDXDNFSLTPDLIHDLLGHVPWLLHPSFSEFFI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTWRQIFTELRKLYPTDACREHNYVFPLLMENCGFREDNIPQLEDVSNFLKDCTGFTLRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLWYRLLSSRFSLWKSYCPR----FFLDYLEAFGLLSDFLDH-QAVIKFFELETHFSYYP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACADMDYDITRMQPQLFVARDFEHLFEVLAEFESTLSWKRGGDFGLTEAL
                                                                                                                                                                                                                                                                                                                  GLLESIPL----YNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWML-----DQGLLESI
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                                                                                                                                                                                                                                              -HSIPRPFSVHYN--PYTQSVEIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438 AA; 49958 MW; 1619297DBDBF5EE7 CRC64;
   (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                   PRELIMINARY;
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24.1%; Pred. No. 2.9e-05;
tive 37; Mismatches 129;
                                                                   PRT;
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                                                                                                                                                                                                                                              409
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                                                                       250
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d insulin-related
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Q9SCZ3
       DARREND DRARKE PRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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Best Local
                           InterPro; IPR000767; Disease resist.
InterPro; IPR001611; LRR.
InterPro; IPR002182; NB-ARC.
InterPro; IPR002187; TIR domain.
Pfam; PF00560; LRR; 6.
Pfam; PF00931; NB-ARC; 1.
Pfam; PF01582; TIR; 1.
PRINTS; PR00364; DISEASERSIST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9SCZ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

EU Arabidopsis sequencing project;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ

SMBL; AL133452; CAB63020.1;

TEMBL; AL133452; CAB63020.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Delseny M., Berger C., Cooke R., Grellet F., Laudie M.,

Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-UN-2002 (TrEMBLrel. 21, Last sennotation update)
Disease resistance-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 WKEVYTTLKGLYATHACR---EHLBAFELLERFSGYREDNIPQLEDVSRFLKERSGFQLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 INMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pro; IPR001273; Aaa_hydroxylase.
PP00351; biopterin_H; 1.
TE; PS00367; BIOPTERIN_HYDROXYL; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 28.2
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
250
; 28548 MW;
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Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 293ECED98F39A46B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53;
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250; 11;

Gaps

2

180

Mewes

Ξ.

12;

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101 FFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV 160
                                                                                                                                                                                                                                                    161 SGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGH-----VPWLLHPSFSE 216
                                                                                                                                                                                                                                                                                                                                      357 -----DNIRIKLDNKIPISSIIGSLTKDKFC-----NLLGHPISKANW-TESSDSD 401
                                                                                                                                                                                                                                                                                                                                                                                                 217 FFINMGRLFTKVIEKVQALPSKKQR------IQTLQSNLIAIVRCFWFTVESGLI 265
                                                                                                                                                                                                                                                                                                                                                                                                                                256 FWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQE 315
                                                                                  190 YCNWKNFD----IKKKLILNPRFFLFLYNSHVCE----YESIFFFLRKRSSHLRSTAY 239
                                                                                                                                62 HKCISILEFFKNL----LPVH----LLSLSKNQ-----REGCSTDMAVVSTP----- 100
                                                                                                                                                                       240 EVLFERILFYAKIOHFLKVFVNNFPAILGLLKDPFLHYVRYHGKSILATKDTPLLMNKWK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lates calcarifer (Barramundi).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;

Centropomidae; Lates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 YCE-RTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 TLF----SIRHFDELVELTSKLEWMLDQ 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BARRAMUNDI;
Collet C., Candy J., Sara V.;
Tyrosine hydroxylase and insulin-like growth factor-II but no insulin are adjacent in the teleost species barramundi (Lates calcarifer).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.6%; Score 106; DB 13; Length 129;
25.0%; Pred. No. 0.16;
tive 14; Mismatches 41; Indels 3
37; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUM-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; APO07942; AAB64194.1; -.
HSBL; PG4177; 1TOH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 AA; 14678 MW; 1AE29C7530AB4D78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
01-DRC-2002 (TrEMBLrel. 20, Last annotation update)
01-MRA-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR01273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyrosine hydroxylase (Fragment).
TH.
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29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 E 266
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SEQUENCE
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Q9GF55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=AALP2;
Koch M., Mitchell-Olds T.;
EVolutionary analysis of plastidic maturase K and nuclear chalcone
synthase and their utility for phylogenetic reconstructions within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; permatophyta; Magnoliophyta; eudicotyledone; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabis.
                                                                                                                                   77 VHLLSLSKNQREGCS-----TDMAVVSTPFFNRNLWYRLLSS------RF 115
                                                                                                                                                               116 SLWKSYCPRFFLDYLEAFG---LLSDFLDHQAV-------IKFFEL----ET 153
                                                                                                                                                                                                                                                    154 HFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSL-------TPD-- 197
                                                                                                                                                                                                                                                                                                                                      198 -LIHDLLGHVPWLLHPSFSEFFINM------GRL------FTKVIE-----KVQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                             593 MLKRIMLCHSQQLVGIQELQIALNMEVIDLQGCARLQRFLATGHFQHLRVINLSGCIKIK 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      234 ALPSKKORIQTL---QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-HAF 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        653 SFPEVPPNIEELYLKQTGIRSIPTVTFSPQDNSFIYDHKDHKFLNREVSSDSQSLSIMVY 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 IDNVRVLP----LELDQIIRLPFNT-----STPQETLFSIRHFDELVEL---TSKLEWM 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       713 LDNLKVLDLSQCLELEDIQGIPKNLRKLYLGGTAIKELPSLMHLSELVVLDLENCKRLHK 772
                                         ch 5.8%; Score 109.5; DB 10; Length 1253;
1 Similarity 20.3%; Pred. No. 1.2;
81; Conservative 61; Mismatches 130; Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106.5; DB 8; Length 506; Pred. No. 0.73;
140809 MW; 4211ADE0566C2B01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast; mRNA processing.
SEQUENCE 506 AA; 60472 MW; 3BD5743D758B9F23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01_MAR-2001 (TrEWBLrel. 16, Created)
01-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       773 LPMGIGNLSSLAVLNLSGCSELEDIQGIPRNLEELYLAG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   337 LDQGL-----LESIPLYNQEKYLSG 356
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InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK.N.
Pfam; PF01348; Intron_maturae2; 1.
Pfam; PF01824; MatK.N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probable intron maturase (Maturase K)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Best Local Similarity
  1253 AA;
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SEQUENCE
                                           Query Match
Best Local (
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                                                                                       Matches
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DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2002 (TrEMBLrel. 16, Last sequence update)
DF Probable intron maturase (Maturase K).
N MATK.
S Cardamine penzesii.
CChloroplast.
Eukarron
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Best Local
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Cardamine.
NCBI_TaxID=125588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast; mRNA processing. SEQUENCE 504 AA; 60332 MW;
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EMBL; AF144337; AAG43306.1; -.
InterPro; IPRO00442; Intron_maturse2.
InterPro; IPRO02866; MatK, N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK, N.
Chloroplast; PNA N. Toccocian
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Koch M., Mitchell-Olds T.;

"Evolutionary analysis of plastidic maturase K and nuclear chalcone synthase and their utility for phylogenetic reconstructions within the Brassicaceae.";
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Cardamine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
FUNCTION: POBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
MITOCHONDRIAL INTRONS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICRNISHYYSGSSKKKFLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFTKVIEKVQALPSKKQR------IQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRIKL--DSKIPISSIIGSLAKDKFC----NVLGHPISKVIW-THSSDSDILNRFVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QCYFSVWFQSQKVHIKQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----IQHFFKVFVNNFPAILGLLKDPFIHYVRYHGRSILATKDTPLLMNKWKYYFVNLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKCISILEFFKNLL--FVHLLSLSKNQ-----REGCSTDMAVVSTP-----FFNRNLW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.6%; Score 106; DB 8; Length 50
(1 Similarity 22.8%; Pred, No. 0.81;
67; Conservative 36; Mismarches 115; Indels
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(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
tron maturase (Maturase K).
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                                                              Rosidae;
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Best Local
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Pfam; PF01824; MatK_N; 1.
Chloroplast; mRNA processing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED
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    414
                                                                            231
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; AF144364; AAG43333.1; -
                                                                                                                                                DSKIPISSIIGSLAKDKFC-----NVLGHPISKVIW-THSSDSDILNRFVRICRNISH
YYSGSSKKKKLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE
                                                                        KVQALPSKKQR------IQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HVCE-----YESIFFFLRKRSSHLRSTSYEVLFERIFFYGKIQHFLKVFV 258
                                                                                                                                                                                                                    DRYFFIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGRLFTKVIE
                                                                                                                                                                                                                                                                                             FQSQKVHIKQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDNVRIKL--
                                                                                                                                                                                                                                                                                                                                                             FSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                     NNFPAILGLLKD-PFIHYV-----RYHGRSILATKDTPLLMNKWKYYFVNLWQCYFSVW
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llarity 22.3%;
Conservative 4
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04 AA; 60292 MW;
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460
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Q9GF30;
01-MAR-2001
01-MAR-2001
01-MAR-2002
                                                                                          Brassicaceae."

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II INTRONS (BY SIMILARITY).

-i- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODE:
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Koch M., Mitchell-Olds T.;

"Evolutionary analysis of plastidic maturase K and "Evolutionary analysis of plastidic maturase K and synthase and their utility for phylogenetic reconst pynthase and their utility for phylogenetic reconst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chloroplast.

Chloroplast.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Cardamine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=82338;
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                                                        MITOCHONDRIAL
     AF144365; AAG43334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
tron maturase (Maturase K).
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                                                                                                                                                                                                                                                                                                                                                                                           for phylogenetic reconstructions within
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                                                                                                     POLYPEPTIDES ENCODED
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the

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SEQUENCE FROM N.A.
Hilu K.W., Alice L.A.;
Hilu K.W., Alice L.A.;
Hilu K.W., Alice L.A.;
A Phylogeny of Ciloriddideae (Poaceae) Based on matk Sequences.";
Submitted (CCT-2000) to the EMBL/GenBank/DDBJ databases.
--- FUNCTION: PROBABLY ASSITSI IN SPLICING CHLOROPLAST GROUP II
INTRONS (BY SIMILARITY).
--- SMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
--- AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast.

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota, Viridiplantae; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Pappophoreae; Enneapogon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               173 LQ-----DRYFPIASVMRTLDKDNFSLTPDLIHDLLGH-VPWLLHPSFSEFFI--NMGR 223
   ----RLLSSRFSL----W 118
                                          | : : | : : | | : : | | 250 HFFRKMEH------FGVMYPGFFQKTIWFFMEPLMHYVRYQGKVILASKGTLLFQKKW 301
                                                                                                                       119 KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                               302 KSYLVNFSQYFFSFWAQPQRICLNÖLTNSCFDFLGYRSNVPINTFLVTNÖML----ENFF 357
                                                                                                                                                                                                                                           179 PIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTK-----V 228
                                                                                                                                                                                                                                                                                 229 IEKVQAL------PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                          406 LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----STV 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  453 RTFMÖRLGSVFLEEFFT---BEBÖVFSLMFSKTT-------HFSFHGSYSERI-WYLD 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 --WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLS---L 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILE---FFKNL 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.5%; Score 104; DB 8; Length 513; 20.3%; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MEX-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K) (Fragment).
   78 HLLSLSKNOREGCSTDMAVVSTPFFNRNLWY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF312360, AAK60051.1; -
InterPro; IPR000442; Introm maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Introm maturas2; 1.
Pfam; PF01824; MatK_N; 1.
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es 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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-!-SIMILARITY WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
EMBL, AFRIASS, AARKO046.1; -.
InterPro; IPR002866, Mark N.
InterPro; IPR002866, Mark N.
Pfam; PF01348; Intro. maturas2; 1.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
Chloridoideae, Eragrostideae, Muhlenbergia.
                                                                                                                                                                                                           Query Match 504;
Best Local Similarity 22.3%; Pred. No. 0.81;
Matches 64; Conservative 41; Mismatches 120; Indels 62; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 NNFPAILGLEKD-PFIHTV-----RYHGRSILATKDTPLLMNKWKYFVNLWQCYFSVW 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 DSKIPISSIIGSLAKDKFC-----NVLGHPXSKVIW-THSSDSDILNRFVRICRNISH 413
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5.5%; Score 104; DB 8; Length 513;
Best Local Similarity 18.6%; Pred. No. 1.2;
Matches 67; Conservative 67; Mismatches 124; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           312 FQSQKVHIKQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDNVRIKL-- 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 DRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGRLFTKVIE 230
                                                                                                                                                                                                                                                                                                                                                                                                  214 HVCE------YESIFPFLRKRSSHLRSTSYEVLFERIFFYGKIQHFLKVFV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 HKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTP-----FFNRNLWYRLLSSR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 FSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQ 174
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                                                                                                                                                                                                                                                                                                                                      2 HYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilu K W., Alice L.A.;
"A Phylogeny of Chloridoideae (Poaceae) Based on matK Sequences.";
submitted (OCT-2000) to the EMBL/GenBank/DDBJ detabases.
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 YYSGSSKKKKLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 KVQALPSKKQR-----IQTLQSNLIAIVRCFWFTVESGLIE 266
InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002865; Matk N.
InterPro; IPR012865; Matk N.
Pfam; PF01148; Intron_maturse2; 1.
Pfam; PF011824; Matk N.
Chloroplast; mark processing.
SEQUENCE 504 AA, 60302 MW; 66AA07E8E2C48C64 CRC64;
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SEQUENCE 513 AA; 61468 MW; 8D6AAD01B14BDEF8 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
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Q95F39;

PRELIMINARY;

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INTRONS (BY SIMILARITY)

-I-SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED MITOCHONDRIAL INTRONS.

EMBL, AF312349; AAK60040.1; -.

InterPro; IPR000442; Intron_maturse2.

InterPro; IPR002666; MatK N.

Pfam; PF01348; Intron_maturss2; 1.

Pfam; PF01348; Intron_maturss2; 1.

Pfam; PF01324; MatK N.; 1.

Chloroplast; mRXA processing.

Chloroplast; mRXA processing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hilu K.W., Alice L.A.;
"A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.",
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukarycha; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; Lillopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Eragrostideae; Monanthochloe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ol-DEC-2001 (TrEMBLrel. 19, Created)
Ol-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Ol-MAR-2002 (TrEMBLrel. 20, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probable intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 SSGTFLERIHFSRKMEH-----FGVMYPGFFRKTIWFFMDPLMHYVRYQGKVILASKGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202 FLLK---KENKRLSRFLYNS-----YVSEYEFFLLFLRKQS------SCLRLA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 KNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWY------RLLSSRFSL 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 YILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFF 71
                                                                            MQRLGSVFLEEFFT---EEEQVFSLMFAKTT---
                                                                                                                                         PQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                      --ESFFPIATRMKKFD-TTAPATP-LIGSLSKAQFCTGLGHPISKPIWTDLSDWDILDRF 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFQKKWKSYLVNFSQYFFSFWTQPQRIRLNQLTNSCFDFLGYRSSVPINTFLVRNQML--
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                                                                                                                                                                                                                                                                                                                                                                                                                       LQDRYFPIASVMRTLDKDNFSLTPDLIHDL-----LGH-VPWLLHPSFSEFFI--NM
                                                                                                                                                                                                                                                                                  GRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISS 281
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                                                                                                                                                                                                                 GRICRNLFH-YHSGSSKKRTLYRLK----YILR---LSCARTLARKHK-----STVRTF 455
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R. M., Bay A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxcandale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bottlar P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt D., Dietz S.M.,
RA Dodson K., Doup L.B., Downes M., Dugans R.D.D., Dew II., Dietz S.M.,
RA Harris N.L., Brangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Ghanr W. Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.B., Kodira C.D., Kratt C., Kravizz S., Kill D., Laiz Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Mozris J., Moshrefi A.,
RA Melson D.R., Nelson K., Sunders R., Warny D.M., Nelson D.L.,
RA Melson D.R., Nelson K., Sungson M., Skupski M.P., Schele F.S., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Romerkulov G., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Romerkulov G., Mishina N.V., Mobarry C., Mozris J., Moshrefi A.,
RA Merkulov G., Mishina R.V., Mobarry C., Mozris J., Moshrefi A.,
RA Menner K., Sender S., Pala S., Pala B., Smith T.,
RA Romerkulov G., Scheeler F., Smith T.,
RA Romerkulov G., Scheeler G., Scheeler F., Sm
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE003590; AAF51561.1; -. FlyBase; FBgn0031216; CG11376. SEQUENCE 1782 AA; 202676 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Musc Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9VPI9
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                                                                                                                                                                                                                                                                              67 ILEF-----FKNLLFVHLLSLSKNQREGCSTDMAV-----VSTPFFNRNLWYR 109
                                                                                                                                     LLSSRFSLWKSYCPRFFLDYLEAFGLLS-----DFLDHQAVIKFFELETH----FSYYP 159
                                                                                                                                                                                                         ILEFPOSATYNPHYSYRNLLFVSPKELNFSSRAGSARNIAVRVQLMAGETPKDAVNATY- 632
                                                                -----GKSSCPKF---STEAFTAVNYHNKCPSFYDEIKIALPASIKQHHHLLFTIYH
                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 13, Created)
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(TrEMBLrel. 14, Last ann
                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  25.0%;
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-HQYLSLLQDRYFPIAS----VMRTLDKDNFSLTPDLIHDLL
                                                                                                                                                                                                                                                                                                                                              32;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                              Score 103.5;
Pred. No. 6.1
                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                              96;
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SEQUENCE FROM N.A.

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Monanthochloe littoralis.

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Query Match Best Local

Local Simhes 75;

Similarity

Conservative

us-09-438-185a-1047.rspt

Page 13

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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                          Bouteloua curtipendula.
   460
                                                                                                                                                                                                         Chloroplast
 459 VE
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                                           RESULT 28
Q9TIB8
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRON.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Koch M., Mitchell-Olds T.,

"Evolutionary analysis of plastidic maturase K and nuclear chalcone synthase and their utility for phylogenetic reconstructions within the
                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae, Aubrieta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161 SGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSE 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 -----DNIRIKLDSKIPISSIMGSLAKDKFC-----NVLGHPISKATWTDSSDFD- 399
Query Match 5.5%; Score 103; DB 8; Length 504;
Best Local Similarity 21.9%; Pred. No. 1.5;
Matches 66; Conservative 37; Mismatches 113; Indels 86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 L--FERILFYGKIHHFLKVFVNNFLTIPGLLKDPFLHYVRYHGKSILATKDTPLLMNKWK 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 FFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        298 FYFVNLWQCYFSVWFQSQKVNINQLSKDNLEFLGYLSSLRLNPLVVRSQMLENSFLI--- 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 FFINMGRLFTKVIEKVQALPSKKQR------IQTLQSNLIAIVRCFWFTVESGL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 400 -ILNRFVRICRNÍSHYYSGSSKKKNLYRIKYILRLCCVKTLARKHKSTVRAFLKRVGSGL 458
                                               204 GHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA-IVRCFWFTVES 262
                                                                           740 PGIXWL-------DNHRAVFSINVEAVTA-----IHTLDSFLDRFFLICEYLDTRN 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 LDPKYILKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISI 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (APR-1999) to the EMBL/GenBank/DDBJ databases.
ON: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                            263 GLIENHEGRKAYGAVLISSPQELGHAFID------NVRVLPLELDQIIRL 306
                                                                                                                                         784 -- IPSHIGEN-----NIETELKKCLLDIEYANREPLVRHLPLVLDKLIEL 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast; mRNA processing.
SEQUENCE 504 AA; 60023 MW; 4620F813810B3AD8 CRC64;
                                                                                                                                                                                                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                                                                          504 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF144352; AAG43321.1; -.
InterPro; IPR00044; Intron_maturse2.
InterPro; IPR012866; MarK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MarK_N; 1.
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                  Aubrieta deltoidea.
                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=81984;
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                                                                                                                                                                                          RESULT 27
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Hilu K.W., Alice L.A.;
Hilu K.W., Alice L.A.;
Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based on matk sequences: A preliminary assessment.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopida; Poales; Poaceae; PACC clade; Colloridoideae; Cynodonteae; Bouteloua.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTRONS (BY SIMILARITY).
-!-SMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 ERIFFSRKMEH-----FGVMYPGFFLKTLMIFMDPLMHYVRYQGKVILASKGTLLFQKKW 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 KSYCPRFFLDYLEAFGLLSDFLD-HQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 FPIASVMRTLDKDNFSLTPDLIHDL-----LGH-VPWLLHPSFSEFFI--NMGRLFT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227 KVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415 NLFH-YHSGSSKKÖTLYRLK----YILR---LSCARTLARKHK-----STVRTFMQRLG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 5.5%; Score 103; DB 8; Length 513; Best Local Similarity 22.0%; Pred. No. 1.5; Matches 78; Conservative 59; Mismatches 127; Indels 90; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 HLLSLSKNQREGCSTDMAVVSTPFFNRNLW------YR---LLSSRFSL----W 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357 FLIATRMKKFD-TTVPATP-LIGSLSKAQFCTGLGHPISKPIWTDLSDWDILDRFGRICR 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 OSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   287 HAPIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 SVFLEEFFT---EEBQVFSLMF----PKATHFSFHGSHSERI-------WYLD 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61519 MW; 223EEA9CBA96DFEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
probable intron maturase (Maturase K).
513 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF144578; AAF20334.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR00286; Matk N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; Matk N.
                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seqn
01-MAR-2002 (TrEMBLrel. 20, Last anno
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PRT;
PRELIMINARY;
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Best Local S
Matches 76
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SEQUENCE FROM N.A.

STRAIN=CV. TEXOKA;

Hill K.W., Alice L.A.;

Hill K.W., Alice L.A.;

"A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.";

"Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

-i- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP IN OTHER PLANT CHLOROPLASTS
                                                                                                                                               Q95F50 PRELIMINAKY; FA., Q95F50; Q95F50; Q1-DEC-2001 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update) Q1-MAR-2002 (TrEMBLrel. 20, Last annotation updat in tron maturase (Maturase K).
                      Schedonnardus paniculatus.
Chloroplast.
Chloroplast.
Enbryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Chlorideae; Schedonnardus.
NCBI_TaxID=160583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK_N; 1.
Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61509 MW; 1162FCC517CA1DID CRC64;
SEQUENCE FROM N.A.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Chloridoldeae; Chlorideae; Buchloe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchloe dactyloides
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SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                   SVFLEEFFT---EEEQVFYLMF----PKTTHFSFHGSHSERI-----
                                                                                                                                                                                                                                                                                                                                                               HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                       NLFH-YHSGSSKKRTLYRLK----YILR---LSCARTLARKHK-----STVRTFMQRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                      KVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLIATRMKKFD-TTVPVTP-LIGSLSKAQFCTGLGHPISKPIWTDLSDGDILDRFGRICR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FPIASVMRTLDKDNFSLTPDLIHDL------LGH---VPWLLHPSFSEFFINMGRLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSYLVN-FSQYFFSFWIQPQRIRVNQLTNSCFDFLGYHSSVPKNTFLVRNQML----ENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSYCPRFFLDYLEAFGLLSDFLD-HQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERIHFSRKMEH-----FGVMYPGFFRKTIWIFMDPLMHYVRYQGKIILASKGTLLFQKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLLSLSKNOREGCSTDMAVVSTPFFNRNLW-----YR---LLSSRFSL-----W 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSIFLFSKENKRLSRFLYNSYVSEYEFFLLFLRKQS------SCLRLTSSGTFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5%; Score 103; DB 8; Length 513; 21.5%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1.5;
59; Mismatches 129;
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                                                                                                                                                                       update)
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RESULT 31
Q95F38
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Best Local
                                                                                                                                                                                                                                                                                                           Q95F38 PRELIMINAN.,
Q95F38;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
The intron maturase (Maturase K).
                              HAID K.W., Alice L.A.;
"A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

-!- SUMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLAS
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCO.

EMBL/ AF312350; AAK6041.1; -...
                                                                                                                                                                                                                        Chloroplast
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Chloridoideae; Eragrostideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002866; MatK_N.
Pfam; PF01348; Intron_maturse3; 1.
Pfam; PF01824; MatK_N.
Pf1.
Chloroplast, mank_processing.
SEQUENCE 513 AA; 61384 MW; 94861F9870BBF8EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilu K.W., Alice L.A.;

"A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY).

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODE
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                             NCBI_TaxID=160560;
                                                                                                                                                                                                                                                                                                Reederochloa eludens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             179 PIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTK------V
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; AF312335; AAK60026.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RTFMQRLGSVFLEEFFT---EEEQVFSLMFAKTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLLSLSKNQREGCSTDMAVVSTPFFNRNLWY------RLLSSRFSL-----W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSIFLFSKENKRLSRFLYNFYVSEYEFFLLFLRKQSSCLRLTSSGTFLERIHFFRKM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSPORIGHAFIONVRVLPLELDOIIRLPFNTSTPORTLFSIRHFDELVELTSKLEWMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----STV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IEKVQAL------PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIATRMK-----KFDTTPPAT-PLIGSL-----SKSQFCTGSGHPISKPIWTDLSDWDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----EHFGVMYPGFFQKTIWFFMEPLMHYVRYQGKVILASKGTLLFQKKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSYLVNÉSQYEFSEWAQRQKICLNQLTNSCÉDELGYRSSVÉINTÉLVTNQML----ENEÉ 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 67; Conserv
IPR000442; Intron_maturse2 IPR002866; MatK_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.6%;
                                                                                                                                                                                                                                Streptophyta; Embryophyta; Tracheophyta; yta; Liliopsida; Poales; Poaceae; PACC clade; eae; Reederochloa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s; Score 103; DB 8; s; Pred. No. 1.5; 64; Mismatches 127
                                                                 NG ORF IN OTHER PLANT CHLOROPLASTS MATURASE-LIKE POLYPEPTIDES ENCODE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NG ORF IN OTHER PLANT CHLOROPLASTS, MATURASE-LIKE POLYPEPTIDES ENCODED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -HFSFHGSHSERI-WYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102;
                                                                   ENCODED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL; AE003617; AAF52504.2; -. HSSP; P08799; 1MND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1143 00 1144
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Q9GF64;
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Q9GF64
ID Q9GF6
AC Q9GF6
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SEQUENCE FROM N.A.

SEQUENCE SECURINE N.A.

MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

A manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A manatides F.A., Lewis S.E., Richards S., Ashburner W., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

A bril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,

Abril J.F., Devlec B. W., Baxendale J., Bayaktaroglu D., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Brokstein P., Brottier P.,

Borkova D., Botchan M.R., Boure B.P., Brokstein P., Brottier P.,

Borkova D., Botchan M.R., Buller H., Cadieu E., Center A., Chandra I.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dunkov B.C., Dunn P.,

Durbin K.J., Brangelista C.C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz M., Galdek A., Gong F., Gorrell J.H., Gul, W.M., Glasser K.,

A Glodek A., Gong F., Gorrell J.H., Gul, W.M., Glasser K.,

A Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

A Harris N.L., Harvey D., Heiman T.J., Kerlush M., Ibegama C.,

A Jalali M., Kalush F., Karpen G.H., K& Z., Kennison J.A., Ketchum K.A.,

A Malali M., Kalush F., Karpen G.H., Kez Z., Kennison J.A., Ketchum K.A.,

A Malali M., Kalush F., Karpen G.H., Re. Z., Kennison J. Lai Z.,

Kimmel B.E., Kodira C.D., Kratt C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Bergota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophilia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||: |: | || || || 358 PIATRMKKFD-TTAPATP-LIGSLSKAQFCTGLGHPISKPIWTDLSDWDLLDRFGRICRN 415
                                                                                                                                             Local Similarity 20.5%; Pred. No. 1.5; ies 72; Conservative 62; Mismatches 133; Indels 84; Gaps
                                                                                                                                                                                                                                                                       199 KSIFLFKKENKRLSRFLYNSYVSEYEFFLLFLRKQS------SCLRLASSGTFL 246
                                                                                                                                                                                                                                                                                                                           78 HLLSLSKNQREGCSTDMAVVSTPFFNRNLWY-------RLLSSRFSL----W 118
                                                                                                                                                                                                                                                                                                                                                           119 KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 VIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGH 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 QSLSLFFQNSQSLQR----AYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFV 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288 AFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.5%; Score 103; DB 8; Length 513; 20.5%; Pred. No. 1.5;
                                                 Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61546 MW; 08330E6C2282C755 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1154 AA.
Pfam; PF01348; Intron maturas2; 1. Pfam; PF01824; MatK N; 1.
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                                                                                                                            Query Match
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A REA BEAR R

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20;
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattels B., McThcoh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nazakern D.M., Reson D.L.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skrong R., Sun E.,
Spier E., Spradling A.C., Turner R., Venere E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A. Cheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 993 V----EMTKDNCRL---LFLRLKKMEGWALGKTKVFLRYYNDEF---LARLYELQVKKV- 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1041 -----IKVOSMMRALLARKR-----VKGGKVFKLGKKGPEHHD------VAASKIOKA 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 GHAFIDNVRVLPLELDQIIRL-----PFNTSTPQETLFSI-----RHFDELVELT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 IASVMRTLDKDNFSLTPDLIHDL-----LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI-----ENHEGRKAYGAVLISSPQEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.4%; Score 102.5; DB 5; Length 1154;
22.7%; Pred. NO. 4.4;
tive 56; Mismatches 129; Indels 95; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     839 PEMIETFRSSLDESIMLMFTNOLTKAGNLTMP---FEAVQHKDESERKSYALNTLSAGCI 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 SILEPPKNLLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSS-RFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    896 SQVN------NLRTLAANFRFTCLTLLKMLSQ---NANLGVHFVRCIRADL--EYKPR 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 FF----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              943 SFHSDVVQQQMKALGVLDTVIARQ---KGFS----SRLPFDEFLRRYQFLAFDFDE--P 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 PKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK----CI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0193; MYOSIN'HEÀVY.
PRODOM; PRO000191; BUK pkinase; 1.
PRODOM; PRO000155; myosin_head; 1.
PROSITE; PSE0011; PROTEIN KINASE DOM; 1.
PROSITE; PSE0011; PROTEIN KINASE TYR; UNKNOWN_1.
ATP-binding; Transferase.
SEQUENCE 1154 AA; 134334 MW; 211CD4A2F295B9A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 506 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; PROMO02938; ninaC.
InterPro; IPR0000139; Euk_pkinase.
InterPro; IPR000049; IQ_region.
InterPro; IPR001469; myosin head,
InterPro; IPR001245; Tyr_pkinase.
Pfam; PP00612; IQ; 2.
Pfam; PP00605; myosin head; 1.
Pfam; PP00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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RESULT 34
O9MV23
ID O9MV2
AC O9MV2
DT 01-0C
DT 01-T
DE Proba
GN MATK.
OS OFFER
OC ENTRA
OC ENTRA
OC Sperr
OC Sperr
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9MV23
Q9MV23;
01-OCT-2000 (TrE)
01-OCT-2000 (TrE)
01-JUN-2002 (TrE)
Probable intron 1
Oryza meyeriana.
Chloroplast.
Enchoroplast.
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=83307;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koch M., Mitchell-Olds T.;
"Evolutionary analysis of plastidic maturase K and nuclear chalcone synthase and their utility for phylogenetic reconstructions of plassicaceae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MATK.
Arabis alpina (Alpine rockcress)
Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-MAR-2001 (TrEWBLrel. 16, Created)
01-MAR-2001 (TrEWBLrel. 16, Last sequence update)
01-JUN-2002 (TrEWBLrel. 21, Last annotation updat
Probable intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=50452;
[1]
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabis.
                                                                                                                                                                                                                                 410
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                                                                                                                                                                                                                                 CRNISHYYSGSSKKKHLYRIKYILRLCCVKTLARKHKSTVRAFLKRLGSGLLE 462
                                                                                                                                                                                                                                                                                                                                                        LLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYCERTLDPKYILKIALKLROSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR
                                                                                                                                                                                                                                                         TKVIEKVQALPSKKQR----
                                                                                                                                                                                                                                                                                                                                 YFSVWFQSQKIHINQLSKDNLEFLGYLSSLRLNPLVVRSQMLENSFLI------DN
                                                                                                                                                                                                                                                                                                                                                                                 H----FLKVFVN-NFPAILGLLKDPFLHYVRYHGKSILATKDTPLLMNKWKFYFVNLWQF
                                                                                                                                                                                                                                                                                                                                                                                                          HKCISILEFFKNLLFVHLLSLSKNQ-----REGCSTDMAVVSTP-----FFNRNLWYR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                  HVCE-----YESIFFFLRKRSSHLRSTAYEVLFERILF-----YAKIQ
                                                                                                                                                                                                                                                                                  IRIKLDNKIPISSIIGSLTKDKFC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up)
(TrEMBLrel. 21, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                  PRELIMINARY;
                                                                                                    maturase (Maturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.4%;
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                                                                                                                                                                                                                                                    -----IQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 102;
Pred. No. 1
                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275A64406C5E9525 CRC64;
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                                                                                                                                                                  519
                                                                                               (Fragment).
                                      Embryophyta; Tracheophyta;
a; Poales; Poaceae;
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Best Local S
Matches 96
SEQUENCE FROM N.A.

STRAIN-AX4;

Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kump Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noe "Sequence and Analysis of Chromosome 2 of Dictyostelium.";

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8T2D4
Q8T2D4;
                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequing the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequing tree of the sequ
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- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

- INTRONS (BY SIMILARITY).

- IS SIMILARITY OF THE PLANT CHLOROPLASTS,
- AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED

MITOCHONDRIAL INTRONS.

EMBL, AF148673; AAE37181.1; --

INTERPROJAGE; INTRON maturse2.

INTERPRO, IPRO02866; Matk.N.
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MEDLINE=20056256; PubMed=10588717;
Ge S., Sang T., Lu B.R., Hong D.Y.;
Phylogeny of rice genomes with emp
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Proc. Natl
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24.5%; Pred. No. 2;
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EXURENCE FROM N.A.

REC STRAINBERRELEY.

RA Manatides P.G., Scherer S.E., 101 P.W., Hoskins R.A., Galle R.F.,

Adams M.D., Celniker S.E., Richards S., Ashburner M., Hendelson S.N.,

RA Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Hendelson S.N.,

RA Barndon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abliew R.M., Baana A., Baxendals J., Bayarkaroglu L., Basaley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolbhakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Brotstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Burler H., Gadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahler K., Downes W., Dugan-Rocha S., Dunkov B.C.,

Burtis K.C., Busam D.A., Burler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahler K., Downes W., Dugan-Rocha S., Dunkov B.C.,

RA Dobson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Dobson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J., Lin Z.,

RA Laako P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Laako P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Harris N., Martei B. M. McIncoh T.C., Kravitz S., Kulp D., Lai Z.,

RA Laako P., Lei Y., Leviteky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Merkulov G., Milshian N.V., Mobarry C., Moread M.P., Moshrein D.,

RA Merkulov G., Milshian R.A., Nixon K., Nusskern D.R., Pacled D.J.M.,

RA Nelson R.A., Nakon K.A., Nakon N., Nalson D.,

RA Nelson D.R., Pattman G.S., Paollard J., Purl V., Resee M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                   403 NDLGLL--SVVKIYKALGLNYTLVLKEEKALNE-----SIIRYFWDNNSFAS 447
183 SYFIQNHEIIFNISKGIWFLEIGVNASPYNSVSALINLNNKEVSQWLNKSRIPKLPDPLL 242
                                                       73 NLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEA 132
                                                                                                            243 KEYFLSLLLIKDDONPYLGT-FAASPSPIYLYS-WVR--DSAFSAIA-----LOO 288
                                                                                                                                                                   133 FGLLSDFLDHQAVIKFF-----ELE----THFSYY---PVSGFVAP----- 166
                                                                                                                                                                                                                        289 AG-----HYNSALKYWLWMANAEQLQPGVWYTRYNFYNGEPDSSFGIPELDSIGLYEIG 342
                                                                                                                                                                                                                                                                               167 -HQYLSLLQDRYF-----PIASVMRTLDKDNFSLTP---DLIHDLLGHVPW---- 208
                                                                                                                                                                                                                                                                                                                   343 VYDYYNLTHNITFLKLVLPRINESVEYQIQQIENDKYHLIPPDLSIWEDRLAYHFWTEAI 402
                                                                                                                                                                                                                                                                                                                                                                                               209 ----LLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFW----FTV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 ESG---LIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 ALGTSVLFENGKSEE----VLTPEPPS-----IDSATLLPIDMGY---LPYNSN----- 489
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Sukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        490 SSVENFDTVIKTLTR-----DGGLARFPDDLYHYSEYL 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 FSIRHFDELVELTSKLEWMLDQGLLESIP--LYNQEKYL 354
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Rubmed=11572479;

Rawarzabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Rawarzabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Poshima T., Kikuchi H.;
                                                                                                                                                                       Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 ---ELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
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                                                                                                                                                                                                                                                                                                                                       95 AVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLL--SDFLDHQAVIKFF--- 149
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19.8%; Pred. No. 2.9;
tive 69; Mismatches 123; Indels 128; Gaps
                                                                                                                                                                                                                                                                            919 YPEIQLKYKNENDFKGPFLNYKLLKLIIKTFDLESFIKLDSLLENHNGNCEQEGSNNRIL 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 SLFFQNSQSLQR-----AYSTPYSYYRIILQKENKE-KQALARHKCISILEFFK 72
                                                                                                                                                                                                                           44 YYRIIL--QKENKEKQALARHKCIS-ILEFFKNLLFVHLLSLSKNQREGCSTD-----M 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sulfolobus tokodaii.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                        5.4%; Score 101.5; DB 5; Length 1615; 20.3%; Pred. No. 8; Live 58; Mismatches 111; Indels 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete genome sequence of an aerobic thermoacidophilic
Trenarchaeon, Sulfolobus tokodaii strain7.";
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                             ll protein.
1615 AA; 192460 MW; ClA5951F24D04A7A CRC64;
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EMBL, AP000985; BAB66140.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 635 AA; 72823 MW; 5219B8F88204794F CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein 871107.
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EMBL; AC115613; AAM10775.1; -. Hypothetical protein. SEQUENCE 1615 AA; 192460 MW
                                                                                                     Query Match
Best Local Similarity 20.3*
Matches 74; Conservative
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Best Local
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EMBL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
ENGL; AE003462; AAR47145.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P97517; P70468;
P97517; P70468;
P97517; P70468;
O1-MAY-1997 (TrEMBLrel. 03, Created)
O1-MAY-1997 (TREMBLrel. 03, Last sequence update)
O1-MAY-1997 (TREMBLrel. 03, Last sequence update)
O1-MAR-2002 (TREMBLrel. 20, Last annotation update)
Tyrosine hydroxylase (Fragment).
Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1128
   NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                         Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases. EMBL; Y09294; CAA70478.1; -. HSSP, P04177; 1TOH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1188
                                                                                              InterPro; IPR001273; Aaa hydroxylase
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=HYPOTHALAMUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAVLEQFDL 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MPQEQVQLLPDWLKLKMIRSSVDRLIEAALNDLTPDQIVLFVQNFGTPVNSMSKLLAMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPOELGHAFID -- NVRVLPLELDQI IRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIHAF--IILLTYSNSNMPESIPILD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMFNNYIIKLREYHEPY-----EWTEYPDLLMVQFDDGVQLP--LH-----IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAPHQYLSLLQDRYFFIASVMRTLDKDNFSLTPDLI---HDLLGHVPWLLHPSFSEFFIN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQFITAHTLNDPVNEMLDHVIDMAQLIVERSTMFQHIIISQEDYDYVPDENRIQTLKCLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSGLKIIFRHSGDF--ENEW--LLKSLOQIPHFYEVKPFIIPQLRAACQVENCPELIMAY 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IINEENSRDAEL------VNFLRNLIFDGNLSHQIVCELLDYIFRRLSSTVKQSRVAA 930
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102
102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
   11433 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.3%; Score 101;
21.1%; Pred. No. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
       52241A9D5DB27795 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 122; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --YWFP-----PGRPAPVAFLPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2042;
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RESULT 39
Q9DQD1
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Best Local S
Matches 62
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Best Local S
Matches 27
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Q9DQD1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF272001; AAG40171.1; -.
InterPro; IPR002877; FtsJ;
InterPro; IPR001016; Viral_RNA_pol_L.
Pfam; PF001728; FtsJ; 1.
Pfam; PF001728; FtsJ; 1.
Pfam; PF001728; FtsJ; 1.
SEQUENCE 2212 AA; 252692 MW; 5E34C0A291603D4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99171703; PubMed=10073695; Volchkov V.E., Volchkov V.A., Chepurnov A.A., Blinov V.M., Dolnik O., Netesov S.V., Feldmann H.; "Characterization of the L gene and 5' trailer region of Ebola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ebola virus (strain Zaire Mayinga) (Ebo).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=MAYINGA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=11062045;
Volchkov V.E., Chepurnov A.A., Volchkova V.A., Ternovoj V.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-MAYINGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=128952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ebola-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology 277:147-155(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klenk H.D.;
"Molecular Characterization of Guinea Pig-Adapted Variants of Ebola
                                        125
                                                                                409
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463
                                                                                                                                                              355
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                                                                                                                                                                                                      13 ILKIALKLROSLSLFFONSOSLORAYSTPYSYYRIILOKENKEKOALARHKCISILEFFK 72
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-HLDHPPLFSTKIISDLSIFIKDRATAVERTCWDAVFEPN----
                                     FFLDYLEAFGL----LSDFLDHQAVI-----KFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                ---CVFKYSIAKHYFDSQGSWYSVTSDRNLTPGLNSYIKRNQFPPLPMIKELLWEFY---
                                                                                                                                                              LIRLEMTPQQLCELF-----SIQKHWGHPVLHSETAIQKVKKHATVLKALRPIVIFETY- 408
                                                                                                                        NLLFVHLLSLSKNOREGCSTDMAVVS----TP----FFNRNLWYRLLSSRFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 5.3%; Score 100.5; l Similarity 29.3%; Pred. No. 0.3! 27; Conservative 15; Mismatches
                                                                                                                                                                                                                                            62; Conservative
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                                                                                                                                                                                                                                                               5.3%; Score 100.5;
23.1%; Pred. No. 14
                                                                                                                                                                                                                                            42;
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                    DB 12; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                              Indels
  - VLGYNPPHKFSTK 514
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                                                                                                                                                                                                                                              69;
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                                                                                                                                                                                                                                            Gaps
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                                                                                462
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477 LMFAKTTHFSFHGSHSERIWYFDIIRIDDLV 507
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                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                       Aegopogon cenchroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         337 LD 338
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Q95F52;
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Q95F52
ID Q95F5:
AC Q95F5:
                                                                                    RESULT 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hilu K.W., Alice L.A.;
"Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based on matK sequences: A preliminary assessment.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTRONS (BY SIMILARITY).
-!- SIMILARITY: WITH CORRESPONDING ORP IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast.
Makaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Eragrostideae; Sporobolus.
                                   515 RVPEQF-----LEQENFS-----IENVLSYAQKLEYLLPQYRNFSFSLKEKELNVGR 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: || : || : || : || : | : | : | : | | | | | | : | : | : | : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 VVSTPFFNRNLWY------RLLSSRFSL-----WKSYCPRFFLDYLEAFGLL 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 QSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIR 305
173 LQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWL--LHPSFSEFF-----INMGR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 EKFLHLHYLSHIEIPYPIHFEILVQLLEYRIQDVPSLHLLRFFLNYYSNWNSLITSMKSI 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 5.3%; Score 99.5; DB 8; Length 513; Local Similarity 23.3%; Pred. No. 3; Conservative 54; Mismatches 153; Indels 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF144601; AAF20357.1; -.
InterPro; IPR000442; Intron maturse2.
InterPro; IPR002866; Mark No.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01348; Mark No.
CENOTOPIA Processing.
SEQUENCE 513 AA; 61561 MW; BF6BB16048B3EC6A CRC64;
                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                                                                                                                                                          513 AA.
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                                                                                                                                                           562 TFGK-----LPYPTRNVQTLCEALLA 582
                                                                                                           224 LFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                          PRT;
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Chloridoideae; Chlorideae; Aegopogon.
NCBI_TaxID=160573;
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5.2%; Score 99; DB 8; Length 513;
Best Local Similarity 19:1%; Pred. No. 3:3;
Matches 69; Conservative 63; Mismatches 124; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 IEKVQAL------PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : | | | :: | | | 453 RTFMQRLGSVFLEEFFT---EBEQVFSLMFS-------WTTYFSFHGSHSBRI--------WY 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 HLLSLSKNQREGCSTDMAVVSTPFFNRNLWYR-------LLSSRFSL----W 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 KSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYF 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            358 LIATRMKKFD-TTAPATP-LIRSL-----SKAQFCTGSGHPISKPIWTDLSDWDI 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 LDRFGRICRNLFHYHSGSSKKQTLYRLK----YILR---LSCARTLARKHK-----STV 452
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED INTROMS.

MITOCHODERAL INTRONS.

EMBL; AF312324; AAK60015.1; -.

INTERPO: IPRO00442; Intron matures2.

Interpo: IPRO00442; Intron matures2.

FEan; PF01348; Intron matures2; 1.

Pfam; PF01348; Intron matures2; 1.

Chloroplast; mRNA processing.

Chloroplast; mRNA processing.

SEQUENCE 513 AA; 61640 MW; E80743D3EA97F086 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilu K.W., Alice L.A.;

"A Phylogeny of Chloridoideae (Poaceae) Based on matK Sequences.";

"A Phylogeny of Chloridoideae (Poaceae) Based on matK Sequences.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-! FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

INTRONS (BY SIMILARITY)

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
                                                                                                            01-DEC-2001 (TrEMBirel. 19, Last sequence update)
01-MAR-2002 (TrEMBirel. 20, Last annotation update)
probale intron maturase (Maturase K).
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513 AA
                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seqn
01-MAR-2002 (TrEMBLrel. 20, Last anno
PRT;
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RESULT
O54921
ID O5
AC O5
DT O1
DT O1
DT O1
DT O1
OS Re
OC Re
OC Me
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Best Local S
Matches 70
                                                                                                                  054921;
01-JUN-1998
01-JUN-1998
01-DEC-2001
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01-DEC-2001
01-MAR-2002
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A Phylogeny of Chloridoideae (Poaceae) Based on matk Sequences.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II

-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODE
MITOCHONDRIAL INTRONS.

MITOCHONDRIAL INTRONS.

MITOCHONDRIAL INTRONS.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO00442; Intron maturse2.
InterPro; IPRO02866; MatK_N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK_N; 1.
Chloroplast; mRNA processing.
SEQUENCE 513 AA; 61432 MW; 56F4A4
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade;
Chloridoldeae; Chlorideae; Gymnopogon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTFMQRLGSVFLEEFFT---EEDQVFSLMF----PKTTHFSFHGSHSERI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIR--HFDELVELTSKLEWM 336
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                                                                                                           (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
tron maturase (Maturase K).
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19.3%; Pred. No.
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   Craniata; Vertebrata;
Sciurognathi; Muridae,
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      Euteleostomi;
; Murinae; Rat
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Best Local :
STRAIN=C2A / ATCC 35395 / DSM 2834;

MEDLINE=21929760; PubMed=11932238;

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98070770; PubMed=9405631;
Kee Y. Yoo J.S., Hazuka C.D., Peterson K.E., Hsu S.C.,
"Subunit structure of the mammalian exocyst complex.";
Proc. Natl. Acad. Sci. U.S.A. 94:14438-14443(1997).
EMBL, AF032666; AR001578.1;
InterPro; IPR002909; IPT_TIG.
Defam. PRO1833. TTG.1
                                                                                                                                                                                                                                                                                                            Methanosarcina acetivorans.
Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                                                 SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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19.9%; Pred. No. 6.7;
Ltive 77; Mismatches 122;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 LD-HQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 ---LIGSL-----SKAQFCTGSGHPISKPVWTDLSDRDILDRFGRICRNLFHYHSGSSK 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 KÖTLYRLK----YILR---LSCARTLARKHK-----STVRTFMÖRLGSVFLEEFFT--- 469
                                                                                                                                                                                                                                                                                                                       147 LHYLSH-IEIPYPLHLEI-LVQILEYRIQDVPSLHLLRFFLNYYSNWNSLISSMKSILLL 204
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                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                     50 QKENKEKQALARHKCISILEFFKNLLFVH----LLSLSKN----QREGCSTDM---AVVS 98
                                                                                                                                                                                                                                                                            1 VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQ--RAYSTPYSYYR-----IIL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni.
Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
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                                                                                                                                                                5.2%; Score 98.5; DB 8; Length 513;
22.0%; Pred. No. 3.6;
iive 62; Mismatches 141; Indels 109;
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                                                                                         Chloroplast; mRNA processing.
SEQUENCE 513 AA; 60865 MW; EFDC47C27343B94C CRC64;
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INEERPY; IPR001440; TPR.
Hypothetical prodection: Complete proteome.
SEQUENCE 584 AA, 69439 MW; CFAD376B1562DE1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DGC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein Cj1679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 ELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         470 EEEQVFSLMF----AKTTRFSF-HGSQ-----SERIWYLD 499
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Nature 403:665-668(2000).
         InterPro; IPR002866; MatK N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK N; 1.
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Matches 81; Conservative
                                                                                                                                                                                            Best Local Similarity 22.08
Matches 88; Conservative
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NCBI_TaxID=197;
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"Phylogenetic relationships in subfamily Chloridoideae (Poaceae) based on matk sequences: A preliminary assessment.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS,
AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY
MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Centotheceae; Zeugites.
Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., M. Sowers K.R., Jaing H., Macario A.J.L., Paulsen I., Metcalf W.W., Birren B., Wannson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B., The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.";

Genome Res. 12:532-542(2002).

EMBL, ABOINGOFS, AMMOS340.1;

Hypothetical protein; Complete protecome.

SEQUENCE 1078 AA, 125949 MW, 9C99FDFB152B13E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     86; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286 YYNLGYVLSELGLIEEAKQRYEESLQIHENLLE----IHPENEEYQALTGSAYYNLGNL 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 PHSLFESIFKFNEKVMLLYKSQDTEEIIEYKIQNQLSSAKIEIDNENYKKALNLLEDTKK 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 RHKCISILEFFKNLLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                196 SDKCVDLQKIHYDIMNLK-LKLCENQ------FEENPENSFLKAQISV--- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YCPRFFLDYLEAFGLLSDFLDHQAVI----KFFELETHFSYYPVSGFVAPHQYLSLLQDR 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             237 -----TLEDFGI----FLINVKLIEKAKKIYEREIQILQDLLNKYPENEEYLSLIGSA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 YFPIASVMRTLD-----KDNFSLTPDLIHDLLGHVPWLLHPSFSEF-----FINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTKV-------IBKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIEN 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::: | | :: | :: | :: | 341 LSELGSIDEATNRYERALKVHIQFIERYPEIKQYHSSVLKNEFKLIESYFYCAENEI--N 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 HEGRKAYGAVLISSPQELGHAFI-----DNVRVLPLELDQIIRLPF-NTSTPQETLFSI 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              399 NQTKMMFFGEVIHMCEQYQDLFIKSDSEDERKKMLEFKIRSQIKFSFLDIEMQKKHELSA 458
                                                                                                                                                                                                                                                                                                                                                                                                                                      10 PKYILKIALKLRQSLSLFFQNSQS---LQRAYSTPYSYYRIILQKENKEK-----QALA 60
                                                                                                                                                                                                                                                                                                                          5.2%; Score 99; DB 17; Length 1078;
16.3%; Pred. No. 8;
Live 79; Mismatches 148; Indels 86
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01-MAY-2000 (TrEWBLrel. 13, Last sequence update)
01-MAR-2002 (TrEWBLrel. 20, Last annotation update)
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InterPro; IPR000442; Intron_maturse2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       459 EKCDEAIKKIKKIK 472
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25;
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RESULT 47
Q94DZ7
ID Q94DZ
AC Q94DZ
AC Q94DZ
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Best Local
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STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
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SEQUENCE
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P0010B10.10.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Q94DZ7;
Q1-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
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                                       LFVDLLA-
                                                                                                         LWYRLLSSRFSLWKSYCPRFFLDYLEAFG-----LLSDFLDHQAVIKFFEL-----
                                                                                                                                                                                            KFPAILRKTPLSRLWYMPDMLFSTPKVHIVIDFHCPLTSHSPE-----AVIST----S
                                                                                                                                                                                                                                                              --QALARHKCISILEFFKNLLF----VHLL----SLSKNQREGCSTDMAVVSTPFFNRN 105
                                                                                                                                                                                                                                                                                                                                                                                                                        FFQNSQSLQRAYSTPYSYYRII------LQKENKEK-----------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTIMYARCLEKLCKIASKVLFAPQSAMYEMFK--NQIKFLN 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGVDDNFEEGKKYYESRLFYAHNETFSTYHYNESLKAFNKFGVDAFKNKEVLVFCEQGFG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGLIEN-HEGRKAYGAVLISSPQELGHAFIDNVRVLPLE---LDQIIR----LPFNTSTPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSLQEANQHHAQFWQN----YAKVLEFNSNYQEAYHAYKKCLSLDSHATYQFDLAYLLMR 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----SEFFINMGRLFTKVIE---KVQALPSKKQRIQTLQSNLIAIVRCFWFTVE 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NINLVKLEDR------LHSKTKENLTISKIEDFLTHQILPQKAYLLFKLFRISDSLELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLSL--LQDRYFPIASVMRTLDKDNFSLT---PDLIHDLLGHVPWLLHPSF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LWKNYAEIYFKHDFTKALNAHEHLCHFMQDLID------KLQ----KGIIAEQT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LWKSYCPRFFL-DYLEAFG------LLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQ 168
                                                                                                                                                                                                                                                                                                                                             FEGTTDSVEPWYCTAYSVENVTPSMIQQWIQKAPTEKLCIPKPNIFIPKDFSLKEAHEKV 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QTLLTRKDDLEDELKLELAFIYKLSNKLEESEQIFKEL--LSKDMYNLN-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----EFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKFALEFATLSSYKLSLFQKALYYAQELFSLNPTSFNGLMLAKSYIEN--LRLDEALNLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        945 AA; 109356 MW; 0B46F635508477F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 98.5;
22.8%; Pred. No. 7.
                                           ----DYLNAYGGYNDKMRILLDAIMKH---ISNFEVKPNRFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ed. No. 7.6;
Mismatches
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Best Local 9
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Q9D4H1;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AKO16522; BAB30290.1; -.
MGD; MGI:1913732; 2410030124Rik.
InterPro; ITRR002999; IPT_TIG.
Pfam; PF01833; TIG; 1.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
        175
                                                                               330
                                                                                                                                                                                                                                    287
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                                                                                                                                                                                                                                                                                                                                                                                     233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    646 KFIPHLISKTFLECYI-QGNIEPNDATSIVQEIEDTIFNTPKSVFKSMSPSQYLIRRVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 GHVPWLLHPSFSEFFINMGRL----FTKVIEKVQ------ALPSKK--QRIQT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152
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                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ETHFSYYPVSGFVAPH----QYLSL-LQDRYFPIASVMRTLDKDNFSLTPDLIHDLL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOSNLIAIVRCF
                                                                               AGIEDL---RELLLKKL-LETPSTLHDQKRYIRYLSDLHAPGDPAWQCIGAQHKWTLKLMQ
                                                                                                                                                         GLLSDFLDHQAVIKFFELETHFSYYPVSGFV-----
                                                                                                                                                                                                                                                                                                          LLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRF----SLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                     KVEGSMTQKLEN--VLNRASNTADTLFQEVLGRKDK---ADSTRNALNVLQRFK-FLFNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENEL - - - - KCY
                                                                                                                                                                                                                                    PLNIKRNIQKG---DYDVVIND-----YEKAKSLFGKTEVQVFKKY-----YAEVE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               924 AA;
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(TremBLrel. 17, Last seq
(TremBLrel. 17, Last ann
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        -RYFPIASVMRTLDKDNFSLTPDLIHDLLGHV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103958 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.2%; Score 98; DB 11; Length 924; 20.0%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457BAD92EAA3040B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 125;
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                                                                                                                                                     ----APHQY-LSLLQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 160;
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239 AA; 28001 MW; D721BD16C7D7B194 CRC64;
                                                                                                                                             Query Match 5.2%; Score 98; DB 9 Best Local Similarity 23.3%; Pred. No. 19; Metches 71; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P04176; 1PHZ:
InterPro; IPR01273; Asa hydroxylase.
Pfam; PF00351; blopterin H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
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NCBI_TaxID=6523;
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207 ----PWLLH--------PSFSEFFINM--GRLFTKVIEKV-QALPSK-- 238
                                                                                                                                                              436 GRDDTWRYKTPHRVAFVEKLTKLVLSQLPNFWKLWISYVNGSLFSETAEKSGQSERSKNV 495
                                                                                                                                                                                                                                                     239 -----KQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLIS---SPQELGHA 288
                                                                                                                                                                                                                                                                                                   496 RQRQNDFKKMIQEVMHSLVKLIRGALLPLS---LREGDGRQ-YGGWEVQAELSGQWLAHV 551
                                                                                                                                                                                                                                                                                                                                                                                              289 FIDNVRV--------HPDELDQIIRLPFNTSTPQETLFSIR--------HFDELVEL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                | :|: | :|: || | :|: || | | : : || | : : | | | : : | | | : : | | | : : | | | : : | | | | : : | | | | | : : | | | | : : | | | | | | : : | | | | | : : | | | | | : : | | | | : : | | | | : : | | | | : : : | | | : : | | | : : | | | : : | | | : : | | | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | | : : | : | | : : | : | | : : | : | : : | | : : | : | : | : | : : | : | : : | | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : | : : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : : | : | : | : : | : | : | : : | : | : : | : | : : | : | : : | : : | : | : : | : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : :
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
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STRAIN=BRISTOL N2;
Waterston N. S.
"Direct Submission.";
Submisted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF067217; AAF99977.1;
HSSP; P08799; 1MND.
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Murray J., Rohlfing T., O'Neal D., Wilson R.;
"The sequence of C. elegans cosmid F56A6,";
Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 214.2 kDa protein.
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SMART; SN00314; RA; 1.
SMART; SN00324; ADGAP; 1.
PROSITE; PS00479; DAG_PE_BIND_DOM_1; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 AEKEDWVVDNEGLTSLPCQFEQSIVHSLQSL 632
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InterPro; IPR000048; IQ_region.
InterPro; IPR000169; MA_domain.
InterPro; IPR000159; RA_domain.
InterPro; IPR000159; RA_domain.
InterPro; IPR000159; RA_domain.
InterPro; IPR000139; RA_domain.
InterPro; IPR000139; RA_domain.
InterPro; IPR000139; RA_domain.
InterPro; IPR000139; RA; I,
IPR00013; RA; I,
IPR00013; RACSIN_IRAY.
IPRODOM; PD000135; MYOSIN_IRAY.
IPRODOM; PD000135; MYOSIN_IRAY.
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MEDLINE=99069613; PubMed=9851916;
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EMBL; AF129815; AAF36488.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 NNNSSRFG-----KFIKINYREN-GAVSG-----ANVEIYLLEKSRIIFQTKGERNYH 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 VFYYLLEGADEEERKKYFLLKPHDYKYLNQNEPFALEGVN---ERNEF-----DRLK 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 HA-----MSSVGFCAKTQQTIFGIISAV------LLLGNITYIKRHGYHSDESGY 452
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YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92; Indels 108; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109 RLLSSRFSLWKSYCPRFF-LDYLEAFGLLSDFLDHQAVIKFFELET------H 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 NPKY-----ARLYPQS----KRLGSLPPHIFAIADVCYHNMLRIKEN----- 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Tryptophan hydroxylase (Fragment).
Lymnaea stagnalis (Great pond snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.2%; Score 97.5; DB 5; Length 239; Best Local Similarity 21.7%; Pred. No. 1.7; Matches 34; Conservative 30; Mismatches 64; Indels 25
                                                                                                                                                                                                                                                                                                                                                DB 5; Length 1887;
19;
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 2.
Hypochhetical protein.
SEQUENCE 1887 A4; 214207 WW; 992DDE7F409D2D84 CRC64;
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중 유
145 HACR---EYLANIPLLVEHCGYREDNVPQLEDIGRFLKERTGFTLRPVAGYLSSRDFLAG 201
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Search completed: January 9, 2003, 16:59:53 Job time: 90 secs

Вþ

30 106.5 5.6 296 2 A40996 31 104.5 5.5 2331 2 S44054 32 102 5.4 563 2 T38766 33 102 5.4 1050 2 C81624 34 100.5 5.3 1157 2 S38160 35 99 5.2 924 2 T09220	98.5 5.2 584 2 98.5 5.2 1024 2 98 5.2 1846 2 97 5.1 492 1	97 5.1 1050 2 96.5 5.1 512 2 96.5 5.1 512 2 96 5.1 529 2	96 5.1 2059 2 95.5 5.1 2059 2	95 5.0 1427 2 95 5.0 1477 2 95 5.0 1475 2	94.5 5.0 699 2 94 5.0 293 2 94 5.0 317 2	93 4.9 307 2 93 4.9 645 2 93 4.9 714 2 93 4.9 1022 2	93 4.9 1391 2 93 4.9 1397 2 92.5 4.9 735 2 92.5 4.9 1084 2 92 4.9 477 2	92 4.9 523 2 92 4.9 544 2 92 4.9 620 2 92 4.9 4563 1	91.5 4.8 293 2 91.5 4.8 670 2 91.5 4.8 907 2	91 4.8 835 1	91 4.8 2183 1 90.5 4.8 314 2	90.5 4.8 616 2	90.5 4.8 2330 1 90 4.8 863 2 90 4.8 863 2	90 4.8 2692 2	89.5 4.7 553 2	89.5 4.7 2136 2 89.5 4.7 2136 2	89.5 4.7 2812 2	89 4.7 355 2	89 4.7 1037 2	89 4.7 1197 1 89 4.7 1197 2	89 4.7 1197 2 88.5 4.7 519 2	88.5 4.7 892 2 88 5 4 7 1967 2	88 4.7 439 2 88 4.7 439 2	00 88 4.7 873 2	88 4.7 2291 2 88 4.7 2629 2
version 5.1.3 - 2003 Compugen Ltd. w model	5:23; Search time 43 Seconds (without alignments) 809.318 Million cell updates/sec	ESIPLYNQEKYLSGFEVLCQ 362	ឆ		parameters: 283224	naries		results predicted by chance to have a . to the score of the result being printed, of the total score distribution.	SUMMARIES	Description	aromatic amino aci aromatic amino aci				trypcopian	tryptophar					phenylalanine 4-mo hypothetical prote			phenylalan	disease resistance 174K ninaC protein
GenCore v Copyright (c) 1993 - OM protein - protein search, using sw	January 9, 2003, 15:1	Title: US-09-438-185A-1047 Perfect score: 1889 Sequence: 1 VHYCERTLDPKYILKIALKL	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.	hed: 283224 seqs, 96134422	Total number of hits satisfying chosen Minimum DB seq length: 0 Maximum DB seq length: 200000000	cessing: Minimum Mar Maximum Mar Listing fi	Database : PIR 73:* 1: $\overline{\mathbf{p}}$ ix1:* 2: $\overline{\mathbf{p}}$ ix2:* 3: $\overline{\mathbf{p}}$ ix3:* 4: $\overline{\mathbf{p}}$ ix4:*	s the number of er than or equal ved by analysis		Result Query No. Score Match Length DB ID	1 1886 99.8 362 2 E72002 2 1886 99.8 362 2 C86621	235.5 12.6 289 2 235.5 12.5 262 2	229.5 12.1 262 2 229.5 12.1 444 2	229.5 12.1 491 2	226.5 12.0 447 2	223.5 11.8 481 2 223 11.8 498 1	221.5 11.7 491 2	219 11.6 579 1	213.5 11.3 452 1	212.5 11.2 453 2 211.5 11.2 491 2	207 11.0 453 2 206.5 10.9 575 2	197 10.4 453 1 194 10.3 452 2	189.5 10.0 294 2 178.5 9.4 404 2	175.5 9.3 457 2	108.5 5.8 1253 2 108.5 5.7 1501 1

phenylalanine 4-mo genome polyprotein probable transcrip exodeoxyribonuclea wupptotherical protein year of the properties of protein year of the protein of the protein of the protein of the protein of the protein of the protein of the protein of the probable and protein of the protein of th

Query Match 99.8%; Score 1886; DB 2; Length 362;	A;ACCESSION: E/2002 A;Status: preliminary A;Status: preliminary A;Molecule type: DNA A;Residues: 1-362 <arn> A;Residues: 1-362 <arn> A;Residues: 1-362 <arn> CBS:AE001685; GB:AE001363; NID:g4377378; PIDN:AAD19183.1; PID:g437738 A;Cross-references: GB:AE001685; GB:AE001363; NID:g4377378; PIDN:AAD19183.1; PID:g437738 A;Experimental source: strain CWL029 C;Genetics: C;Genetics:</arn></arn></arn>	R;Kalman, S; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606; PMID:10192388	aromatic amino acid hyroxylase - Chlamydophila pneumoniae (strain CWL029) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000 C:Accession: F72002	RESULT 1	84 4.4 240 2 F70409 conserved hypothet	84.5 4.5 1748 1 JQ1555 genome polyprotein 84.5 4.5 3068 1 A44062 genome polyprotein	84.5 4.5 1070 2 G84982 exodeoxyribonuclea 84.5 4.5 1107 1 S52517 myosin I heavy cha	84.5 4.5 719 2 C88216 protein 80495.2 [1 84.5 4.5 820 2 T27909 hypothetical prote	84.5 4.5 553 2 E95160 hypothetical prote 84.5 4.5 585 2 S48951 hypothetical prote	84.5 4.5 531 2 B84442 hypothetical prote	85 4.5 938 2 G70472 hypothetical prote 84.5 4.5 2 T22823 hypothetical prote 84.5 4.5 2 C71150 hypothetical prote	85 4.5 567 2 B69166 hypothetical hypothetical hypothetical	85 4.5 493 2 H95209 transcription 85 4.5 549 2 F64640 conserved hyp	85 4.5 462 85 4.5 471	85 4.5 238 1 B64313 85 4.5 328 2 T32210	85.5 4.5 1808 2 AB1847 85.5 4.5 2039 2 864540	85.5 4.5 1489 2 85.5 4.5 1613 2	123 86 4.6 1822 2 544849 KI2H4.8 protein - 124 85.5 4.5 321 2 D90154 transposase ISC143 125 85.5 4.5 816 2 T95788 hypotherical prote	86 4.6 565 2 D72222 86 4.6 1405 1 DJZPA	86 4.6 422 2 A72309 86 4.6 512 2 D98074	86.5 4.6 1202 2 A48773 86 4.6 339 2 T20960	86.5 4.6 710 2 B89252 protein 2C455.4 [86.5 4.6 990 2 S23416 lantibiotic epide	86.5 4.6 128 2 AH2322 86.5 4.6 533 2 T27589	87 4.6 324 1 A48993 choloyigiycin 87 4.6 741 2 H90607 atp-dependent	87 4.6 293 2 F64558 conserved hypothe	87.5 4.6 1122 2 A97814 transcrip 87.5 4.6 1237 2 AC1583 internali	87.5 4.6 694 2 D81280	87.5 4.6 334 2 E7168
Qy 241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300	Db 181 ASVMRTLDKONFSLTPDLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240	61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLMYRLLSSRFSLWKS	Qy 1 VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA 60 :	Query Match 99.8%; Score 1886; DB 2; Length 362; Best Local Similarity 99.7%; Pred. No. 2e-144; Matches 361; Conservative 1; Mismatches 0; Indels 0; Gaps	A,Experimental Bource: strain J138 C;Genetics: A;Gene: CPj1046	A;Residues: 1-362 <sto> A;Cross-references: GB:BA000008; NID:g8979419; PIDN:BAA99253.1; GSPDB:GN0014</sto>	A,Status: preliminary A,Molecule type: DNA	A;Reference number: A86491; MUID:20330349; PMID:10871362 A;Accession: C86621	ımoniae i	C;Accession: Csbs21 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; S	C;Species: Chiamydophila pneumoniae, Chiamydia pneumoniae C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001	C86621 aromatic amino acid hyroxylase [imported] - Chlamydophila pneumoniae (strain	RESULT 2	Db 361 cQ 362	Qy 361 CQ 362	Db 301 DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQSLLESIPLYNQEKYLSGFEVL 360	Qy 301 DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360	Db 241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300	241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL	181 ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ	181 ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ	121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI	Qy 121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFFI 180	Db 61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLMYRLLSSRFSLMKS 120	QY 61 RHKCISILEFFKNILFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS 120	Db 1 MHYCERTLDPKYILKIALKLROSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA 60	Qy 1 VHYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALA 60	Best Local Similarity 99.7%; Pred. No. 2e-144; Matches 361; Conservative 1; Mismatches 0; Indels 0; Gaps

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HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240
                                                                                                                                                                                                                                                        LSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                      7%; Pred. No. 2e-144;
1; Mismatches 0; Indels 0; Gaps
                                                          JESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
|||||||||||||||||
|JESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
                                                                                                                                                                                       JDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI 180
RHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                  RHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                         0;
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08; NID:g8979419; PIDN:BAA99253.1; GSPDB:GN00142 J138 imoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.
314, 2000
genome sequences of chlamydia pneumoniae J138.
UID:20330349; PMID:10871362 e [imported] - Chlamydophila pneumoniae (strain J138) moniae, Chlamydia pneumoniae _revision 02-Mar-2001 #text_change 02-Mar-2001

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ò g à g RESULT 3

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A; Description: catalyzes the oxidation of tryptophan to 5'-hydroxytryptophan by tetrahydd A; Pathway: melatonin biosynthesis; scrotconin biosynthesis; tryptophan catabolism C; Superfamily: phenylalanine 4-monooxygenase C; Superfamily: phenylalanine 4-monooxygenase; oxidc C; Keywords: biopterin; iron; melatonin biosynthesis; metalloprotein; monooxygenase; oxidc F; SKH inding alte: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicte F; 260, 443/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status F; 272, 277, 317/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
Residues: 1-18,'T',20-67,'T',69-89,'TP',92-96,'M',98-99,'E',101-103,'S',105-150,'S',155
35,'G', 437-444 «TLP.
A;Cross-references: GB:L29306; NID:g531192; PIDN:AAA67050.1; PID:g531193
    A;Cross-references: GB:AE004522; GB:AE004091; NID:g9946768; PIDN:AAG04261.1; GSPDB:GN001: A;Bxperimental source: strain PAO1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1_444 ~800T.
A;Residues: 1_444 ~800T.
A;Crosa-references: EMBL:X52836; NID:g37954; PIDN:CAA37018.1; PID:g37955
A;Crosa-references: EMBL:X52836; NID:g37954; PIDN:CAA37018.1; PID:g37955
Arch. Biochem. Biophys. 315, 445-455, 1994
A;Itile: Cloning and expression of rabbit and human brain tryptophan hydroxylase CDNA in A;Reference number: S51199; NUID:95077422; PMID:7986090
                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 RVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
12.3%; Gcore 231.5; DB 1; Length 444;
Best Local Similarity 27.8%; Pred. No. 5.8e-11; Indels 27; Gaps Matches 64; Conservative 43; Mismatches 96; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                       93 DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 -----THFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 PLLTNPWFAEFTHTYGKLGLKA-----SKEER-----VFLARLYWMTIEFGLVE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267 NHEGRKAYGAVLISSPQELGHAFID---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 13 DNGFIHYPETEHQVWNTLITRQLKVIEGRACQEYLDGIEQLG-----LPHERIPQLDEIN 67
                                                                                                                                                                                                                     Query Match
12.5%; Score 235.5; DB 2; Length 262;
Best Local Similarity 24.5%; Pred. No. 1.4e-11;
Matches 61; Conservative 52; Mismatches 103; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120732; OMIM:191060
A;Map position: 11p15.1-11p14.3
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 DELVELTSK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 KRĽFQĽAQE 237
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                                                                                                                                                 A; Gene: phhA; PA0872
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C;Species: Pseudomonas aeruginosa
C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83535
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Braddman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Laxbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Teference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: GB:AE004410; GB:AE003853; NID:g9658244; PIDN:AAF96726.1; GSPDB:GN001
A,Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phenylalanine-4-hydroxylase VCA0828 [imported] - Vibrio cholerae (strain N16961 serogrou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.P.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
                                                                                                                       301 DQIIRLPFNISTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 GAKATPKERSY------LARLYWFTVEFGLVQEQGQTKIYGGGILSSPGE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 RIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLEL 300
                                                                        301 DQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 VWHELITRQGEVVKTRACQAYLDGLNMLNLPTDRLPQLPEINRVLQRETGWQVEPVPALI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 FTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQE 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 LGHAFIDNV-RVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSK----LEWM-LD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 LWYRLLSSRFSLWKSYCPRFFLDYLBAFGLLSDFLDHQAVI-KFFELETHFSYYPVSGFV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 APHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.6%; Score 256.5; DB 2; Length 289; Best Local Similarity 25.6%; Pred. No. 3.2e-13; Matches 65; Conservative 56; Mismatches 108; Indels 25;
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Status: preliminary Molecule type: DNA Residues: 1-289 <HEI>

A; Map position: 2

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A; Gene: VCA0828 C;Genetics:

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A;Status: preliminary A;Molecule type: DNA

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C;Accession: A53452
R;Zhao, G.S.; Xia, T.; Song, J.; Roy, R.A.
Proc. Natl. Acad. Sci. U.S.A. 91, 1366-1370, 1994
A;Title: Pseudomonas aeruginosa possesses homologues of mammalian phenylalanine hydroxy
A;Reference number: A53452; MUID:9415131; PMID:8108417
A;Accession: A53452
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C;Species: Pseudomonas aeruginosa
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 08-Oct-1999
C;Accession: A53452
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A; Residues: 1-262 < RES >
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              INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
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Tyrosine 3-monooxygenase (EC 1.14.16.2) - quail

N;Alternate names: tyrosine 3-hydroxylase
C;Species: Phasianidae gen. sp. (quail)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 31-Mar-2000
C;Accession: A28582; PHI524
R;Fauquet, M.; Grima, B.; Lamouroux, A.; Mallet, J.
J. Neurochem. 50, 142-148, 1988
A;Title: Cloning of quail tyrosine hydroxylase: amino acid homology with other hydro.
A;Reference number: A28582; MUID:88089590; PMID:2447231
A;Accession: A28582
                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-30 cFA2>
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; catecholamine biosynthesis; iron; metalloprotein; oxidoreduct
F;324,329,369/Binding site: iron (His, His, Glu) #status predicted
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A;Cross-references: GB.M17250, ND:9165771; PID:AAA31487.1; PID:9165772
C;Superfamily: phenylalanine 4-monoxygenase
C;Keywords: biopterin; iron; metalloprotein; oxidoreductase; phosphoprotein
F;272,277,317/Binding site: iron (His, His, Glu) #status predicted
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Proc. Natl. Acad. Sci. U.S.A. 84, 5530-5534, 1987
A;Title: Full-length cDNA for rabbit tryptophan hydroxylase: functional domains A;Reference number: A32699; MUID:87289638; PMID:3475690
A;Accession: A32699
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-101 (L',103-150,'L',152-201,'ND',204-206,'R',208-389,'K',391-444 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Fauquet, M.; Boni, C.
J. Neurochem. 60, 274-281, 1993
A;Title: The quail tyrosine hydroxylase gene promoter contains A;Reference number: PH1524; MUID:93107923; PMID:8093261
A;Accession: PH1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-491 - FAND
A;Cross-references: GB:M24778; NID:g213649; PIDN:AAA49514.1; PID:g213650
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                                                                                                                                                                                            107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                     PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                            WKEVYSTLKSLYPTHACK---EYLEAFNILEKFCGYNENNIPQLEEVSRFLKERTGFQLR 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELLGHVPLLAEPSFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WGTVFRELNKLYPTHACR---EYLKNLPLLSKYCGYQEDNIPQLEDISNFLKERTGFSIR 230
PVRGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADKTFAQFS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            h 12.1%;
Similarity 27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LASLGASEEAVQKLAT--
                                                                                                                                                                                                                                                                                       12.1%;
                                                                                                                                                                                                                                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 8.
                                                                                                                                                                                                                                                                                           Score 229.5; DB 2
Pred. No. 9.7e-11;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----CYFFTVEFGLCKQDGQLRVFGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5e-11;
ches 97;
                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                100;
                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                             Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an active cyclic
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RESULT 9

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JUNGORS

Lyrosine 3-monooxygenase (EC 1.14.16.2) - mouse
Lyrosine names: tyrosine hydroxylase
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Species: Musculus (house mouse)
C.Species: Ju-De-1991 #sequence_revision 31-De-1991 #text_change 31-Mar-2000
C.Apcession: JN0068; MUD: 91248263; PMID:1674869
A; Reference number: JN0068; MUID:91248263; PMID:1674869
A; Residues: 1-498 a.ICH>
A; Residues: 1-498 a.ICH>
A; Residues: 1-498 a.ICH>
A; Residues: 1-498 a.ICH>
A; Residues: 1-498 a.ICH>
A; Experimental source: Drain
B; Monlecule type: DRA
A; Residues: 1-20 a. Sharpy, Z.D.
Submitted to the EMBL Data Library, June 1990
A; Description: DC-12 Nuclear Extracts Produce Tissue-Specific Protection of Several Seque
A; Residues: 1-30 a.MORA
A; Residues: 1-30 a.MORA
A; Residues: 1-30 a.MORA
A; Residues: Las a.Mora
A; Residues: Las a.Mora
A; Residues: Las a.Mora
A; Residues: Las a.Mora
A; Residues: Las a.Mora
A; Residues: Las a.Mora
C; Comment: This enzyme, which requires ferrous iron, catalyzes the hydroxylation of tyros
c; C; Comment: This enzyme, which requires ferrous are c; Superfamily: phenylalanin at 4-monooxygenase; oxidoreductase; phosphoprote;
C; Superfamily: phenylalanin at monooxygenase; oxidoreductase; phosphoprote;
F; 331, 336, 376/Binding site: iron (His, His, Glu) #status predicted
                                Arystophan 5-monooxygenase (EC 1.14.16.4) - mouse tryptophan 5-monooxygenase (EC 1.14.16.4) - mouse (Specias: Mus musculus (house mouse)
C. Specias: Mus musculus (house mouse)
C. Accession: A34582
R. Stoll, J. Gozak, C.A.; Goldman, D.
Genomics 7, 88-96, 1990
A.Title: Characterization and chromosomal mapping of a cDNA encoding tryptophan hydroxyle A, Reference number: A34582; MUID:90243261; PMID:2110547
A, Reference number: A34582; MUID:90243261; PMID:2110547
A, Residues: preliminary
A, Stoll Minary
A, Residues: 1447 <STO>
A, Residues: L447 <STO>
A, Coresion: A34582; MID:9020113; PIDN:AAA63401.1; PID:9202114
A, Coresion: A34582; MID:9020113; A) A, Coresion: A34582; MID:9202113; A, Moterian auchors translated the codon AAC for residue 405 as Gln
A, Corestfanily: phenylalainie 4-monooxygenase
C, Superfanily: phenylalainie 4-monooxygenase
C, Reywords: biopterin; iron; metalloprotein; oxidoreductase; phosphoprotein
F, 275, 280, 320/Binding site: iron (His, His, Glu) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.0%; Score 226.5; DB 2; Length 447; ilarity 27.4%; Pred. No. 1.5e-10; Conservative 43; Mismatches 97; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 11.9%; Score 225.5; DB 2; Length 498; 1 Similarity 27.5%; Pred. No. 2.1e-10; 66; Conservative 42; Mismatches 101; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
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Best Local Similarity
Matches 66; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Rescidues: 1-444 «Authorian raphe nucleus
A; Experimental source: dorsal raphe nucleus
R; Darmon, M.C.; Grima, B.; Cash, C.D.; Maitre, M.; Mallet, J.
R; Darmon, M.C.; Grima, B.; Cash, C.D.; Maitre, M.; Mallet, J.
A; Title: Isolation of a rat pineal gland cDNA clone homologous to tyrosine and phenylala A; Rifelerence number: A24367; MUID:87005247; PMID:2875901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-444 cDAR>
A; Cross-references: GB:X53501; NID:g57760; PIDN:CAA37579.1; PID:g57761
A; Experimental source: pineal gland and state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of t
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A;Residues: 167-261 - DA2.
A;Cross-references: GB:M28000; NID:g207432; PIDN:AAA42262.1; PID:g207433
C;Comment: This enzyme has different physical properties in pineal gland and in dorsal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tryptophan 5-monooxygenase (EC 1.14.16.4) - rat

N.Alternate names: tryptophan 5-hydroxylase
C,Alternate names: tryptophan 5-hydroxylase
C,Species: Rattus norvegicus (Norway rat)
C,Accession: JL0034; A60034; A24367
R,Darmon, M.C.; Guibert, B.; Leviel, V.; Ehret, M.; Maitre, M.; Mallet, J.
N. Neurochem. 51, 312-316, 1988
A;Title: Sequence of two mRNs encoding active rat tryptophan hydroxylase.
A;Reference number: JL0034; MUID:88244702; PMID:337941
174 WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNVPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
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231 PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFS 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
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12.0%; Score 227.5; DB 1; Length 444;
Best Local Similarity 27.4%; Pred. No. 1.2e-10;
Matches 63; Conservative 43; Mismatches 97; Indels 27; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
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                                                                                                                                                                  279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDE 325
                                                                                                                                                                                                                                                                           387 LSSYGELIHSLSDEPEVRDFDPAAAVQPCQDQPYQPVYFVSESFSD 433
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::| ::: | ::: | 343 QDIG-----LASLGATDEEIEKLATL---
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Function:

Gaps

RESULT 10

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tyrosine 3-monooxygenase (EC 1.14.16.2) - rat
tyrosine 3-monooxygenase (EC 1.14.16.2) - rat
tylernate names: tyrosine 3-hydroxylase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 03-Mar-2000
C;Accession: A00510; A44714; S03026; I58264
R;Grima, B.; Lamouroux, A.; Blanot, F.; Faucon Biguet, N.; Mallet, J.
Proc. Natl. Acad. Sci. U.S.A. 82, 617-621, 1985
A;Title: Complete coding sequence of rat tyrosine hydroxylase mRNA.
A;Reference number: A00510; MUID:85113249; PMID:2857492
A;Accession: A00510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tryptophan 5-monooxygenase (EC 1.14.16.4) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 31-Mar-2000
C;Accession: I51567
A;Molecule type: mRNA
A;Residues: 1-498 <GRI>
A;Cross-references: GB:M10244; NID:g207408; PIDN:AAA42257.1; PID:g207409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-481 cGRE>
A;Cross-references: GB:L20679; NID:g450644; PIDN:AAA21306.1; PID:g450645
A;Cross-references: GB:L20679; NID:g450644; PIDN:AAA21306.1; PID:g450645
C;Superfamily: phenylalanine 4-monoxygenase
C;Keywords: biopterin; iron; metalloprotein; oxidoreductase
C;Keywords: biopterin; iron; metalloprotein; oxidoreductase
C;Keywords: biopterin; iron; metalloprotein; oxidoreductase
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. Neurochem. 62, 2420-2428, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAV 277
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70; Conservative
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tyrosine 3-monooxygenase (EC 1.14.16.2) - bovine c;Species: Bos primigenius teatrus (cattle) c;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000 c;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 31-Mar-2000 c;Accession: 145983 #sequence of a cDNA clone encoding bovine & J. Neurosci. Res. 19, 440-449, 1988 #sequence of a cDNA clone encoding bovine & Fittle: Isolation and nucleotide sequence of a cDNA clone encoding bovine & A;Reference number: 145983; MUID:88259287; PMID:2898537 #s,PAccession: 145983 #SUID:88259287; PMID:2898537 #s,PAccession: 145983 #sequence of a cDNA clone encoding bovine & A;Reference number: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #SUID:88259287; PMID:2898537 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PACCESSION: 145983 #s,PA
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A;Title: Role of the N-terminus of rat pheochromocytoma tyrosine A;Reference number: S03026; MUID:88271342; PMID:2899026
A;Accession: S03026
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Nucleic Acids Res. 15, 2363-2384, 1987
A;Title: Identification and cell type specificity of the tyrosine hydroxylase
A;Reference number: I58264, MUID:87174758; PMID:2882469
A;Recessione number: I58264
A;Status: translated from GB/EMBL/DDBJ
A;Status: translated from GB/EMBL/DDBJ
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A;Molecule type: protein
A;Residues: 2-12;16-24;38-47;151-157
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J. Biol. Chem. 261, 10489-10492, 1986
A;Title: Identification of four phosphorylation sites in the N-terminal region of tyr
A;Reference number: A44714; MUID:86278113; PMID:2874140
A;Accession: A44714
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A; Modecule type: DNA
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A; Residues: 1-30,35-135 < KOB3>
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A; Reperimental source: Splice form 3
A; Note: this splice form is produced by an alternative donor site within exon 1
R; Note: this splice form is produced by an alternative donor site within exon 1
R; Rightla: A single human gene encoding multiple tyrosine hydroxylases with different predia A; Reference number: A93393; MUID:8713064; PMID:2882428
A; Reference number: A93393; MUID:8713064; PMID:2882428
A; Residues: 1-30,62-528 < GRII>
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A; Reperimental source: splice form 1
A; Note: this splice form 1s produced by an alternative donor site within exon 1
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Ajstatus: translated from GB/EMBL/DDBJ
Ajmolecule type: DNA
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Ajmolecule type: DNA
Ajmolecule Acids Res. 15, 6733, 1987
Ajmile: Isolation of a full-length cDNA clone encoding human tyrosine hydroxylase type: Ajmile: Isolation of a full-length cDNA clone bundor: 138340; MUID:87316931; PMID:2888085
Ajmolecule type: JNA
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A;Scatus: pre-liminary; translated from GB/EMBL/DDBJ
A;Scatus: pre-liminary; translated from GB/EMBL/DDBJ
A;Scatus: 1-30,35-528 «KOB4»
A;Cross-references: EMBL:Y00414; NID:g37126; PIDN:CAA68472.1; PID:g37127
A;Cross-references: EMBL:Y00414; NID:g37126; PIDN:CAA68472.1; PID:g37127
J: Biol. Chem. 263, 7466-7410, 1988
A;Title: Expression of human tyrosine hydroxylase cDNA in invertebrate cells using a back A;Reference number: 155282; MUID:88213428; PMID:2896667
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y, Residues: 30,35-528 (SR13>
y, Cross-references: GB:X05290; NID:g32501
y, Experimental source: splice form 3
y, Note: this isozyme is produced by use of an alternative donor site within exon 1
y, Inchinose, H; Obye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.
slochem: Biophys. Res. Commun. 195, 158-165, 1993
y, Rate increased heterogeneity of tyrosine hydroxylase in humans.
y, Raterence number: PN0575; MUID:91371398; PMID:7689834
y, Accession: PN0575
y, Stadues: translation not shown
y, Molecule type: DNA
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A;Ressidues: GB:M20911; NID:g339636; PIDN:AAA61167.1; PID:g339637
A;Accession: 170056
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A, Status: translation not shown
A, Molecule type: DNA
A, Residues: 35-61 <ICH2>
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A, Residues: 1-94 × ARGA
A, Cross-references: GB:M7589; NID:g139680; PIDN:AAA61179.1; PID:g139681
R, Le Bourdelles, B.; Boularand, S.; Boni, C.; Horellou, P.; Dumas, S.; Grima, B.; Mallet
R, Le Bourdelles, B.; Boularand, S.; Boni, C.; Horellou, P.; Dumas, S.; Grima, B.; Mallet
A, Fittle: Analysis of the S' region of the human tyrosine hydroxylase gene: combinatorial
A, Recession: A60201
A, Rollecule type: mRNA
A, Rocession: A60201
A, Rollecule type: mRNA
A, Residues: 1-65 a, LEBA
A, Residues: 1-65 a, LEBA
A, Residues: 1-65 a, LEBA
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A, Residues: 1-65 a, LEBA
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A, Residues: 1-65 a, LEBA
A, Residues: 1-65 a, LEBA
A, Residues: 1-65 a, LEBA
A, Residues: 1-65 a, Rulonose, H.; Kishi, R.; Nakazawa, A.; Kurosawa, Y.; Fujitä
A, Tile: Structure of the human tyrosine hydroxylase gene: alternative splicing from a s
A, Reference number: JE0012; MUID:89008200; PMID:2902075
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NiAlternate names: Vyrosine 3-hydroxylase
NiContains: tyrosine 3-monooxygenase, splice form 1; tyrosine 3-monooxygenase, splice for C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #text_change 16-Jun-2000
C;Dates 31-Mar-1989 #text_change 16-Jun-2000
C;Datesibn: A30002; A26825; A60201; J20012; J20013; J20014; A27791; B27791; PNQ
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A; Residues: 1-528 (ANG1>
A; Cross-references: GB:M7589; NID: 9339680; PIDN: AAA61179.1; PID: 9339681
R; Kaneda, N.; Kobayashi, K.; Ichinose, H.; Kishi, F.; Nakazawa, A.; Kurosawa, Y.; Fujita
Biochem. Biochem. Biochem. 146, 971-975, 1987
A; Title: Isolation of a novel cDNA clone for human tyrosine hydroxylase: alternative RNP
A; Reference number: A90136; MUID: 87298614; PMID: 2887169
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A;Residues: 1-491 <DXM>
A;Cross-references: GB:M36794; NID:g163750; PIDN:AAA30779.1; PID:g163751
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: biopterin; iron; metalloprotein; monooxygenase; oxidoreductase
F;324,329,369/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          283 PAAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPECCHELLGHVPMLADRTFAQFS 342
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                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 221.5; DB 2; Length 491;
ilarity 27.1%; Pred. NO. 4.38-10;
Conservative 42; Mismatches 102; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE 334
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A;Residues: 1-14,62-135 <KOB2>
A;Cossa-references: GB:D00269; NID:g220099; PIDN:BAA25097.1; PID:g2951767
A;Experimental source: splice form 2
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submitted to GenBank, December 1987
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Matches 65, Conserve
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A;Residues: 1-34,62-64 <GIN2>
A;Cross references: GB:M20912; NID:g339642; PIDN:AAA61168.1; PID:g339643
C;Comment: The expression of the four distinct proteins produced by alternate splicing v C;Genetics:
A;Gene: GDB:TH
A;Cross references: GDB:119612; OMIM:191290
A;Gene: GDB:TH
A;Cross references: GDB:119612; OMIM:191290
A;Map position: lip15.5-11p15.5
A;Introns: 34/3; 61/3; 135/3
A;Note: the list of introns is incomplete
C;Function:
A;Pathway: catecholamine biosynthesis
A;Note: this is the rate-limiting step in catecholamine biosynthesis; iron; metallopx C;Keywords: alternative splicing; biopterin; catecholamine biosynthesis
C;Superfamily: phenylalanine 4-monooxygenase, splice form 4 #status predicted <MAT2>
F;1-30,Froduct: tyrosine 3-monooxygenase, splice form 3 #status predicted <MAT2>
F;1-30,62-528/Product: tyrosine 3-monooxygenase, splice form 1 #status predicted <MAT1>
F;1-30,62-528/Product: tyrosine 3-monooxygenase, splice form 1 #status predicted <MAT1>
F;1-18/Binding site: phosphate (Thr) (covalent) (by unidentified kinase) #status predicted F;19/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus predicted firstatus
                                                                                                           tyrosine 3-monooxygenase (EC 1.14.16.2), major splice form - fruit fly (Drosoph N;Alternate names: tyrosine 3-hydroxylase, type I; tyrosine 3-hydroxylase, type N;Contains: tyrosine 3-monoxygenase, minor splice form
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 21-Jul-2000
C;Accession: A55369; B55369; JN0010
R;Birman, S; Morgan, B; Anzivino, M; Hirsh, J.
J. Biol. Chem. 269, 26559-26567, 1994
A;Fille: A novel and major isoform of tyrosine hydroxylase in Drosophila is gen
A;Reference number: A55369; MUID:95014502; PMID:7929381
A;Accession: A55369
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-579 <BIRL>
A;Rotesidues: 1-579 <BIRL>
A;Rotesidues: GB:U14395; NID:959799; PIDN:AAA62876.1; PID:9598800
A;Note: authors translated the codon CGC for residue 219 as Ser, and TCC for re
A;Accession: B55369
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
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Best Local S
Matches 65
Residues: 1-61,133-579 <BIR2>;Cross-references: GB:U14395;;Note: authors translated the
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         NID:g595799; PIDN:AAAA62877.1; PID:g595801 codon CGC for residue 219 as Ser, and TCC
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3-hydroxylase, type II
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C;Genetics:
A;Gene: FlyBase:ple
A;Cross-references: FlyBase:FBgn0005626
A;Cross-references: FlyBase:FBgn0005626
A;Map position: 3L 65B
A;Map position: 3L 165B
A;Introns: 23/3; 61/1; 101/1; 132/1; 405/2; 447/3
A;Introns: 23/3; 61/1; 101/1; 132/1; 405/2; 447/3
C;Superfamily: phenylalanine 4-monooxygenase
C;Keywords: alternative splicing; biopterin; iron; metalloprotein;
C;Keywords: alternative splicing; biopterin; dron; metalloprotein;
F;409,414,454/Binding site: iron (His, His, Glu) #status predicted
                                                              A;Molecule type: mRNA
A;Residues: 208-453 <ROB>
A;Residues: 208-453 <ROB>
A;Cross-references: GB:K02599; NID:g205961; PIDN:AAA41794.1; PID:g205962
A;Cross-references: GB:K02599; NID:g205961; PIDN:AAA41794.1; PID:g205962
A;Wretborn, M.; Humble, E.; Ragnarsson, U.; Engstrom, L.
Blochem. Blophys. Res. Commun. 93, 403-408, 1980
Blochem. Blophys. Res. Commun. 93, 403-408, 1980
A;Title: Amino acid sequence at the phosphorylated site of rat liver phenylalanine A;Reference number: A14970; MUID:80220293; PMID:7387651
A;Accession: A14970
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references. GB.M12337; NID:g206120; PIDN.AAAA1843.1; PID:g206121 R;Robson, K.J.H.; Beattie, W.; James, R.J.; Cotton, R.C.H.; Morgan, F.J.; Woo, S.L.C Biochemistry 23, 5671-5675, 1984 A;Title: Sequence comparison of rat liver phenylalanine hydroxylase and its cDNA clo. A;Reference number: A00509; MUID:85122617; PMID:6098294 A;Accession: A00509;
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Neuron 2, 1167-1175, 1989
A;Title: Isolation and characterization of the gene for drosophila tyrosine hydroxyl
A;Reference number: JN0010; MUID:90166583; PMID:2483109
A;Accession: JN0010
A;Accession: JN0010
A;Molecule type: mRNA
A;Residues: 1-61,133-579 <NEC>
A;Cross-references: GB:X76209; NID:g433469; PIDN:CAA53802.1; PID:g433470
C;Genetis:
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J. Biol. Chem. 261, 4148-4153, 1986
A;Title: Isolation and sequence of a cDNA clone which contains A;Reference number: A25321; MUID:86140234; PMID:2869038
A;Accession: A25321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phenylalanine 4-monooxygenase (EC 1.14.16.1) - rat
N;Alternate names: phenylalanine 4-hydroxylase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Dec-1986 #sequence revision 19-Oct-1995 #text_change 03-Mar-2000
C;Accession: A25321; A00509; A14970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-453 < DAH >
;Molecule type: protein
;Residues: 12-16,'B',18-19,'ZZ'
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Similarity 28.6%; Pr
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Pred. No. 8.4e-10;
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Query Match
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NyAlternate names: phenylalanine 4-hydroxylase
NyAlternate names: phenylalanine 4-hydroxylase
C;Decies: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 21-Jul-2000
R;Kwok, S.C.M.; Ledley, P.D.; Dilella, A.G.; Robson, K.J.H.; Woo, S.L.C.
Biochemistry 24, 556-561, 1985
A;Title: Nucleotide sequence of a full-length complementary DNA clone and amino acid seq
A;Reference number: A00508; MUID:85199778; PMID:2986678
A; Description: catalyzes the 4'-hydroxylation of phenylalanine to tyrosine by tetrahydrd A; Pathway: tyrosine biosynthesis; phenylalanine catabolism cisuperfamily: phenylalanine 4-monooxygenase C; Keywords: biopterin; homodimer; iron; metalloprotein; monooxygenase; oxidoreductase; F; 16/Falhading site: phosphate (Ser) (covalent) (by calmodilin-dependent kinase) #status F; 23/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict F; 285,290,330/Binding site: iron (His, His, Glu) #status predicted
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A; Molecule type: protein
A; Residues: 131-144 <CCT>
A; Residues: 131-144 <CCT>
B; Konecki, D.S.; Wang, Y.; Trefz, F.K.; Lichter-Konecki, U.; Woo, S.L.
Biochemietry 31, 8363-8368, 1992
A; Title: Structural characterization of the 5' regions of the human phenylalanine hydrox
A; Reference unuber: IS2416; WUID:92399453; PMID:1326329
A; Accession: IS2416
A; Accession: IS2416
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R;Abadie, V.; Jarucaleska, J.; Lyonnet, S.; Millasseau, P.; Berthelon, M.; Rey, F.; Munni Hum. Mol. Genet. 2, 31-34, 1993
A;Title: Illegitimate transcription of the phenylalanine hydroxylase gene in lymphocytes A;Reference number: I54346; MUID:93258345; PMID:8098245
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A;Residues: 1-452 cKWO.
A;Cross-references: GB:KO3020; NID:g189936; PIDN:AAAG0082.1; PID:g189937
A;Cross-references: GB:KO3020; NID:g189936; FIDN:AAAG0082.1; PID:g189937
B;Coctton, R.G.H.; McAdam, W.; Jennings, I.; Morgan, F.J.
Biochem. J. 255, 193-196, 1988
A;Title: A monoclonal antibody to aromatic amino acid hydroxylases. Identification of A;Reference number: S02687; WUID:89061656; PMID:2461704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 FPLLEKYC------GFREDNIPQLEDVSQFLQTCTGFRLRPVAGLLSSRDFLGGL 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 AFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIG-----LA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :| : | : | : | : | 310 SLGAPDEYIEKLAT-----IYWFTVEFGLCKEGDSIKAYGAGLLSSFGELQYCLSDKP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 FSLWKSYCPRFFLDYLEAFGLLSDFLDH-QAVIKFFELETHFSYYPVSGFVAPHQYLSLL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 ODRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVO 233
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A;Molecule type: mRNA
A;Residues: 381-389, 'G', 391-405 <ABA>
A;Cross-references: GB:S61296; NID:g300410; PIDN:AAD13926.1; PID:g4261626
A;Experimental source: 1ymphocytes, mutant form
R;Kowlessur, D.; Gitron, B.A.; Kaufman, S.
Arch. Biochem. Biophys: 333, 85-95, 1996
                                                                                                                                                                                                                                                                                                                                           Query Match 11.3%; Score 214; DB 1; Length 453; Best Local Similarity 28.4%; Pred. No. 1.5e-09; Matches 61; Conservative 37; Mismatches 89; Indels 3
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A; Residues: 1-20 < KON>
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A,5Catus: translated from GB/EMBL/DDBJ
A,5Catus: translated from GB/EMBL/DDBJ
A,8Catus: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Rolecule type: DNA
A,Rolecule type: DNA
A,7Cross-references: GB:865592; NID:9238240; PIDN:AAB20205.1; PID:9238241
A,6Cross-references: GB:8119470; OMIM:261600
A,6Gene: GDB:PDH
A,Cross-references: GDB:119470; OMIM:261600
A,Map position: 12q24.1-12q24.1
A,Note: a defect in this gene can cause phenylketonuria
C,Complex: homodimer
C,Complex: homodimer
C,Function:
A,Description: catalyzes the 4'-hydroxylation of phenylalanine to tyrosine by tetrahydrol
A,Description: catalyzes the 4'-hydroxylation of phenylalanine catabolism
C,Superfamily: phenylalanine 4-monoxygenase
C,Keywords: biopterin; homodimer; iron; metalloprotein; monoxygenase; oxidoreductase; p?15/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predicte
F;285,290,330/Binding site: iron (His, His, Glu) #status predicted
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A; Accession: $74142
A; Molecule type: protein
A; Molecule type: protein
A; Residues: $2-1 < KKOWN
B; Eigel, A; Dworniczak, B.; Kalaydjieva, L.; Horst, J.
Hum. Genet. 87, 739-741, 1991
A; Title: A frameshiff mutation in exon 2 of the phenylalanine hydroxylase gene linked to A; A; Accession: 154257; MUID:92039642; PMID:1682235
A; Accession: 154257
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tyrosine 3-monooxygenase (EC 1.14.16.2) - bovine
tyrosine 3-monooxygenase (EC 1.14.16.2) - bovine
KyAlternate names: tyrosine 3-hydroxylase
CySpecies: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 31-Mar-2000
C;Accession: JL003; A27687
R;Saadat S.; Stehle, A.D.; Lamouroux, A.; Mallet, J.; Thoenen, H.
J. Neurochem. 51, 572-578, 1988
J,Title: Predicted amino acid sequence of bovine tyrosine hydroxylase and its similarity
A;Reference number: JL0039; MUID:88274405; PMID:2899135
A;Accession: JL0039
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A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
A;Residues: 153-158,160,162-169 <ABA>
C;Comment: This protein is the rate-limiting enzyme in the biosynthesis of catecholamine C;Superfamily: phenylalanine 4-monoxygenase
C;Keywords: biopterin; iron; metalloprotein; oxidoreductase; phosphoprotein
F;24-91/Product: tyrosine 3-monoxygenase #status predicted <AMI>
F;8/Binding site: phosphate (Ser) (covalent) (by unidentified kinase) #status predicted
F;19/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predict
F;19/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase) #status predict
F;324,329,369/Binding site: tron (His, His, Glu) #status predicted
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A;Experimental source: adrenal medulla
R;Abate, C; Smith, J.A., Joh, T.H.
Biochem. Biophys. Res. Commun. 151, 1446-1453, 1988
A;Title: Characterization of the catalytic domain of bovine adrenal tyrosine hydroxylase
A;Reference number: A27687; MUID:88183482; PMID:2895648
A;Accession: A27687
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A; Residues: 1-491 <SAA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                          279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE 334
                                                                                                                                                                                                                                                                                                                                                            219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226 WKEVYSTLRGLYPTHACR---EHLEAFELLERFCGYREDRIPQLEDVSRFLKERTGFQLR 282
                                                                                                                                                                                                                                                                                             QDIG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QEIG------LASLGAPDEYİEKLAT-----IYWFTVEFGLCKEGDSIKAYGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSSFGELQYCLSDKPKLLPLELEK 371
                                                                                                                                                                                                                                                                                                                                                                                                                           PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLAHGPMLADRTFAQFS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSPQELGHAFIDNVRVLPLELDQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                               LSSYGELLHSLSEEPEIRAFDPDAAAVQPYQDQTYQPVYFVSESFSDAKDKLRSYASRIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAF-GLLSDFLDH-QAVIKFFELETHFSYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 11.2%; Score 211.5; DB 2; Similarity 26.7%; Pred. No. 2.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
   (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41; Mismatches 104;
                                                                                                                                                                                                                                                                                                ----LYWFTVEFGLCKQNGEVNAYGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 491;
                                                                                                                                                                  446
                                                                                                                                                                                                                                                                                                386
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Matches

70;

Conservative

47;

Mismatches

116;

Indels

45;

Gaps

Similarity

294

104 RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155

RKTWGIIYRKLR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 350

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RESULT 22
T34509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N;Alternate names: phenylalanine 4-hydroxylase; tryptophan hydroxylase C;Species: Drosophila melanogaster C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 31-Mar-2000 C;Accession: J00766 R;Morales, G.; Requena, J.M.; Jimenez-Ruiz, A.; Lopez, M.C.; Ugarte, M.; Alonso, C Gene 93, 213-219, 1990 A;Title: Sequence and expression of the Drosophila phenylalanine hydroxylase mRNA. A;Accession: J00766; MUID:91033030; PMID:2121612 A;Accession: J00766
                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein ZK1290.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T34509 R;Taich, A.
                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-575 <TAI>
A;Cross-references: EMBL:U21308; PIDN:AAB93319.1; GSPDB:GN00020; CESP:ZK1290.2
A;Experimental source: strain Bristol N2; clone ZK1290
                                                                                                                                                                                                                                                                                                      submitted to the RMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid ZK1290
A;Reference number: Z21535
A;Accession: T34509
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C;Ksywords: biopterin; iron; metalloprotein; monooxygenase; oxidoreductase; phenylke:
F;285,290,330/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references:
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-453 <MOR>
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                                                                              A; Introns: 49/3;
                                                                                                                                A;Gene: CESP:ZK1290.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: FlyBase: Tph
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Best Local Similarity
     Query Match
Best Local :
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                                                                                                         position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTIKFANSIPRPFGVRYN--AYTQSVEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGL--LESIP----LYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEIG-----LASIGAPDDYIEKIST----IFWFTVEYGLLAKEGELKAYGAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WGIIFRNLTKLYKTHACR---BYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LŚŚYGELEYCLTDKPQLKDFE-----PESTGV---TKYPITQFQPLYYVADSFETAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSPOSIGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                           72/2; 105/3; 223/1; 257/3; 280/2; 310/2; 346/1; 391/2; 433/3; 523/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.0%;
10.9%; Score 206.5; DB 2
25.2%; Pred. No. 8.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 207; DB 2; Length 453 Pred. No. 5.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 109;
                       DB 2;
                          Length 575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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phenylalanine-4-hydroxylase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Calobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C;Accession: C87449
R;Nierman, W.C.; Reldhlyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.F.B.; Laub, M.T.; DeBoy, R.T.; Dodasva, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koloné
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Ttle: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                Afficial type: mRNA
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Biochem. Biophys. Res. Commun. 225, 238-242, 1996
A;Title: Structure of the phenylalanine hydroxylase gene in Drosophila melanogaster and
A;Reference number: JC4888; MUID:96332435; PMID:8769124
A;Accession: JC4888
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A;Cross-references: GB:AE005673; NID:g13423011; PIDN:AAK23591.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYY 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 LSSYGELEYCLTDKPQLKDFE-----PEVTGV---TKYPITQFQPLYYVADSFETAKE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFB----LETHFSYYP-------- 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 -----VSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSF 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Match 10.3%; Score 194; DB 2; Length 452; Local Similarity 27.1%; Pred. No. 6.3e-08; les 73; Conservative 39; Mismatches 111; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 QGL--LESIP----LYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 KTIKFANSIPRPFGVRYN--AYTQSVEVL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
C;Accession: A42271
K;Neckameyer, W.S.; White, K.
J. Biol. Chem. 267, 4199-4206, 1992
A;Title: A single locus encodes both phenylalanine hydroxylase and tryptophan hydroxylase
A;Reference number: A42271; MUID:92156168; PMID:1371286
A;Accession: A42271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: FlyBase:FBgn0005770
C;Superfamily: phenylalanine 4-monoxygenase
C;Keywords: biopterin; iron; metalloprotein; monoxygenase; oxidoreductase; phosphoprote
F;284,289,329/Binding site: iron (His, His, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phenylalanine 4-monooxygenase (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)
N/Alternate names: phenylalaninase; phenylalanine 4-hydroxylase
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1996 #sequence_revision 18-Oct-1996 #text_change 20-Jun-2000
C;Accession: JC4888
R;Ruiz-Vazquez, P.; Moulard, M.; Silva, F.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryptophan 5-monooxygenase (EC 1.14.16.4) - fruit fly (Drosophila sp.)
NiAlternate names: tryptophan hydroxylase
C;Species: Drosophila sp.
C;Date: 10-Sep.1199 #sequence_revision 10-Sep-1999 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 PVAGLLSSRDFLAGLAFRVFHSTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPAFAQFS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 QEIG-----LASLGAPDDYIEKLST----IFWFTVEYGLCRQEGELKAYGAGL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 ISSPQELGHAPIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 SYYPYSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                      351 RVRPVAGYLSARDFLAGLAYRVFFCTQYVRHHADPFYTPEPDTVHELMGHMALFADPDFA 410
                                                                                                                                                                                                                   216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI----- 265
                                                                                                                                                                                                                                                                                                                                                                                                   ---ENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 WGIIFRNLTKLYKTHACR----EYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                           411 QFSQEIG-----LASLGASEEDLKKLATL-----YFFSIEFGLSSDDAADSPVK 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.4%; Score 197; DB 1; Length 453;
ilarity 27.5%; Pred. No. 3.6e-08;
Conservative 38; Mismatches 111; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence extracted from NCBI backbone (NCBIN:82902, NCBIP:82903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEEAQQ --- KLRMFTNNMKRPFIVRYN--PYTESVEVL 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    339 QGL--LESIP-----LYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 397 KTIKFANSIPRPFGVRYN--AYTQSVEVL 423
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es 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule type: mRNA
Residues: 1-453 <NEC>
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                                                                                                                                                                                                                                                                                                                                                                                                   266
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submitted to the EMBL Data Library, October 1995	RESULT 27 T23494 phenylalanine 4-monooxygenase (EC 1.14.16.1) K08F8.4 [similarity] - Caenorhabditis elega C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 19-May-2000 C;Accession: T23494 R;Smye, R.	Qy 275 GAVLISSPQELGHAFID 291 	Qy 215 SEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAY 274 :: :: :: :: :: :: :: :: :: :: :: :: ::	155 FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTBDLIHDLLGHVPWLLHPSF 	Qy 130 LEAFGLLSDF-LDHQAVIKFELETH 154	Qy 70 FFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLMYRLLSSRFSLWKSYCPRFFLDY 129	Qy 19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQA-LARHKCISILE 69	Query Match 9.4%; Score 178.5; DB 2; Length 404; Best Local Similarity 24.3%; Pred. No. 9.6e-07; Matches 77; Conservative 41; Mismatches 114; Indels 85; Gaps 11;	A; Map position: 2 A; Map position: 2 A; Introns: 117/2; 183/1; 273/2; 302/3; 369/3 A; Introns: 117/2; 183/1; 273/2; 302/3; 369/3 C; Superfamily: phenylalanine 4-monooxygenase C; Keywords: biopterin; oxidoreductase	A, Cross-vace: . 1-704 C. M. A. (1908) A, (1908) A, (1908) G. (1908) G. (1908) A, (1908) G. (1908) A, (1908) G. (190	A; Reference number: 220038 A; Accession: T25433 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	C;ACCESSION: T25453 R;Henkhaus, J; Wohldmann, P. submitted to the EMBL Data Library, December 1996 submitted to the EMBL Data Library, December 1996 A;Description: The sequence of C. elegans cosmid B0432.	T23453 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 19-May-2000	Qy 331SKLEWMLDQGLLESIP 346 SKLEWMLDQGLLESIP 346	Qy 275 GAVLISSPQELGHAFID-NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELT 330	Qy 215 SEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAY 274
Qy 198 -LIHDLLGHVPWLLHPSFSEFFIN	Qy 116 SLWKSYCPRFFLDYLEAFGLLS	Qy 77 VHLLSLSKNQREGCSD	Query Match Best Local Similarity 20.3%; Matches 81; Conservative 61		A; Molecule type: DNA A; Residues: 1-1253 A; Cross-references: EMBL: AL133452 A; Experimental source: cultivar Co	A;Reference number: Z23013 A;Accession: T45787 A;Status: preliminary	- 2 4	145787 145787 disease resistance-like protein - / N/Alternate names: protein F26013.: C:Species: Arabidopsis thaliana (m	388 LAESFASAKNKLKSWAATINRP		203 LC 288 LC	228 Q	Query Mato Best Local Matches	A;Gene: CESP:K08F8.4 A;Map position: 2 A;Map position: 2 A;Matrons: 12/3; 51/3; 116/1; 170/; A;Introns: 12/3; 51/3; 116/1; 170/; C;Superfamily: phenylalanine 4-monn C;Keywords: biopterin; oxidoreducts	A;Residues: 1-457 -WIL> A;Cross-references: EMBL:Z66497; P A;Experimental source: clone K08F8 C:Genetics:	A;Reference number: Z19747 A;Accession: T23494 A;Status: preliminary; translated A:Molecule type: DNA A:Molecule type: DNA

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0/2; 236/1; 281/2; 323/3; 400/2
pnooxygenase
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                                :||: |: : | :
HPPLLSLPQDFNTRNLVILNMCYSKLQRLWEGTKELG 592
                                                           EAIFLDPSALSFDVNPMAFENMYNLRYLKICSSNPGN 532
                                                                                                                                    LSDFLDHQAV----ET 153
                                                                                                                                                                        Score 109.5; DB 2; Length 1253;
Pred. No. 1.6;
11; Mismatches 130; Indels 127; Gaps
                                                                                                                                                                                                                                                                                                                                     047/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----TKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRDFLAGLAFRVFHSTQYIRHHSAPKYTPEPDICHEL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 175.5; DB 2; Length 457;
Pred. No. 2e-06;
95; Mismatches 80; Indels 49; Gaps
NM-----KVQ 233
                                                                                                                                                                                                           --TDMAVVSTPFFNRNLWYRLLSS-----RF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse-ear cress)
ision 04-Feb-2000 #text_change 04-Feb-2000
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QIRYNAYTQRVEILDKV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGELQYALSDKPEVVDFDPAVCCVTKYPITEYQPKYF 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQELGHAFIDNVRVLPLE--LDQIIRLPFNTSTPQET 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olumbia; BAC clone F26013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.; Grellet, P.; Laudie, M.; Mewes, H.W.; Lemcke, F. Database, December 1999
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bb 1143QVHIYNQ 1150 RESULT 30 A40996 phenylalanine 4-moncoxygenase (EC 1.14.16.1) - Chromobacterium violaceum NyAlternate names: phenylalaninase; phenylalanine 4-hydroxylase C;Species: Chromobacterium violaceum C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 31-Mar-2000 C;Accession: A40996; B40996 R;Onishi, A.; Liotta, L.J.; Benkovic, S.J. J Biol. Chem. 266, 1844-18459, 1991 A;Title: Cloning and expression of Chromobacterium violaceum phenylalanine hydroxylase ir A;Reference number: A40996; MUID:92011593; PMID:1655752 A;Molecule tvoe: DNA	A; Residues: 17-296 < CONIS A; Cross-treferences: GB: M55915; NID:g144481; PIDN:AAA23115.1; PID:g144482 A; Accession: B40996 A; Molecule type: protein A; Residues: 1.20 < CONS. A; Residues: 1.20 < CONS. A; Residues: 1.20 < CONS. A; Experimental source: strain ATCC 12540 C; Keywords: biopterin; oxidoreductase Query Match Best Local Similarity 27.3%; Pred. No. 0.4; Matches 27; Conservative 22; Mismatches 49; Indels 1; Gaps 1; Matches 27; Conservative 22; Mismatches 49; Indels 1; Hilling Application Applicat	Db 63	A;Variety: strain Popp C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999 C;Accession: 544054; 532776 R;Bukreyo, A.A.; Volchkov, V.E.; Blinov, V.M.; Dryga, S.A.; Netesov, S.V. R;Bukreyo, A.A.; Volchkov, V.E.; Blinov, V.M.; Dryga, S.A.; Netesov, S.V. R;Bukreyo, A.A.; Volchkov, V.E.; Blinov, V.M.; Dryga, S.A.; Netesov, S.V. A;Reference number: 544049 A;Reference number: 544054 A;Residue: 1231 - 54054 A;Residue: 1-231 - 54054 A;Gross-references: EMBL: 229337; NID: 9450908; PIDN: CAA82542.1; PID: 9450915 A;Cross-references: EMBL: 229337; NID: 9450908; PIDN: CAA82542.1; PID: 9450915 A;Experimental source: strain Popp R;Bukreyov, A.A.; Netesov, S.V. submitted to the EMBL Data Library, September 1992	A,Description: The partial nucleotide sequence of Marburg virus genome. A,Reference number: 832775 A,Accession: 832775 A,Accession: 832776 A,Molecule type: genomic RNA A,Residues: 1-2331 cBUM3 A,FEXPERIMENTAL: EMBL:X68494; NID:g296962; PIDN:CAA48508.1; PID:g296963 A,FEXPERIMENTAL SOURCE: Strain POPP C,Genetics: A,Gene: L C,Genetics: A;Fexperimental source strain Popp C,Genetics: A,Gene: L C,Superimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Gene: L C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental source strain Popp C,Genetics: A;Fexperimental S,Fexperiment
	inac protein - fruit fly (Drosophila melanogaster) inas: protein kinase (EC 2.7.1) les: Drosophila melanogaster is 1-Dec-1993 #sequence_revision 31-Dec-1993 #text_chansion: B29813 ell, C.; Rubin G.M. 2. 757-772, 1988 2. TS7-772, 1988 2. TS7-775, 1988 2. TS7-775, 1988 2. THe Drosophila ninac locus encodes two photoreceptor cence number: A90898; MUID:88151067; PMID:2449973 Sign: B29813 Sign: B29813 Auther : 1-1501 **NON-	nices: GB:MZ0230; NID:gls/yb/; FIDN:AAAZ8/Z1.1; FID:gls/ e:ninac ninac protein; myosin motor domain homology; protein k ninac protein; myosin motor domain homology; protein k tin binding; alternative splicing; ATP; nucleotide bind in: protein kinase homology «MMOT» ain: myosin motor domain homology «MMOT» on: actin binding #stetus predicted nain: carboxyl-terminal «CBT» live site: Lys, Glu, Asp #status predicted site: ATP (Lys) #status predicted	uery Match set Local Similarity 22.4%; Pred. No. 2.4, atches 85; Conservative 58; Mismatches 130; Indels 107; Gaps 21; atches 85; Conservative 58; Mismatches 130; Indels 107; Gaps 21; 10 PKYILKIALKIROSISIPPONSOSLORAYSTPYSYYRILOKENKEKQALARHKCI 65 11 PKYILKIALKIROSISIPPONSOSLORAYSTPYSYYRILOKENKEKQALARHKCI 65 12 PKYILKIALKIROSISIPPONSOSLORAYSTPYSYRILOKENKEKQALARHKCI 65 13 PEMIETFRASLDESIMLMFTNQLIKAGNLIMPFEAVQHKDESERKSYALNTLSAGCI 895 66 SILEFFKNILFVHILISISKNOREGCSTDMAVVSTPFFNRNLWYRLLSS-RFSIWKSYCPR 124 1	ALGVLDTVIARQKGFSSRLPPDEFLRRY FSLTPDLIHDLLGHVPWLLHPSFSEFFINM CRLLFLRLKOMGGWALGKTKVFLRYNDEF SSNLIAIVRCFWFTVESGLIENHEGRRA

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molocule type: DNA
A;Molocule type: DNA
A;Residues: 1-563 <GEN'
A;Cross-references: EMBL:Z69086; PIDN:CAA93165.1; GSPDB:GN00066; SPDB:SPAC3H8.08c
A;Experimental source: strain 972h-; cosmid c3H8
C;Genetics:
A;Gene: SPDB:SPAC3H8.08c
A;Gene: SPDB:SPAC3H8.08c
A;Map position: 1
C;Superfamily: transcription regulator SPBC16G5.17; GAL4 zinc binuclear cluster ho
F;14-50/Domain: GAL4 zinc binuclear cluster homology <GL4>
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             A;Molecule type: DNA
A,Residues: 1-1157 cBAL>
A,Residues: 1-1157 cBAL>
A,Residues: 1-1157 cBAL>
A,Residues: 1-1157 cBAL>
A,Cross-references: EMBL:228307; NID:g486562; PID:g486563; MIPS:YKR082w
A,Experimental source: strain S288C
R;Garcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santos, M.A.; Bou, G.; Remacha
Yeast 10, 231-245, 1994
A,Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae
A,Title: The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae
A,Reference number: S42009; MUID:94262327; PMID:8203164
                                                                                                                                                                                                                                RESULT 34

$38107

NUP133 protein - yeast (Saccharomyces cerevisiae)

NJAlternate names: protein YKR082w; protein YKR402

C;Species: Saccharomyces cerevisiae

C;Date: 03-May-1994 #sequence revision 03-May-1994 #text_change 21-Jul-2000

C;Accession: $3816(0; $42011); $51915; $39130; $39130;

R;Baladdron, V.; Ballesta, J.P.G.; Bou, G.; del Rey, F.; Esteban, P.F.; Garcia-Cantal-
submitted to the Protein Sequence Database, March 1994

A;Reference number: $38158

A;Accession: $38160
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hick, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzb-Nucleic Acids Res. 28, 1197-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR3. A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exodeoxyribonuclease V, beta chain, probable CP0007 [imported] - Chlamydophila pneumor. C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: C81624 R;Read, T.D.; Brunham, R.C.; Shen. C. Gill and the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of th
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A;Experimental source: strain AR39, HL cells
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 WVERTLEFCNLDRIFNTLLVDLQEYLKQNYTPW-LSPDESVF-----ALEKLLSS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 RLIHKKPALTHSQLVLHHITNYLKQDLWKNVLFQEQFHLLAVRYNVTSKHTSSLVDKLLA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 ----VVSTPFFNR-----NLWY-RLLSSRFSLWKSYCPRFFLDYLEA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 RIILQXENKEKQALARHKCISIL--EFFKNLLF---VHLLSLSKNQREGCSTDMA----- 95
LFISPKFTGSL----FLIGDPKQSIYEWRSADLPTYLTAKSSFSEDKQL 434
                                                                                                                                                  VRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYTQPISSYFSSRVERLEQISLWHQQIYNSLLEIPK----QVFLDQLTAHISGFKKQPFS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -VMRTLDKDNF-----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILDDL--HHFVDLLYTSETHSSLFSFFKIAETFNFKHRLA-----RYKPCAAFTVLENMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSDFLDHQAVIKFFELETH---FSYYPVS-GFVAPHQYLSLLQDRYFPIAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAYLISSPQELGH---AFIDN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    $; Score 102; DB 2; Length 1050;
$; Pred. No. 5;
51; Mismatches 116; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                  REQYQLVLIDEFODTDKQQWSIFSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -FG 134
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Db 233 KVEGBMTQKLEN-VLANAASNTADTLEQELIGRKOKADSTRNALNVLORFK-PLFNL 286 Cy 19 LISLSROREGGSTDMAVVSTPFFNRALMSRFSLWKSYCRFFLDYLEAF 133 Db 287 PLNIKRNIQKGDYDVNINDYEKAKSLFGKTEVQVFKKYYAEVE 329 Cy 134 GLLSDPLDHQAVIKFFELSTHFSYYEVSGFVAPHQY-LSILQ 174 :	RESULT 36 Deposite the protein Cji679 [imported] - Campylobacter jejuni (strain NCTC 11168) Nypochetical protein Cji679 [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni C;Species: Campylobacter jejuni C;Species: Oampylobacter jejuni C;Species: Oampylobacter jejuni C;Species: Oampylobacter jejuni C;Species: Oampylobacter jejuni C;Species: Oampylobacter jejuni C;Species: Oampylobacter jejuni C;Species: Oampylobacter jejuni reveals hype Nature 403, 665-668, 2000 A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype A;Reference number: A81250; MUID:20150912; PMID:10688204 A;Reference number: A81250; MUID:20150912; PMID:10688204 A;Reference pathonianary A;Molecule type: DNA A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D434 c-PAB A;Residues: D544 c-PAB A;Resid	OY 169 YLSLLODRYFPIASVWRTLDKDNPSLTPDLIHDLLGHVPWLLHPSF 214
Residues Cross-re Cross-re Cross-re Bo J. 13 Bo J. 13 Rattles A Ra	Qy 143 QAVIKFPELETHFSYYPVSGFYAPHQYLSLIQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202 11 1 1 1 1 1 1 1 1	Query Match 5.2%; Score 99; DB 2; Length 924; Best Local Similarity 19.9%; Pred. No. 7.4; Matches 90; Conservative 77; Mismatches 122; Indels 164; Gaps 27; Qy 19 KLRQSLSLFFONSQSLQRAYSTPYSYYRILLQKENKEKQALARHKCISILEFFKNLLFVH 78

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hypothetical protein MG075 - Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: Mycoplasma genitalium C;Species: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1999 C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 07-Dec-1999 C;Accession: C64208 C;Accession: C64208 R;Fraser C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Genetic code: SGC3
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A;Experimental source: strain G-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1024 <TIGR>
A;Cross-references: GB:U39687; GB:L43967; NID:g1045744; PID:g1045751; TI
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Best Local
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                                                                                                                                                                                                                                                                                                                     811 LKKEYTFKDNLKFFPFKADGSSRLEFDLSKPDQRVIPFAFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        614 -----ELLNFFPDTKDITPT 647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KSIRDLFADML-FGKSLESVNDSDSFIKINGSFTLKYHGDNLNLLPNYHSLITKNVGYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QQTDSLKNLFSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL----- 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ETLFSIRHFDELVELTSKLEWMLDQGLLESIPLYNQEKYLS 355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFT-----KVIEKVQALPSKKQRIQT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI-----DKT
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                                                                                                                                                                                                                                                                                                                                                                      ----HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD 324
                                                                                                                                                                                                                                                                                                                                                                                                                          VNVNFHIDARLLTAELQNTVFSNPK-----PVIKSPVELSKSLFEVWKTIFENSVNQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 98.5; DB 2;
Pred. No. 9.3;
1; Mismatches 134;
                                                                                                                                         #text_change 23-Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytochrome P450 2L - spiny lobster N; Contains: oxidoreductase (EC 1. - . - .)
N; Contains: oxidoreductase (EC 1. - . - .)
C; Species: Panulirus argus (spiny lobster)
C; Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 19-May-2000
C; Accession: S68856; S74194
R; James, M.O.; Boyle, S.M.; Trapido-Rosenthal, H.G.; Smith, W.C.; Greenberg, Arch. Biochem. Biophys. 329, 31-38, 1996
A; Title: CDNA and protein sequence of a major form of P450, CYP2L, in the ha; Reference number: S68856; MUID:96201120; PMID:8619632
                                                                                                                                               A;Gene: CYP2L1
C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: chromoprotein; electron transfer; endoplasmic reticulum; l F;295-458/Domain: cytochrome P450 homology <CYP>F;295-458/Domain: cytochrome P450 homology <CYP>F;436/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Residues: 1-10, 'X', 12-39 <JAN>
C; Genetics:
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A; Residues: 1-492 < JAM>
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                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source: hepatopancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S68856
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                                                                                                                     Query Match
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                      56 KQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: U44826; NID: g1304739;
                                                                                              5.1%; Score 97;
19.9%; Pred. No.
                                                                          56;
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                                                                          Mismatches 106;
                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAB03106.1;
                                                                                                                     Length 492;
                                                                       Indels 136;
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PID: g1304740

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A;Introns: 71/1; 165/3; 247/2; 335/2; 356/2; 389/3; 441/3; 497/3; 539/1; 607/3; 636/2 06/1; 1714/3; 1756/2 C;Superfamily: rat myosin heavy chain; myosin motor domain homology; protein kinase (
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1846 < MUR>
A;Residues: 1-1846 < MUR>
A;Cross-references: EMBL:AF067217; PIDN:AAC17015.1; GSPDB:GN00019; CESP:F56A6.2
A;Experimental source: strain Bristol N2; clone F56A6
C;Genetics:
A;Gene: CESP:F56A6.2
A;Map position: 1
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                          255 --QCVVİSGESGSGKTESTNHLMSHLİSLSQKGSTGCSTEQTLLSAGPVLEAFGNAVTLT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 NPKY-----ARLYFQS----KRLGSLPPHIFAIADVCYHNMLRIKEN-----
                                                                                                                                                                                                                                                                                                                                      61 RHKCISI------LEFFKNLLFVHLLSLSKNQREGCSTDMAVVST-----PFFNRNLWY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 DPKYILKIALKLRQSLSLFFQNSQSLQRAYSTP-----YSYYRIILQKENKEKQALA 60
                                                           HVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGL 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.2%; Score 98; DB 2; Length 1846; (larity 23.3%; Pred. No. 22; Conservative 34; Mismatches 92; Indels 1
                                                                                                                                                                                                                                                                       -KFIKINYREN-GMVSG-----ANVEIYLLEKSRIIFQTKGERNYH
                                                                                                                                                                                                   ----FVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLG 204
----LLLGNITY I KRHGYHSDESGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108;
                                                                                                                                   ---DRLR
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                                                                                                                                   408
452
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Glacose-6-P dehyrogenase [imported] - Chlamydophila pneumoniae (strain J138)
Glamydophila pneumoniae, Chlamydaphila pneumoniae
Glspecies: Chlamydaphila pneumoniae, Chlamydia pneumoniae
Glspecies: Chlamydaphila pneumoniae, Chlamydia pneumoniae
Glacossion: F86520
Glacossion: F86520
Glacossion: F86520
Alirakawa H.; Kimoto, NW.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ish Nucleic Acids Res. 28, 2311-2314, 2000
Alirite. Comparison of whole genome sequences of chlamydia pneumoniae J138.
Alirite Comparison of whole genome sequences of chlamydia pneumoniae J138.
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Glucose-6-p dehyrogenase - Chlamydophila pneumoniae
Glucose-121-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
Gluct: 21-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
Gluct: 21-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
Gluct: 21-Apr-1999 #sequence_revision 23-389, 1999
Altitle: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
Alterence number: A72000; MUID:99206606; PMID:10192388
Alteresion: CT2103
Alterence number: A72000; MUID:99206606; PMID:10192388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 FFKNLLFVHLLSLSKNQREGCSTDMAVVSTPF-------FNRNLWY---- 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186 -----TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 VSVLGYREEENVDKDSRVETYVALKTVINNPRWLGVP----FYLRAGKRLAKKSTDISII 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373 FKKS------PYNLFAAEECSRCPIENDLL------IIRIQPDE-GVALKFNCKV 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 PGTNNIVRPVKMDFRYDSYFQTTTPEAYERLLCDCIIGDRTLFTGGDEVMASWKLFTPVL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVR- 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 5.1%; Score 96.5; DB 2; Length 512; Local Similarity 18.8%; Pred No. 5.3% indels 177; Gaps es 83; Conservative 57; Mismatches 124; Indels 177; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 LRQSLSLFFQNSQSLQRAY-----STPYSYYRIILQKENKEKQALARHKCISILE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 LKDSL-----EDLDKTYGTRGNRLFYLSTPPQYFSRIIENLNKHK--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 -----LFY------KNODOGKPWSRVIIEKPFGRDLDSAKOLOOCINENLNENSVYHIDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 ------RLLSSRF-----SLWKSYCPRFFLDYLE-----AFGLLSDFLDHQAVIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 YLGKETVQNILTTRFANTIFESCWNSQ----YIDHVQISLSETIGIGSRGNFFEKSGMLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148 -----FFELETHFSYYPVSGFVAPH---OYLSLLODRYFPI---ASVMR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELTSKLEWMLDQGLLESIPLY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 E----EW--DODSSPSFPNY 488
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Rishitation: Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;References: G858000008; NID:38979110; PIDN:BAA98945.1; GSPDB:GN00142
A;Experimental source: strain J138
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C,Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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5.1%; Score 97; DB 2; Length 1050;
Best Local Similarity 22.1%; Pred. No. 13;
Marches 77; Conservative 51; Mismatches 117; Indels 104; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 - VMRTLDKDNF----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
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79 KTALSKFECSDRPDFYTFKLF------113
                                                                                                                                                                                                                                                                                           162 ---GFVAPHQYLSLLQD---RYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL--HPS 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FIKEHO---- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------ 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 -ATLDPSNPKDLLDAYLIDLQERKEDPLSTWNIETVRAVIMDLFGAGTETTSTMIRWTIL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           299 -----ELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPL---- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 ----VVSTPFFNR-----NLWY-RLLSSRFSLWKSYCPRFFLDYLEA-----FG 134
                                                                                                116 SLWKSYCPRFFLDYLEAFGL----LSDFLDHQAVIKFFELETHFSY---YPVS----- 161
                                                                                                                                                                                     114 -MWQTH-RRFILRQLRDLGMGKSRLEAAIQHEAACLVQELKKHTDQPMPLPKSINLAVLN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46 RIILQKENKEKOALARHKCISIL--EFFKNLLF---VHLLSLSKNOREGCSTDMA---- 95
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178 FPIASVMRTLDKDNFSLTPDLI-HDLLGHVPWLLHPSFSEFF 218	9 7	
120 SYCPREFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177 :	Qу 12 рь 13	
ery Match 5.1%; Score 96; DB 2; Length 529; st Local Similarity 22.0%; Pred. No. 6.1; tches 66; Conservative 35; Mismatches 127; Indels 72; Gaps 11;	Query Best L Matche	
RESULT 43 \$62468 \$62468 \$c;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 16:May-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000 C;Accession: T38579; \$62468 R;Badcock, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, October 1995 A;Reference number: Z21745 A;Accession: T38579 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-529 <ba2 1l<="" a;cross-references:="" a;map="" c;gene:="" embl:z54354;="" gspdb:gn00="" nid:g1019398;="" pid:g1019411;="" pidn:caa91178.1;="" position:="" spac2g11.13="" td=""><td>RESULT 43 \$62468 probable m Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Ayreferency Ayr</td><td></td></ba2>	RESULT 43 \$62468 probable m Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Cyspecies: Ayreferency Ayr	
328 ELTSKLEWMLDQGLLESIPLY 348 	Qy 32 Db 47	
295VLPLELDQIIRLPFNTSTPQETLFSIRHFDELV 327	Qу 29 Db 4 1	•
236 PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVR- 294	Оу 23 рь 37	
186TLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235	Qу 18 Db 31	
148 FFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMR 185	Qy 14 Db 25	
109RLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIK 147	Qy 10 Db 20	
70 FFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFIRNLMY 108	Qу 7 рь 15	
20 LRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILE 69 :	Qy 2 pb 11	
ery Match 5.1%; Score 96.5; DB 2; Length 512; st Local Similarity 18.8%; Pred. No. 5.3; tches 83; Conservative 57; Mismatches 124; Indels 177; Gaps 22;	Query Best L Matche	
A;Cross-references: GB:AE001609; GB:AE001363; NID:g4376502; PIDN:AAD18391.1; PID:g437651 A;Experimental source: strain CWL029 C;Genetics: A;Gene: zwf C;Superfamily: glucose-6-phosphate dehydrogenase	A;Cross- A;Experi C;Geneti A;Gene: C;Superf	

RESULT T41933 large C;Spec: A;Vari- C;Acce R;Nich submit A;Desc: A;Refe:	B 8	B 8	ß 8	B 8	B 8	유 성	Ma Ma	RESULT H72041 exodeo. C. Spec: C. Date C. Acce. Reture A. Titl A. Rece. A. Rete. A. Res. A. Res. A. Res. A. Fees. A. Fees. A. Gene A. Gene	å å	유	g &
4 4 4 0 8 · 8 · 6	293 390	236 355	183	135 253	96 197	46 137	Query Matc Best Local Matches	Codeoxyribon Codeoxyribon Species: Ch Date: 23 Ap Accession: Kalman, S.; Kalman, S.; Kalture Genet. Pittle: Comp Reference n Accession: Status: pre-	320 362	271 303	219 250
15 gument prote ss: human her y: strain JI (3-Dec-1999 jion: T4193) alas, J the EMB iption: Deters prione number:	VRVLPL : : LFISPK	PSKKORIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLI 	-VMRTLDKDNFSLTPDLIHDL-LGHVPWL 	LLSDFLDHQAVIKFFELETHFSYYPVS-GFVAPHQYLSLLQDRYFFIAS	VVSTPPFNRNLWY-RLLSSRFSLWKS 	RIILQKENKEKQALARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMA	7 7	RESULT 44 H72041 H72041 H72041 H72041 C;Species: Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila pneumoniae, Chlamydophila plate: 23-Apr-1999 Heccession: H72041 R;Kalman, S; Mitchell, W.; Marathe, R.; L Rature Genet. 21, 385-389, 1999 A;Title: Comparative genomes of Clamydia plate (Comparative genomes of Clamydia plate (Comparative genomes of Clamydia plate (Comparative genomes of Clamydia plate (Comparative genomes of Clamydia plate (Comparative genomes of Clamydia plate (Comparative genomes of Clamydia plate (Clamydia plate) A;Reference preliminary A;Gross-references: GB:AE001655; GB:AE0013 A;Experimental source: strain CWL029 C;Genetics: A;Genetics:	NFQLTLLGMGISS	RKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFN	-INMGR
ны нно	PLELDQII : PKFTGSL-	IQTLQS QAL	DKDNF-	DHQAVI -HHFVD	VVSTPFFNR- : : : PISSYFSSRV	enkeko Palths	similarity 7; Conser	ease v, ydophila 999 #8eq 041 385-38 110e gen er: A720 041 11nary 11nary 11nary 1041 50 <arns< td=""><td>LGMGIS</td><td>ASNATT : : ASSITA</td><td>FTFIL</td></arns<>	LGMGIS	ASNATT : : ASSITA	FTFIL
2 ic Ph	RLPFNT FLI	NLIAIV	RIFNTL	KFFELE : LLYTSE	R RVERLE	IIILQKENKEKQALARHKCIS 	vat	, beta la pne equenc , w.; , w.; la 389, 1 389, 1 2000; strai	SFALLG	QELGHA : : KESYHS	INMGRLETKVIEKVQALPS
n he 7 _rev _brar	STPQET ::: GDPKQS	RCFWFT	TADTOR HITOGE	THSSLF	HMTSIÖ : XMTN	CISIL	5.1%; 22.1%; ;ive 51	v, beta - Chlamydoph hila pneumoniae, Chla #sequence_revision 23 !ll, W.; Marathe, R.; !S-389, 199 !genomes of Clamydia A72000; MUID:99206606 Y ARN> GB:AE001655; GB:AE001	IRH : TVIIPY	FIDNVR	PSKKQR
pesvi sion , Dec	LFSIRE	VESGLI	DL-LGF	SFFKIF	-RLLSS ::: QQIYNS	-EFFKNLLF- : : : QDLWKNVLFQ	Pre	amydop e, Chl sion 2 ee, R.; ee, R.; ee, P.; 20660	TTEYFO	VLPLEI : : ISSIRI	IQTLQS
.rus 7 (03-Dec- ;ember 1	PLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGL 	ENHEGE	-SLTPDLIHDL-LGHVPWLLHPSFSEFF 	HQAVIKFFELETHFSYYPVS-GFVAPHQYLS 	-nlwy-rllssrfslwksycprffldylba- : : slwhqqiynsllbipkqvfldqltah	ILLF	ore 96; DB ed. No. 15; Mismatches	Chlamydophila pneumoniae niae, Chlamydia pneumoni eniae, Chlamydia pneumoni evision 23-Apr-1999 #tex evision 23-Apr-1999 #cx fathe, R.; Lammel, C.; Fa Clamydia pneumoniae and D:99206606; PMID:1019238	irhfdelveltsklemmldogllesiplynoekylsgf 	TSTPQETLFSDAILITELPGIIRLPFNTSTPQETLFSDAILITLLYNSVKESYHSFKHAMSISSIRLFLFSRLFINCGIQTSLSSAVIFGKARLNLS	INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHE
stra 1999 1995 he c	ELTSKLI : CLTAKS	RKAYGAVLIS : REQYQLVLID	LHPSFSEFF	»HQYLSL : CHRLA	· ×	-VHLLSLSKNQREGCSTDMA- :: GFHLLAVRYNITSKHTSSLVD)B 2; L 5; 8 117;	nila pneumoniae amydia pneumonia 3-Apr-1999 #text Lammel, C.; Pan pneumoniae and 5; PMID:10192388	VMIIS:	FINCG:	RCFWFT
JI) text	EWMLDQGL : : SFSEDKQL	Δ	FINMG	LIQDRY RY	CPRFFLDYLEA ; QVFLDQLTAHISG	SKNQR 	en	0 0 5 10	TLLESI	TSTP	FVESGL
_change e nucle	GL 341 434	SPQELGHA : EFQDTDKQQWS	INMGRLFTKVIEKVQAL :: ALEKLLSS	RYFPIAS : RYKPCAAFTVLENMS	ISG	EGCSTD :: SKHTSS	1050 els	tra tr	PLYGLL 	TSTPQETLFS ; TSLSSAVIFG	CTIVIL
21-Jan		AFIDN : QWSIFSN	VIEKVQA : :: ALEKLLS	TVLENM	FKKQP	MA ! LVDKLL	104;	in CWL029) ge 05-May- Olinger, achomatis	KYLSGF : GYIPGF	KARLNL	- IENHEG PVENHEG
-200		N 292 N 389	L 235	- 182 IS 305	FG 134 FS 252	- 95 A 196	Gaps	y-2000 y-1000 y-2000 y-2000 y-2000 y-2000 y-2000	E 358	- 319 .S 361	G 270 S 302
nce of							19;	Grimwood			
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probable zinc proteinase [imported] - Arabidopsis thaliana (Specias: Arabidopsis thaliana (mouse-ear cress) (C;Specias: Arabidopsis thaliana (mouse-ear cress) (C;Accession: B84846 (Specias) (Special Esquence_revision 02-Feb-2001 #text_change 16-Feb-2001 (C;Accession: B84846 (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Special Estate) (Sp
A;Cross-references: GB:Z99122; GB:AL009126; NID:g2636029; PIDN:CAB15644.1; PID:g2636152
A;Experimental source: strain 168
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A, Status: preliminary
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-970 <STO>
A, Residues: 1-970 <STO>
A, Cross references: GB: AE002093; NID: 92335108; PIDN: AAC02769.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 WYRLLSSRFSLWKSYCPR-----FPLDYLEAF------GLLSDFLDHQAV---IKF 148
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21.7%; Pred. No. 17;
tive 48; Mismatches 128; Indels 174; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    93; Indels 81; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 WLAFFDSEFSLWQARTPEGSQNMQGLYYGYLSALKKHAPNKPELKSLYQIHSAIAVCLRM 201
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                                                                                                                                                                                                                                                                                                         Match 5.1%; Score 95.5; DB 2; Length 536; Local Similarity 21.8%; Pred. No. 6.8; J. Conservative 30; Mismatches 93; Indels 81 es 57; Conservative 180;
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C;Superfamily: Bacillus subtilis hypothetical protein ywqB
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Deccies: Bacillus subtilis
C;Deccies: Bacillus subtilis
C;Deccies: Bacillus subtilis
C;Accession: E70066
R;Kunst, F: Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S; Brouillet, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997 Henaut, A.; Hibbert, H.; Holsappel, S.; Hossono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Hullo, M.F.
Koetter, P.; Roningstein, G.; Krogh, S.; Kose, M.; Sakosno, S.; Hullo, M.F.
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell
Y, M.; Glawar, K.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sektguchi, J.; Sckowska, A.; Seror
A;Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sektguchi, J.; Sckowska, A.; Seror
A;Authors: Yoshikawa, H.; Zumetelle, K.; Yasumoto, K.; Yaca, K.; Yaca, K.; Yoshida, K.;
A;Authors: Yoshikawa, H.; Zumetelle, E.; Koshikawa, H.; Danchin, A.
A;Ttle: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: Asserter number: A;Reference of the Gram-positive bacterium Bacillus subtilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1378 FD--LLDNIAHFRFAFDFNHQQNLILKLKDKFKTLRTDTVFERFFNLDDTFVSSMNVENF 1435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.1%; Score 96; DB 2; Length 2059;
Best Local Similarity 20.6%; Pred. No. 37;
Matches 90; Conservative 62; Mismatches 164; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 CPRFFLDYLEAFGLLSDFLDHQAVI------KFFELETHFSYYP-----VSGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 VAPHQYLS-----TP- 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 FFKNL--LFVHLLSLSKNQREGCSTD----MAVVSTPFFNRNLWYRLLSSRF--SLWKSY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 ILKIALKLRQSLSLFFQNSQS-LQRAYSTPYSYYRIILQKENKEKQALARHK--CISILE 69
                                                                                                                                                                                                                                                                                                                                                        A;Note: U31
C;Superfamily: varicella-zoster virus 240K tegument protein
                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-2059, ANIC>
A;CsGs-references: EMBL:143400; PIDN:AAC54693.1
A;Experimental source: strain JI
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     Accession: T41933
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A;Residues: 1-1427 <WED>
A;Cross-references: EMBL:X59720; NID:g1907116; PID:g1907218; MIPS:YCR081w R;Ballesta, J.P.G.; Pranco, L.; Hoenicka, J.; Jimenez, A.; Remacha, M.; Sa submitted to the Protein Sequence Database, March 1992
A;Reference number: S19486
A;Accession: S19496
A;Molecule
                                         A;Molecule type: DNA
A;Residues: 1-133,'RFV',136-137,'PDWS',142,'LASLYLTA' <JIM>A;Residues: 1-133,'RFV',136-137,'PDWS',142,'LASLYLTA' <JIM>A;Cross-references: EMBL.X59720
R;Rodriguez-Cousino, N.; Lill, R.; Neupert, W.; Court, D.A.
Yeast 1, 581-585, 1995
Yeast 1, 581-585, 1995
A;Reference number: S55867; MUID:95373282; PMID:7645349
A;Accession: S55868
A;Accession: S55868
                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X59720; MIDS:YCR080W R;Hengartner, C.J.; Thompson, C.M.; Zhang, J.; Chao, D.M.; Liao, S.M.; Koleske, Genes Dev. 9, 897-910, 1995 A;Title: Association of an activator with an RNA polymerase II holoenzyme. A;Reference number: A57062; MUID:95293223; PMID:7774808 A;Accession: C57062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 202-863 <BAL>
A; Cross-references: EMBL:X59720; MIPS:YCR080w
A:Crossion: S19495
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N;Alternate names: cyclin-dependent kinase 5 activator homolog; probable membrane protei
C;Species: Saccharomyces cerevisiae
C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S74293; S19496; S19495; S19766; C57062; S53594; S55868; S68611; S59988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Wedler, H.; Wambutt, R. submitted to the Protein Sequence Database, September 1996 A;Reference number: S74288
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A; Residues: 531-1427 <FEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Feldmann, H.; Mannhaupt, G.; Vetter, I. submitted to the Protein Sequence Database, March 1992 A;Reference number: S19429
A;Accession: S19766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A,Residues: 'MSFFCLENSGNARDGPLDFEESYKGYGEHELEENDYLNDETFGDNVQVGTDFDFGNPHSSGSS',4,'NAIGGNC
A;Cross-references: EMBL:X59720; MIPS:YCR080w
A;Cross-reference has been revised in reference $55867
A;Note: this sequence has been revised in reference $55867
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submitted to the EMBL Data Library,
A;Reference number: S53589
A;Accession: S53594
;Molecule type: DNA
;Residues: 1-133,'RFV',136-137,'FDWS',142,'LASLYLTA' <ROD>
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                                                                                            cytosolic protein Ycr77p
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                                                                                                                                                             RESULT 49
A60026
  cell communication-mediating membrane protein pTra2A - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 03-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C;Accession: A60026 R;Kuwabara, P.E.; Okkema, P.G.; Kimble, J. Mol. Biol. Cell 3, 461-473, 1992 Mol. Biol. Cell 3, 461-473, 1992
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C; Genetics:
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Best Local :
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A;Gene: SGD:SRB8
A;Gene: SGD:SRB8
A;Cross-references: SGD:S0000677; MIPS:YCR080w; MIPS:YCR081w
A;Map position: 3R
C;Superfamily: Saccharomyces cerevisiae SRB8 protein
C;Keywords: nucleus; transmembrane protein
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F;277-293/Domain: transmembrane #status predicted <TM2>
F;353-369/Domain: transmembrane #status predicted <TM3>
F;566-582/Domain: transmembrane #status predicted <TM3>
F;724-740/Domain: transmembrane #status predicted <TM6>
F;724-740/Domain: transmembrane #status predicted <TM6>
F;1081-1087/Domain: transmembrane #status predicted <TM7>
F;1081-1081/Domain: transmembrane #status predicted <TM7>
F;1169-1185/Domain: transmembrane #status predicted <TM8>
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R;Huang, O.O.; Lee, K.Y.; Wang, J.H.
FEBS Lett. 378, 48-50, 1996
A;Title: A novel yeast protein showing specific association A;Reference number: S68611; MUID:96140706; PMID:8549800
A;Recession: S68611
A;Molecule type: protein
A;Residues: 701-1011,1013-1056 <HUA>
                                                                                                                              605 LLINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQLVEITEQIKMRILSNDITNLQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               438 DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLD-DNPTEFDWPTYVDQNPLTMHKIIQLIL
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                                                                                                                                                                                                                                                                                                                                   264 LIENHEGRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 YILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI
                                                                                                                                                                                                ---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKL---------
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KTPLSIKIMVAEWYLSHLCSGILSSV---NRTVLLKIFKIFC 703
                                                                                                                                                                                                                                                         LAKNFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLQDSNDKFVHVQ 604
                                                                                                                                                                                                                                                                                                                                                                                                WSIHPSRQFDHYESN-----QLVAKLLLL-----RINSTDEDLHEFQIEDAIWSLVFQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLLHPS--FSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNL--IAIVRCFWFTVESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HQYLSLLQDRYFPIASVM-----RTLDKDN-----FSLTPDLIHDLLGHVP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 326
                                                         -----EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKPLLFEIVSNADTNONSDMKKKLELISYRNESLKNNSSIR-----NVIMSASNAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YYIVSSSKSMINDENYIINDIKKNNKIKLNILKILSSLILKIFQEQSLEVFIFPTSNWEI
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98; Conservative
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C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C./Accession: C81321
R.Parkhill, J. Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin, C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVllet, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
A.Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hythieterence number: A81250; MID:20150912; PMID:10868204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;Status: preliminary
;Molecule type: DNA
;Mosidues: 1-699 «PAR»
;Cross-references: GB:ALi39077; GB:ALi11168; NID:g6968444; PIDN:CAB73415.1; PID:g696859
;Experimental source: serotype O2, strain NCTC 11168
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C,Superfamily: Thermotoga maritima P-type cation-transporting ATPase, ATPase nucleotide-
F,8-37/Domain: heavy-metal-associated homology <HMA>
F,8-37/Domain: ATPase nucleotide-binding domain homology <ATN>
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                                                                                                                                                                                                                                                                     19;
A,Status: preliminary
A,Mocaule types: mRNA
A,Rocaule types: mRNA
A,Rocaiduces: 1.1475 < KUWA
A,Rocaiduces: 1.1475 < KUWA
A,Crosa references: GB:S42187; NID:9253436; PIDN:AAB22845.1; PID:9253437
A,Note: sequence extracted from NCBI backbone (NCBIN:110873, NCBIP:110874)
C,Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 5.0%; Score 94.5; DB 2; Length 699; Best Local Similarity 22.5%; Pred. No. 12; Matches 76; Conservative 54; Mismatches 101; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                -----VQALPSKKORIQTLQSNLIAIV----- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 EKPDYPNVVNQTCDKIFHDLNSTGIEFFDGSRSFSSTKSQFDTMQTEIVLLTPEMLLSAM 378
                                                                                                                                                                                                                                                                                                                                                                                                                                          49 LOKENKEKQALARHKCISILEFFKNLLFVH--LLSLSKNQREGCSTDMAVVSTPFFNRNL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 WYRLLSSRFSLWKSYCPRFFLDYLEAFG------LLSDFLDHQAVIKFFEL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 --RLRNS------MIBAIGENDERPYVKSNYGPSLIKSWADH-----MFDL 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 ETHFSYYPVSGF------VAPHQY-----LSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    213 -----PSKSFTNSTKDALFQKIKLWLLSIEPRQKTCAASIHSCDTPLDSEHYFNICTD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 MRTLDK-------DNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 -----RCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDN-----VRVLPLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 QHSDFVNGFESIW-TIEKAEELIHEFRLAL-----KEETEKFKENRMSKMIRVTSRV 429
                                                                                                                                                                                                  Query Match 5.0%; Score 95; DB 2; Length 1475;
Best Local Similarity 16.7%; Pred. No. 29;
Matches 75; Conservative 65; Mismatches 120; Indels 188; Gaps
                                                                                                                                                                                                                                                                                                                           1 VHYCERTLDPKYILKIALKIRQS------LSLFFQNSQSLQRAYSTPYSYRII 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          430 LDNTVTTKLQSFSEKQTIHFVVNVHSLI 457
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Q27712 panulirus a Q927g7 chlamydia p Q928u6 chlamydia p Q09812 schizosacch P52362 human herpe	P41001 plasmodium P25648 saccharomyc P34709 caenorhabdi P47342 mycoplasma P47311 mycoplasma	P13783 kluyveromyc P56784 arabidopsis P48190 zea mays (m P04114 homo sapien Q57761 methanococc	measles vi measles vi buchnera a	P34/90 saccharomyc Q03660 saccharomyc P31352 marburg vir	P15736 simian 11 r P35911 galdieria s P46578 caenorhabdi	Q14517 nomo sapien P09975 marchantia Q12496 saccharomyc P58402 escherichia	P30855 escherichia Q12774 homo sapien	F55105 Hellochacte P53137 saccharomyc Q60260 methanococc Q13619 homo sapien	P40309 saccharomyc P18458 berne virus Q92448 rattus norv	V8zari yersinia pe P12175 oryza sativ Ogomno camovlobact		P30195 stapnylococ Q02773 saccharomyc P70705 rattus norv	P40016 saccharomyc P28040 schizosacch			P07236 saccharomyc Q97p44 streptococc	P38818 saccharomyc	P57528 buchnera ap	Q01500 p genome po O67305 aquifex aeo	P49022 lactococcus P18544 saccharomyc	escherichi	P48055 oryctolagus		P18588 rattus norv P95979 sulfolobus	Q10201 schizosacch O14077 schizosacch
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5.1.3 Compugen Ltd.	; Search time 25 Seconds (without alignments) 600.577 Million cell updates/sec	E.		ers: 112892		1		cted by chance to have a of the result being printed, score distribution.		Description	m αo ·	P4334 pseudomonas P70080 gallus gall P17752 homo sapien	P11982 phasianidae P19810 rattus norv	F1/552 Musculu P1/290 oryctolagus O42091 anguilla an	P24529 mus musculu Q92142 xenopus lae			017446 schistosma				P90986 caenobacter P90986 caenorhabdi		F35262 Malburg VII Q10144 schizosacch P36161 saccharomyc	
GenCore version Copyright (c) 1993 - 2003	<pre>protein - protein search, using sw model i on:</pre>	Title: US-09-438-185A-1047 Perfect score: 1889 Sequence: 1 VHYCERTLDPKYILKIALKL	table: BLOSUM62 Gapop 10.0 , Gapext 0.5	Searched: 11289/ 8648, 414/03/8 residues Total number of hits satisfying chosen parameters	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 150 summaries	Database : SwissProt_40:*	Pred. No. is the number of results predicted by chance to score greater than or equal to the score of the result by and is derived by analysis of the total score distributi	SUMMARIES	No. Score Match Length DB ID	1886 99.8 362 1 256.5 13.6 289 1	235.5 12.5 262 1 231 12.2 445 1 230.5 12.2 444 1	6 229.5 12.1 491 1 TY3H_PHASP 7 227.5 12.0 444 1 TR5H_RAT	225.5 11.9 444 1 225.5 11.9 488 1	225.5 11.9 498 1 223.5 11.8 481 1	223 11.8 498 221.5 11.7 490 231 11.7 490	220 11.6 528 1	216.5 11.5 465 1	213.5 11.3 452 212.5 11.2 453	201 10.6 313 1	194 10.3 452 1	178.5 9.4 524	106.5 5.6 1501 1	104:5 5:5 2531 1 102 5:4 563 1 100.5 5:3 1157 1	100.5 5.3 2212 1 RRE 98.5 5.2 1024 1 YO7

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STRALN=CWL029;

MEDLINE=99206606; PubMed=10192388;

MEDLINE=99206606; PubMed=10192388;

Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,

Colinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

Nat. Genet. 21:385-389(1999).
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STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAINEEL TOR NIG61 / Serotype O1;
STRAINEEL TOR NIG661 / Serotype O1;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 SFDRFFALLADKKFPVATFLRRREEFDYLQEPDFFHEVYGHCAMLTHPDFAAFTHVYGQL 168
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25.6%; Pred. No. 3.39—13;
tive 56; Mismatches 108; Indels 25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001273; Aaa hydroxylase.
Pfam; PR00151; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE
TIGRFAMs; TIGR01267; Phedhydrox mono; 1.
PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron; Complete proteome.
                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 149 IRON (POTENTIAL).
289 AA; 33445 MW; 2D68B31C6E31D521 CRC64;
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                                                                                                                                                    289 AA
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Best Local Similarity 25.61
Matches 65; Conservative
                                                                                                                                                 STANDARD;
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VCA0828; -
                                                                                                                                                                                                                                                                                                                                      monooxygenase).
PHHA OR VCA0828.
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361 CQ 362
                                                                                                                                                 VIBCH
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STRAIN=ATC 15692 / PAO1;
MEDIANS=ATC 15692 / PAO1;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Sencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Composter M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an Opportunistic pathogen.",
Nature 406:959-964(2000).
                                                            -!- COFACTOR: Binds if ferrous ion.
-!- COFACTOR: Binds if ferrous ion.
-!- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-!- SUBUNIT: MONOMER.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACI
285 LGHAFIDNV-RVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSK----LEWM-LD 338
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SEQUENCE FROM N.A.

MEDLINE=9415131: PubMed=8108417;

Zhao G., Xia T., Song J., Roy R.A.;

Zhao G., Xia T., Song J., Roy R.A.;

"Pseudomonas aeruginosa possesses homologues of mammalian

"Phenylalanine hydroxylase and 4 alpha-carbinolamine dehydratase/DCOH
as part of a three-component gene cluster.";

Proc. Natl. Acad. Sci. U.S.A. 91:1366-1370(1994).
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L-tyrosine + dihydrobiopterin + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of chick pineal tryptophan hydroxylase and clircadian oscillation of its mRNA levels.";

Brain Res. Mol. Brain Res. 42:25-20(1996).

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5-

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5-

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5-

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + H(2)O.

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + H(2)O.

1- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + H(2)O.

1- CATALYTIC ACTIVITY: BALDINGS OF MELATONIN IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL MERVOUS SYSTEM AND CATALYZES THE FIRST STEP OF THE SYNTHESIS OF MELATONIN IN THE FINEAL GLAND.

1- SUBUNIT: MULTIMER OF IDENTICAL SUBUNITS (BY SIMILARITY).

1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
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METAL
CONFLICT
SEQUENCE
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-White leghorn; TISSUE-Pineal gland; MEDLINE-97072811; PubMed-8915576; Florez J.C., Seidenman K.J., Barrett R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tryptophan 5-monooxygenase (EC 1.14.16.4) (Tryptophan 5-hydroxylase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLTNPWFAEFTHTYGKLGLKA----
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       U26428; AAC60036.1;
P04176; 1PHZ.
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135
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IRON (BY SIMILARITY).
F -> L (IN REF. 1).
MW; A5665839C5961A45 CRC64;
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Pred. No. 1.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Barrett R.K., Sangoram A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 103; Indels
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P17752; Q16736; O95188; O1-AUG-1990 (Rel. 15, Create 16-OCT-2001 (Rel. 40, Last s. 15-JUN-2002 (Rel. 41, Last at Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptophan 5-monooxygenase (Fight of Tryptopha
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METAL
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PROSITE; I
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InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                       Tipper J.P., Citron B.A., Ribeiro P., Kauf "Cloning and expression of rabbit and huma hydroxylase CDNA in Escherichia coli.", Arch. Biochem. Biophys. 315:445-453(1994).
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
TISSUE=Carcinoma;
MEDLINE=90332431; PubMed=2377472;
Boulalard S., Darmon M.C., Ganem Y., Launay J.M., Mallet J.
"Complete coding sequence of human tryptophan hydroxylase."
Nucleic Acids Res. 18:4257-4257(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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    Neurochem. 71:1769-1772(1998).
    -I- CARIALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine hydroxy-L-tryptophan + dihydropteridine + H(2)0.

                                                                                     SEQUENCE OF 388-444 FROM N.A. (ISOFORM MEDLINE=98421834; PubMed=9751214; Wang G.A., Coon S.L., Kaufman S.; "Alternative splicing at the 3'-cDNA o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                               hydroxylase.";
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                    WEDLINE=95077422; PubMed=7986090;
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larity 28.4%;
Conservative 4
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BIOPTERIN_HYDROXYL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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annotation update)
(EC 1.14.16.4) (Tr
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IRON
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Pred. No. 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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(BY SIMILARITY).
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                                                                                             of human
                                                                                                                                                                                                                                                       human
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human brain
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COFACTOR: FERROUS ION.

219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278

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12.1%;
29.1%;
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Best Local Similarity
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P11982,
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                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                 EMBL, X52836; CAA37018.1; -. SWRL; L29306; AAA67050.1; -.
                                                                                                                                                         -!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 WGTVFRELNKLYPTHACR---EYLKNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLNEDVLQVSVFALLLFLPSLHGECHPDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96; Indels 27; Gaps
            -i- PATHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL MERVOUS SYSTEM AND CATALYZES THE FIRST STEP OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.
-i- SUBDNIT: MULTIMER OF IDENTICAL SUBUNITS.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: ISOFORM 2 SEEMS TO BE LESS WIDELY EXPRESSED THAN ISOFORM 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Phosphorylation; Alternative splicing.
MOD_RES 58 58 PHOSPHORYLATION (BY PKA) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2%; Score 230.5; DB 1; Length 444; 27.8%; Pred. No. 6.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS, PRO0372; FVWHYDRXLASE.

PRINTS, TIGROL270; TTP 5 moncox, 1.

PROSITE; PS00367; BIOPERIM HYDROXYL; 1.

Oxidoreductase; Moncoxygenase; Serotonin biosynthesis; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S -> N (IN REF. 2).
Q -> R (IN REF. 2).
A -> G (IN REF. 2).
; 86C398869ABE120A CRC64;
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-> I (IN REF. 1).
P -> NL (IN REF. 1)
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43; Mismatches
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InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; blopterin_H; 1.
Pfam; PF01842; ACT; 1.
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PIR, S10489; S10489.
HSSP; P04177; 1TOH.
Genew; HGNC:12008; TPH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY.
--- PATHWAY: Catecholamine biosynthesis; first step.
--- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydxoyt-L-phenylalanine + dihydropteridine + H(2)O.
-!- COFACTOR: FERROUS ION.
-!- ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUB-Adrenal gland;
TISSUB-Adrenal gland;
TISSUB-Adrenal gland;
MEDIJINE-88089590; PubMed-2447231;
Fauquet M., Grima B., Lamouroux A., Mallet J.;
Forgining of quail tyrosine hydroxylase: amino acid homology with
other hydroxylases discloses functional domains.";
J. Neurochem. 50:142-148(1988).
I- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
NEURONES.
                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH....---QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226 WKEVYSTLKSLYPTHACK---EYLEAFNLLEKFCGYNENNIPQLEEVSRFLKERTGFQLR 282
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae.
NCBI TaxID=9006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 491;
                                                                                      279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                               335 LSSISBLKHALSGHAKVKPFDPKITCKQECLITTFQDVYFVSESFEDAKE 384
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; Pred. No. 8.7e-11;
34; Mismatches 100; Indels
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324 324 IRON (BY SIMILARITY).
329 329 IRON (BY SIMILARITY).
369 369 IRON (BY SIMILARITY).
491 AA, 56066 MW, AFB363220F70C0A0 CRC64;
                                                                                                                                                                                                                                                                                                                 491 AA.
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P09810;

P09810;

Ol-MAR-1989 (Rel. 10, Created)

Ol-OCT-1989 (Rel. 12, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                 MEDLINE=87005247; PubMed=2875901;
Darmon M.C., Grima B., Cash C.D., Maitre M., Mallet J.;
Darmon M.C., Grima B., Cash C.D., Maitre M., Mallet J.;
"Isolation of a rat pineal gland cDNA clone homologous to tyrosine and phenylalanine hydroxylases.";
FEBS Lett. 206:43-46(1986)
-i- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5
-i- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5
-i- COPACTOR: FERROUS 10N.
-i- COPACTOR: FERROUS 10N.
-i- PATHMAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL NERVOUS SYSTEM AND CATALYZES THE FIRST STED OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.
-i- SUBUNIT: MULTIMER OF IDENTICAL SUBUNITS.
-i- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACI HYDROXYLASES FAMILY.
                                                   EMBL; M28000; AAA42262.1; -.
EMBL; X53501; CAA37579.1; -.
EIR; JL0034; WHRTW.
PIR; A24367; A24367.
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91245924; PubMed=1645430; Kim K.S., Wessel T.C., Stone D.M., Carver C.H., Joh T.H., Park D.H.; "Molecular cloning and characterization of cDNA encoding tryptophan hydroxylase from rat central serotonergic neurons."; Brain Res. Mol. Brain Res. 9:277-283(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Pineal gland;
MEDLINE-88244702; PubMedd-3379411;
Darmon M.C., Guibert B., Leviel V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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"Sequence of two mRNAs encoding active
J. Neurochem. 51:312-316(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 167-261 FROM N.A
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t tryptophan hydroxylase.";
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Best Local
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MOD RES 58
METĀL 272
METĀL 277
METĀL 277
METĀL 317
SEQUENCE 444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TR5H_MOUSE
P17532;
01-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                 tryptophan hydroxylase from a mouse mastocytoma cell line."; Genomics 7:88-96(1990)
-i-CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + hydroxy-L-tryptophan + dihydropteridine + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90243261; PubMed=2110547;
Stoll J. Kozak C.A., Goldman D.;
"Characterization and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGRRAMS; TIGRO1270; Trp. 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Serotonin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                     + +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tryptophan 5-monooxygenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1990
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001273, Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231
                                                                                                                                                                                                                         hydroxy-L-tryptophan + dihydropteridine + H(2)0.

COFACTOR: FERROUS ION.

PATHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL MERVOUS SYSTEM AND CATALYZES THE FIRST STEP OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.

SUBUNIT: MULTIMER OF IDENTICAL SUBUNITS.

SIMILARITY: BELONGS TO THE BIOFTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSSISELRHALSGHAKVKPFDPKVACKQECLITSFQDVYFVSESFEDAKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEIG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNVPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 15, Created)
(Rel. 15, Last sec
(Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LASLGASEETVOKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58
272
277
317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12.0%;
27.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update)
annotation update)
(EC 1.14.16.4) (Tryptophan 5-hydroxylase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 227.5; DB 1;
Pred. No. 1.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (BY PKA)
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
; C3CF5245727CC825 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mapping of a dise mastocytoma
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a cell line.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                 0(2)
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collaboration -

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11.9%; Score 225.5; DB 1 ilarity 27.0%; Pred. No. 1.6e-10; Conservative 44; Mismatches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     488 AA.
                                                                                                                                                                                                               HSSP, P04177, 1TOH.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; blopterin H; 1.
Pfam; PF01842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                         EMBL; M17250; AAA31487.1; -. EMBL; L29305; AAA67051.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      444 AA;
                                                                                                                                                                                                      PIR; A32699; A32699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anguilla.
NCBI_TaxID=7936;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TY3H ANGAN
                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
CONFLICT
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SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                               294 QEIG-----LASLGASEETVQKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p17290; Q29523;
01-MUG-1990 (Rel. 15, Created)
01-MUV-1997 (Rel. 35, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Tryptophan 5-monooxygenase (EC 1.14.16.4) (Tryptophan 5-hydroxylase).
                                                                                                                                                                                                                                                                                                          107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                  177 WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 233
                                                                                                                                                                                                                                                                                                                                                              159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;

TISSUE=Brain;

TISSUE=Brain;

Tipper J.P., Citron B.A., Ribeit and human brain tryptophan of rabbit and human brain tryptophan hydroxylase cDNA in Escherichia coli.";

Arch. Biochem. Biochem. Biophys. 315:445-453(1994).

-!- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5 hydroxyl--tryptophan + dihydropteridine + H(2)O.

-!- COFACTOR: FERROUS ION.

-!- COFACTOR: FERROUS ION.

-!- PATHWAY: FHIS IS THE RAIE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROTONIN IN THE CENTRAL NERVOUS SYSTEM AND CATALYZES THE FIRST
                                                                                                                                                                                                                                                                                 97; Indels 27; Gaps
                                                                                                                                                                        PHOSPHORYLATION (BY PKA) (POTENTIAL).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IGC839F22A138BCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87289638; PubMed=3475690; Grentt H.E., Ledley F.D., Reed L.L., Woo S.L.C.; Full-length cDNA for rabbit tryptophan hydroxylase: functional domains and evolution of aromatic amino acid hydroxylases."; Proc. Natl. Acad. Sci. U.S.A. 84:5530-5534(1987).
                                                                                                                                                                                                                                                       DB 1; Length 447;
                                                                                                       PRINTS; PRO03/2; FYMHYDRXLASE.
TIGRRAM; TIGROL270, TTP 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXTL; 1.
Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 LSSISELKHALSGHAKVKPPDPKIACKQECLITSFQDVYFVSESFEDAKE 387
                                                                                                                                                                                                                                                                  .3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              444 AA.
                                                                                                                                                                                                                                                                                43; Mismatches
                                                                                                                                                                                                                                                      12.0%; Score 226.5; 27.4%; Pred. No. 1.3
                                         MGD; MGI:98796; Tph.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                         61 61 PH
275 275 IRC
280 280 IRC
320 320 IRC
447 AA; 51343 MW; :
EMBL, J04758; AAA63401.1;
PIR; A34582; A34582.
HSSP; P04177; 1TOH.
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                             Local Similarity
es 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                             Phosphorylation.
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SEQUENCE
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STEP OF THE SYNTHESIS OF MELATONIN IN THE PINEAL GLAND.
SUBUNIT: MULTIMER OF IDENTICAL SUBUNITS.
SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 PHOSPHORYLATION (BY PKA) (POTENTIAL).
272 IRON (BY SIMILARITY).
317 IRON (BY SIMILARITY).
317 IRON (BY SIMILARITY).
102 M -> LIN REP. 1).
151 L -> S (IN REF. 1).
203 KY -> ND (IN REF. 1).
207 R -> Q (IN REF. 2).
390 T -> K (IN REF. 2).
390 T -> K (IN REF. 1).
390 T -> K (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 WYRLLSSRFSLWKSYCPRFFLDYLBAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLJHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 WGTVFRELNKLYPTHACR---EYLKNLPLLSKYCGYREDNIPQLEDISNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygli; Neopterygli; Teleostei; Anguilliformes; Anguillidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 444;
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TGRRAMs; TIGROLY, TEP_S. monoox; 1.
PROSITE; PS00367; BIOPTERIM HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron; Phosphorylation.
Phosphorylation.
Phosphorylation.
Phosphorylation.
Phosphorylation.
Phosphorylation.
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RESULT
TY3H_MC
AC P2
DT 01
DT 115
DT 15
DT 15
CGN TF
CGN TF
CGN TE
CCC EV
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Best Local S
Matches 65
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MEDILINE-98344760; PubMed=9681435;
BOULARDAG S., Biguet N.F., Vidal B., Veron M., Mallet J.,

Vincent J.D., Dufour S., Vernier P.;

Vincent J.D., Dufour S., Vernier P.;

Vincent J.D., Dufour S., Vernier P.;

Vincent J.D., Dufour S., Vernier P.;

J. Neurochem. 71:460-470(1998)

J. Neurochem. 71:460-470(1998)

J. Neurochem. 71:460-470(1998)

J. Neurochem. 71:460-470(1998)

J. Neurochem. 71:460-470(1998)

J. Neurochem. 71:460-470(1998)

J. Neurochem. 71:460-470(1998)

J. CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,

GATALYTIC ACTIVITY: (BY SIMILARITY)

LENDYMER REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN THE CATALYTIC ACTIVITY (BY SIMILARITY)

LENDYMER REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN THE CATALYTIC ACTIVITY (BY SIMILARITY)
    TYSH_MOUSE STANDARD; PRT; 498 AA.

F24529;
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monoxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase)
TH.
Mus musculus (Mouse).
The musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        MOUSE
  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGRFAMS; TIGRO1269; TYr 3 monoox; 1.
PROSITE; PS00367; BIOPTERIM HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AJ000731; CAA04264.1; -. HSSP; P04177; 1TOH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PATHWAY: Catecholamine biosynthesis; first step.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
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                                                                                                                                                                                                                                                                                                                                                           339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 WYRLLSSRFSLWKSY-CPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEF 217
                                                                                                                                                                                                                                                                           LLSSYGELVHSLSDEPERREFDPEAAAAEPYQDQNYQSVYFVSESFTDAKE
                                                                                                                                                                                                                                                                                                                  LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE
                                                                                                                                                                                                                                                                                                                                                                                               FINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                RPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCVHELLGHVPMLADRTFAQF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WREVYSTLRDLYTTHACS----EHLEAFRLLERHCGYSPNSIPQLEDVSHFLKERTGFQL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ransmitter biosynthesis; Phosphorylation.
S 38 38 PHOSPHORYLATION (BY PKA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 488 AA;
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Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.9%;
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Pred. No. 1.8e-10;
8; Mismatches 99;
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IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
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SEQUENCE
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Submitted (APR-1992) to
-i- FUNCTION: PLAYS AN
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MOD_RES
DOMAIN
METAL
METAL
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EMBL; X53503; CAA37580.1; -.
PIR; JN0068; JN0068
HSSP; P04177; 1TOH.
MGD; MGI:98735; Th.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
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MEDLINE=91248263; PubMed=1674869;
IChikawa S., Sasaoka T., Nagatsu T.;
"Primary structure of mouse tyrosine hydroxylase deduced
                        279
                                                               350
                                                                                                        219
                                                                                                                                                 290
                                                                                                                                                                                           159
                                                                                                                                                                                                                                    233
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PATHWAY: Catecholamine biosynthesis; first step.
SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROXYLASES FAMILY
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                                                               QDIG-----
                                                                                                                                                                                                                                                                                                                  66; Conser
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40
51
331
336
376
376
498 AA;
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40
59
331
376
                                                                                                                                                                                                                                                                                                                                     11.9%;
                                                                                                                                                                                                                                                                                                                                                                                                       55992 MW;
                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                  Score 225.5; DB 1
Pred. No. 1.8e-10;
2; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                          IRON
IRON
IRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
PHOSPHORYLATION
PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                         DB 1;
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
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from

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Biochem. Biophys. Res. Commun. 176:1610-1616(1991)

Bermudez J., Sharp Z.D.; RR-1992) to the EMBL/GenBank/DDBJ databases. : PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC

CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
COFACTOR: FERROUS ION. Ħ

AMINO

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PRINTS; PR00372; FYWHYDRXLASE.
TIGREAMS; TIGR01269; TYr 3 monoox; 1.
TIGREAMS; TIGR01269; TYr 3 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
Catecholamine biosynthesis; Phosphorylation.
Neurotransmitter biosynthesis; Phosphorylation.
Neurotransmitter biosynthesis; Phosphorylation (BY CAMK2) (BY MOD_RES 19 19 PHOSPHORYLATION (BY CAMK2)) (BY (BY

RON (BY SIMILARITY).

RON (BY SIMILARITY).

RON (BY SIMILARITY).

62790179664F6DC6 CRC64; SIMILARITY).
PKA) (BY SIMILARITY). Length 498;

Indels

Gaps

<u>ن</u>

107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF WKEVYATLKGLYATHACR---EHLEAFQLLERYCGYREDSIPQLEDVSHFLKERTGFQLR 289 PVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFS LASLGASDEEIEKLST-----VYWFTVEFGLCKQNGELKAYGAGL 334 349 218 393

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                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                  -i- PATHWAY: THIS IS THE RATE-LIMITING ENZYME IN THE BIOSYNTHESIS OF SEROYOUIN IN THE CENTRAL NERVOUS SYSTEM AND CATALZES THE FIRST STEP OF THE SYNTHESIS OF MELAYONIN IN THE PINEAL GLAND.
-i- SUBLINIT: MULTIMER OF IDENTICAL SUBUNITS (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLARES PAMILY.
                                                                                                                                                                                                                                                                                                  Green C.B., Besharse J.C.;
"Tryptophan hydroxylase expression is regulated by a circadian clock in Xenopus laevis retina."
J. Neurochem. 62:2420-2428(1994).
-!- CATALYTIC ACTIVITY: L-tryptophan + tetrahydropteridine + O(2) = 5-hydroxy-L-tryptophan + dihydroxy-L-tryptophan + dihydroxy-L-tryptophan + copections. PERROUS ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 SQEIG------LASLGASDEAVQKLAT------CYFFTVEFGLCKQEGKLKVYGAG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       211 WGTVFRELNKLYPTHACR---EYLKNLPLLSKHCGYREDNIPQLEDVSRFLRERTGFTIR 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268 PVAGYLSPRDFLAGLAFRVFHCTQYVRH-DSDPLNTPEPDTCHELLGHVPLLAEPSFAQF 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSL-TPDLJHDLLGHVPWLLHPSFSEF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 FINMGRLFTKVIEKVQALPSKKQRIQTLQSNLJAIVRCFWFTVESGLIENHEGRKAYGAV 277
394 LSSYGELLHSLSEEPEVRAFDPDTAAVQPYQDQTYQPVYFVSESFSDAKDKLRNYASRIQ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                               ÎS-JUL-1998 (Rel. 36, Created)
18-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Tryptophan 5-monooxygenase (EC 1.14.16.4) (Tryptophan 5-hydroxylase).
                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        llarity 29:5%; Score 223.5; DB 1; Length 481; Pred. No. 2.5e-10; Conservative 38; Mismatches 90; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Monooxygenase; Serotonin biosynthesis; Iron. METAL 309 309 IRON (BY SIMILARITY). METAL 314 IRON (BY SIMILARITY). METAL 354 354 IRON (BY SIMILARITY). SEQUENCE 481 AA; 55406 MW; 6852C33EFFBDEBAO CRC64;
                                                                       481 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00372; FYWHYDRXLASE.
TIGRPAMs; TIGR01270; Trp 5 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
                                                                                                                                                                     Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                      MEDLINE=94246419; PubMed=8189245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L20679; AAA21306.1; -.
                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 70; Conserv
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                             NCBI_TaxID=8355;
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                                                                    TR5H XENLA
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-i- SUBLINITH HOMOTETRAMER.
-i- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anton X.X., Manaster J.S., Kordower X.X., Markham X.X., Bredesen D.E.; Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
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-!- COFACTOR: FERROUS ION.
-!- ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN THE CATALYTIC ACTIVITY.
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-- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                             20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JWA-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                        371 LLSSISELKHSLSGNAKVKPFD------PMVTCN-QECI--ITSFQELYFVSESFE 417
278 LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLE 334
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MEDLINE-97372896; PubMed-9228951;
Goodwill K.E., Sabatier C., Marks C., Raag R., Fitzpatrick P.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91170235; PubMed=1672315; Haycock D.A.; Haycock J.W., Haycock D.A.; "Tyrosine hydroxylase in rat brain dopaminergic nerve terminals. Multiple-site phosphorylation in vivo and in synaptosomes."; J. Biol. Chem. 266:5650-5657(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-8511249; PubMed=2857492;
Grima B., Lamouroux A., Blanc, F., Faucon Biguet N., Mallet J.;
Gromplete coding sequence of rat tyrosine hydroxylase mRNA.";
Proc. Natl. Acad. Sci. U.S.A. 82:617-621(1985).
                                                                                                                                                                                                                                                                                 498 AA.
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InterPro; IFR001273; Aaa_hydroxylase.
PEam; PF00351; blopterin H; 1.
PRINTS; PR00372; FYWHYDRÄLASE.
TIGREAMS; TIGR01269; Tyr 3 monoox; 1.
PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.
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                                                                                                                                                                                                                                                                                 STANDARD;
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P04177;
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TY3H_RAT
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RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TYSH EN COLOR RESULT TY
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MOD RES 31
MOD RES 31
MOD RES 31
MOD RES 51
MOD SES 51
METAL 336
METAL 336
                                                                                                                                                                 MEDLINE=88274405; PubMed=2899135; Saadat S., Stehle A.D., Lamouroux A., Mallet J., Thoenen H.; Saadat S. Stehle A.D., Lamouroux by the tyrosine hydroxylase similarity to tyrosine hydroxylases from other species."; J. Neurochem. 51:572-578(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Cre. 01-FEB-1996 (Rel. 33, Las 15-JUN-2002 (Rel. 41, Las Tyrosine 3-moncoxygenase
                                           SEQUENCE OF 153-169.
MEDLINE=88183482; PubMed=2895648;
Abate C., Smith J.A., Joh T.H.;
Characterization of the catalytic domain of bovine
                                                                                                                                                                                                                                                                                                                                 "Isolation and nucleotide sequence of a cDNA clone encoding bovine adrenal tyrosine hydroxylase: comparative analysis of tyrosine hydroxylase gene products."

J. Neurosci. Res. 19:440-449(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=88259287; PubMed=2898537;

D'Mello S.R., Weisberg E.P., Stachowiak M.K.,

Kaplan B.B.;
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P17289;
  Biochem. Biophys. Res.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
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65; Conserv
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nonooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
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26.7%;
     Commun. 151:1446-1453(1988)
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-!- FUNCTION:
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SEQUENCE OF 1-27
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                                                                                          INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                           PAAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPECCHELLGHVPMLADRTFAQFS
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                                              -LASLGVSDEEIEKLST-----LYWFTVEFGLCKQNGEVKAYGAGL
                                                                                                                                                                                                                                                                                                                                                         11.7%;
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InterPro; IFAVOLETIN H; 1.

Pfam, PF00351, biopterin H; 1.

PRINTS; PR00372; FYWHYDRXLASE.

TIGRRAMS; TIGR01269; TYF 3 monoox; 1.

TIGRPAMS; TIGR01269; TYF 3 monoox; 1.

PROSITE; PS00367; BIOPTERIN HYDROXYL; FALSE NEG.

Catecholamine biosynthesis; Oxidoreductase; Monc

Catecholamine biosynthesis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M36794; AAA30779.1; -.
EMBL; M36705; AAA30798.1; -.
PIR; A27687; A27687.
PIR; JL0039; JL0039.
HSSP; P04177; 1TOH.
InterPro; IPR001273; Aaa_hydroxylase.
Pfam: PF00351; biopterin H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88163736; PubMed=2894860;
Haavik J., Andersson K.K., Petersson L., Flatmark T.;
"Soluble tyrosine hydroxylase (tyrosine 3-monooxygenase) from bovine
adrenal medulla: large-scale purification and physicochemical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) dihydroxy-L-phenylalanine + dihydropteridine + H(2)O. COFACTOR: FERROUS ION. ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE IN TOTALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: Catecholamine biosynthesis; first step SIMILARITY; BELONGS TO THE BIOPTERIN-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               him. Biophys. Acta 953:142-156(1988).
FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF
                                                                                                    54992 MW;
                                                                                     PHOSPHORYLATION (BY PKA).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
AAMI -> GSLV (IN REF. 2).
P -> K (IN REF. 2).
P -> K (IN REF. 2).
R -> V (IN REF. 2).
R -> V (IN REF. 2).
GHV -> AHG (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> N (IN REF. 2).
K -> R (IN REF. 2).
Score 221.5; DB:
Pred. No. 3.7e-10
                                  DB 1;
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                               Length
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                                  490;
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Mismatches

Indels

31;

Gaps

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281

341

218

334 385 278 us-09-438-185a-1047.rsp

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STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
                                                                                          317 LFSIRHFDEL 326
                                                                                                                                  239 YFVLPSFDAL 248
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                                                                                                                                                                                                                                                                                                                                                                                          OR TYH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Res. 7:331-338(2000).
-!- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-Ltyrosine + dihydrobiopterin + H(2)O.
-!- COFACTOR: Binds 1 ferrous ion (By similarity).
-!- COFACTOR: Binds 1 ferrous ion (By similarity).
-!- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-!- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRANS-MAPF303099;
STRANS-MAPF303099;
MADAINE-APF303099;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watamabe A., Idesawa K., Ishikawa A., Kawatima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 CSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPR------FFLDYLEAFGLLSD 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                199 IHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40; Mismatches 109; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 CRADFTVAQD-----YDYSDEEQAVWRTLCDRQTKLTRKLAHHSYLDGVEKLGLLDR 73
                                                                                                                                                                                                                                                                                                                     Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Poteria; Mesorhizobium.
NCBI_TAXID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRIRPAMS; TIGRO1267; Phe4hydrox mono; 1.
PROSITE; PS00367; BIOPTERIN_HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 221; DB 1; Length 275; 26.0%; Pred. No. 2e-10;
                                                                                                                                                                                ]5-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 140 IRON (POTENTIAL).
275 AA; 31347 MW; BC29D255534BC215 CRC64;
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                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
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Matches 65; Conservative
                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                             nonooxygenase).
PHHA OR MLR4831.
                                                                                                                                                                        15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                          LT 15
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PH4H RHILO
Q98D72;
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P07101; Q15588; Q15589; Q15585;

01-APR-1988 (Rel. 07, Created)

01-UUL-1989 (Rel. 11, Last sequence update)

15-UUN-2002 (Rel. 41, Last annotation update)

Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
259 TVESGLI-ENHEGRKAYGAVLISSPQELGHAFI-DNVRVLPLELDQIIRLPFNTSTPQET 316
                                                                                MEDLINE=88213428; NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 NUMELE 1882 
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MEDLINE-88117543; PubMed=2892893;
le Bourdelles B., Boularand S., Boni C., Horellou P., Dumas S.,
Grima B., Mallet J.;
"Analysis of the S' region of the human tyrosine hydroxylase gene:
combinatorial patterns of exon splicing generate multiple regulated
tyrosine hydroxylase isoforms.";
J. Neurochem. 50:988-991(1988).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Nature 326:707-711(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (TYPES 1 TO 4).
MEDILINE=890003200; PubMed=2902075;
KOBAYASHI K., Kaneda N., Ichinose H., Kishi F., Nakazawa A.,
KUrosawa Y., Fujita K., Nagatsu T.;
"Structure of the human tyrosine hydroxylase gene: alternative splicing from a single gene accounts for generation of four mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-94 FROM N.A. (TYPE 3).
MEDLINE=87298614; PubMed=2881769;
Kaneda N., Kobayashi K., Ichinose H., Kishi F., Nakazawa A.,
Kurosawa Y., Fujita K., Nagatsu T.;
"Isolation of a novel DNA clone for human tyrosine hydroxylass:
"Isolation of a novel cond clone for human a ships allernative RNA splicing produces four kinds of mRNA from a ships
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (TYPE 3).
MEDLINE=87316931; PubMed=2888085;
Kobayashi K., Kaneda N., Ichinose H., Kishi F., Nakazawa A.,
Kurosawa Y., Fujita K., Nagatsu T.;
"Isolation of a full-length cDNA clone encoding human tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grima B., Lamouroux A., Boni C., Julien J.-F., Javoy-Agid F.,
Mallet J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene.";
Biochem. Biophys. Res. Commun. 146:971-975(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hydroxylase type 3.";
Nucleic Acids Res. 15:6733-6733(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (TYPES 1 TO 4).
MEDLINE=87173064; PubMed=2882428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. 103:907-912(1988).
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(W Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
MAIternative splicing; Neurotransmitter biosynthesis; Phosphorylation.
T DOMAIN 85 90 POLY-ALA.

METAL 361 S61 IRON (BY SIMILARITY).

METAL 366 366 IRON (BY SIMILARITY).

METAL 406 406 IRON (BY SIMILARITY).

METAL 406 406 IRON (BY SIMILARITY).

VARSPLIC 34 34 MISSING (IN ISOFORM 4).

VARSPLIC 35 61 MISSING (IN ISOFORM 4).

VARSPLIC 35 61 MISSING (IN ISOFORM 4).
                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00414; CAA68472.1; ALT_SEQ.
EMBL; M17589; AAA61179.1; --
EMBL; M25290; CAA28908.1; --
EMBL; M24791; AAA61173.1; JOINED.
EMBL; M24787; AAA61173.1; JOINED.
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61170.1; --
EMBL; M24789; AAA61167.1; --
EMBL; M24789; MAHUY1.
PIR; A27791; WHHUY1.
PIR; B27791; WHHUY2.
PIR; B27791; WHHUY3.
PIR; B27891; WHHUY3.
PIR; D26825; WHHUY4.
PIR; JE0012; JE0013.
PIR; JE0014; JE0013.
PIR; JE0014; JE0014.
HSSP; P04177; 1704.
HSSP; P04177; 1704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@sisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew; HGNC::
MIM; 191290;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXLASE
                                                                                                        257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PLAYS AN IMPORTANT ROLE IN THE PHYSIOLOGY OF A NEURONBS.

CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + C dihydroxy-L-phenylalanine + dihydropteridine + H(2)O. COFACTOR: FERROUS ION.

ENZYME REGULATION: PHOSPHORYLATION LEADS TO AN INCREASE CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHMAY: Catecholamine biosynthesis; first step.
ALTERNATURE PRODUCTS: 4 ISOFORMS; 1, 2, 3 (SHOWN HERE)
ARE PRODUCED BY ALTERNATIVE SPLICING.
 QFSQDIG----
                        EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG
                                                                                                                                 SSRFSLWKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                   QURPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA
                                                                            SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                        AEEIATWKEVYTTLKGLYATHACGEHLEÄFALLERFSGYREDNIPQLEDVSRFLKERTGF 316
                                                                                                                                                         1 Similarity
65; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGNC:11782; TH.
                                                                                                                                                           Conservative
 -LASLGASDEEIEKLSTLS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AN IMPORTANT ROLE IN THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                    11.6%;
                                                                                                                                                           38;
                                                                                                                                                         Score 220; DB 1; L
Pred. No. 5.3e-10;
B; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
 WFTVEFGLCKONGEVKAYG
                                                                                                                                                                                  Length 528;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                           36;
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                                                   Query Match
Best Local S
Matches 74
                                                                                                        SEQUENCE
                                                                                                                                               METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuron
                                                                                                                                                                    TIGRFAMS; TIGRO1269; Tyr 3 monoox; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
                                                                                                                                                                                                PRINTS; PR00372; FYWHYDRXLASE.
TIGRFAMs; TIGR01269; TYr_3_mor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            276
258 EYRAAFQKLQDEQIFVETRLPQLQEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQ 317
                        128 DYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                         leurotransmitter biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421
                                                   Similarity
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508 AA;

57861 MW; 2D194E0E8495E66F CRC64;

IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).

11.6%; ilarity 28.6%; Conservative 3

37;

Score 219; DB 1; I Pred. No. 6.1e-10; 7; Mismatches 94;

1; Length 508; Indels

54;

Gaps

8 '-

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EMBL; U14395; AAA62877.1; -.
EMBL; X76209; CAA53802.1; -.
PIR; JN0010; JN0010.
HSSp; P04177; 1TOH.
FlyBase; FBgn0005626; ple.
                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo.
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TY3H DROME STANDARD; PRT; 508 AA.

118459;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UU-1998 (Rel. 36, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyro:
(Protein Pale).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neckameyer W.S., Quinn W.G.,
"Isolation and characterization of the gene for Drosophila tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=90166583;
InterPro; IPR001273; Aaa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 RIQ 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 KLE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O. COFACTOR: FERROUS ION. PERROUS ION. PATHWAY: Catecholamine biosynthesis; first step. SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PLAYS AN I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRHF----DELVELTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pubMed=2483109;
Quinn W.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMPORTANT ROLE IN
                                                                                                                                                                                                                                                                        noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Tyrosine 3-hydroxylase) (TH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE PHYSIOLOGY OF ADRENERGIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              + O(2) = 3,4-
                                                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                      outstation
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X-RX CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X-RX CRYSTALLOGRAPHY (2.2 ANGSTROMS).

X MEDLINE=99260738; PubMed=10331871;

X MEDLINE=99260738; PubMed=10331871;

X SALTATSIS I.G., House C.M., Michell B.J., Goodwill K.E.,

X SALTATSIS S.G., Stevens R.C., Cotton R.G., Kemp B.E.;

X STANCTURIAL Baiss of autorequilation of phenylalanine hydroxylase.";

NAT. Struct. Biol. 6:442-446 (1999).

-1-CYTALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =

-1-tyrosine + dihydrobiopterin + H(2)O.

-1-CATALTIC ACTIVITY: N-TERMINAL REGION OF PAH IS THOUGHT TO CONTAIN

ALLOGYTOR: DOMAIN THAT REGILATES THE ACTIVITY OF A CATALYTIC

DOMAIN IN THE C-TERMINAL PORTION OF THE MOLECULE.

-1- PATHWAY: CAtabolism of phenylalanine; first (rate-limiting) step.

-1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID

-1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID

-1- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
                                                                            1: || || :|| || :|| || 328 TRLSTL------YWFTVEFGLCNENGETRALGAGIMSSYGELENAF----- 367
                                              180 IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
                                                                                                                                               240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE 299
214 EYIDGFQLLEKYCNYNSESIPQLQTICEFMHRTSGFRIRPVAGLVSPKDFLASLAFRVFQ 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dahl H.-H.M., Mercer J.F.B.; Isolation and sequence of a cDNA clone which contains the complete coding region of rat phenylalanine hydroxylase. Structural homology with tyrosine hydroxylase, glucocorticoid regulation, and use of alternate polyadenylation sites."; Biol. Chem. 26.141494153(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence comparison of rat liver phenylalanine hydroxylase and its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 208-453 FROM N.A.
MEDLINE-85122617; PubMed-6098294;
Robson K.J.H., Beattie W., James R.J., Cotton R.C.H., Morgan F.J.,
                                                                                                                                                                                                                                                   300 LDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWM-----LDQGLLESIPLYN 349
                                                                                                                                                                                                                                                                                   368 SDLSVKEPFNINDAAVQVYDDVGYQKIYFVTESIESMKRELRNYINTSGKSTIPIYD 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wretborn M., Humble E., Ragnarsson U., Engstrom L., Manino acid sequence at the phosphorylated site of rat liver phosphalanine hydroxylase and phosphorylation of a corresponding synthetic peptide.", Biochem. Blophys. Res. Commun. 93:403-408(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-1987 (Rel. 04, Created)
113-MQT-1987 (Rel. 05, Last sequence update)
15-JUN-2002 (Rel. 11, Last amnotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                453 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=86140234; PubMed=2869038;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 23:5671-5675(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 12-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monooxygenase).
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                                                                                                                                                                                                                                                                                                                                                                                                                             PH4H RAT P04176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hamdan F.F., Ribeiro P.,
"Cloning and characterization of a novel form of tyrosine hydroxylase from the human parasite, Schistosoma mansoni.";
-! CATALWITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PATHWAY: Catecholamine biosynthesis; first step.
-!- SMILMATIY: BELODOGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
                                              318 STQYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIG-----LASLGASD 368
                    180 IASVMRTLDKDNFSLTPDLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
                                                                                                                                                  292 --NVRVLPLE--------LDQIIRLPFNTSTPQETLFSIRHFD--ELVELT 330
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                                                                                                                                                                                                                                                                       422 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma
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                                                                                                                  240 QRIQTLOSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
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Pfan. PP00315, biopterin_H; 1.
TGRRAMS, TIGR01269; Tyr 3 monoox, 1.
PROSITE; PS00367; BJOPTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron; Neurotransmitter biosynthesis.
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0DE47B4A474665CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                     481 DKLETLVHOMNTEILHLTN 499
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MEDLINE=98421787; Pul
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017446;
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DT 21-JUL
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R TIGREAMS; TIGR01268; Phe4hydrox tetr; 1.

R PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.

V Oxidoreductase; Monooxygenase; Phosphorylation;
Phenylalanine catabolism; Iron; 3D-structure.

MOD RES 16 16 PHOSPHORYLATION (BY PK METAL 285 285 IRON.

METAL 290 290 IRON.

METAL 330 330 IRON.

METAL 330 330 IRON.

SEQUENCE 453 AA; 51821 MW; 7667771
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Best Local S
Matches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M12337; AAA41843.1; -.
EMBL; K02599; AAA41794.1; -.
PIR; A00509; WHRTF.
PIR; A14970; A14970.
PIR; A25321; A25321.
PDB; 1PF2; 30-APR-99.
PDB; 2PHM; 30-APR-99.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aasa_hydroxylase.
Pfam; PF00351; biopterin_H; 1.
Pffam; PF00351; ACT; 1.
PRINTS: PR00372; FYWHYDRXLASE.
                                                                                                                                                                                                                                                                                                                                                       PH4H HUMAN STANDARD; PRT; 452 AA. P00439; Q16717; P00439; Q16717; P17011-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH)
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MEDLINE=85199778; PubMed=2986678;
Kwok S.C.M., Ledley F.D., Dilella A.G., Robson K.J.H., Woo
"Nucleotide sequence of a full-length complementary DNA c:
amino acid sequence of human phenylalanine hydroxylase.";
                                                                                                                   TISSUE=Liver;
                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                          monooxygenase).
                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   domo sapiens (Human)
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llarity 28.4%;
Conservative 3:
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Primates;
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MW; 365D9E8A7E498D52 C
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Pred. No. 1.3e-
37; Mismatches
                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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..3e-09;
les 89;
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A clone a
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Lyonnet S., Caillaud C., Rey F., BETTHELOH M., LICHLE T. Munnich A.; Munnich A.; "Molecular genetics of phenylketonuria in Mediterranean mutation associated with partial phenylalanine hydroxyla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REVIEW ON PKU VARIANTS.
MEDLINE=91348681; PubMed=1679029;
Konecki D.S., Lichter-Konecki U.;
Withe phenylketonuria locus: current knowledge about mutations of the phenylalanine hydroxylase gene in variations of the phenylalanine hydroxylase gene in variations.
                                                                                                                                                    MEDILINE-88294030; PubMed=2840952;
Lichter-Konecki U., Konecki D.S., Dilella A.G., Brayton K., Ma.
Hahn T.M., Trefz F.K., Woo S.L.C.;
"Phenylalanine hydroxylase deficiency caused by a single base
substitution in an exon of the human phenylalanine hydroxylase
                                                                                                                                                                                                                                                                       DATABASE OF PKU VARIANTS.

MEDLINE=96174613; Prevost L., Scriver
Hoang L., Byck S., Prevost L., Scriver
"PAH Mutation Analysis Consortium Data
producing and other allelic variation
Nucleic Acids Res. 24:127-131(1996).
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE=93244826; PubMed=1301187;
Eisensmith R.C., Woo S.L.C.;
"Molecular basis of phenylketonuria and related
"Molecular basis of phenylketonus and polymorph:
hyperphenylalaninemias: mutations and polymorph:
phenylalanine hydroxylase gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [8]
REVIEW ON PKU VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91061429; PubMed=2246858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusetti F., Erlandsen H., Flatmark T., Stevens R.C.; "Structure of tetrameric human phenylalanine hydroxylase implications for phenylketonuria.", Biol. Chem. 273:16962-16967(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS)
MEDLINE=98307935; PubMed=9642259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE=99060040; PubMed=9843368; Erlandsen H., Flatmark T., Stevens R.C., Hough E.; Crystallographic analysis of the human phenylalanine hydroxylase catalytic domain with bound catechol inhibitors at 2.0-A resolution biochemistry 37:15638-15646(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Crystal structure of the catalytic domai hydroxylase reveals the structural basis hat. Struct. Biol. 4:995-1000(1997).
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Stevens R.C.;
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Scriver C.R., Nowacki P.M.,
Submitted (SEP-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 24:556-561(1985) [2]
                                                                             VARIANT LYS-280:
MEDLINE=89190664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  populations."
                                                                                                                                                                                                                                           VARIANT PRO-311
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MEDLINE=99060040; PubMed=9843368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heterogeneity of phenylketonuria at the clinical, levels.";
                                                                                                                            liochemistry 27:2881-2885(1988).
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                                                                             PubMed=2564729;
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EMBL/GenBank/DDBJ da
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Scriver C.R.;
ium Database: a database
ium patabase the human PAH
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pasis for phenylketonuria.";
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1.3%; Score 213.5; DB 1; Length 452;
1.8imilarity 26.6%; Pred. No. 1.4e-09;
62; Conservative 44; Mismatches 100; Indels 27; Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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01-AUG-1990 (Rel. 15, Last sequence update)
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MEDLINE=94172999; PubMed=8068076;
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MEDLINE=92380641; PubMed=1355066;
                                                                                                                                                                                                                                   mutation.";
Mol. Biol. Med. 6:245-250(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                      hydroxylase gene.";
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InterPro; IPR002912; ACT.
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Pfam; PF00351; biopterin_H; 1.
Pfam; PF01842; ACT; 1.
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MCDOnald J.D., Charlton C.K.;
"Characterization of mutations at the mouse phenylalanine hydroxylase
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MEDLINE=80220293; PubMed=7387651;

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SEQUENCE
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MEDLINE=85122617; PubMed=6098294;
Robson K.J.H., Beattle W., James
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RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

RA Arlat M., Billault A., Brottier P., Camus J.C., Cunnac S., Demange N.,

RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

RA Gaspin C., Inbaualt P., Whalen M., Wincker P., Levy M.,

RA Siguier P., Thabault P., Whalen M., Wincker P., Levy M.,

RA Weissenbach J., Boucher C.A.,

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

RI Nature 415:497-502(2002).

"I - CATALYTIC ACTUITY: L-phenylalanine + tetrahydrobiopterin + O(2) =

"I - CATALYTIC ACTUITY: L-phenylalanine + tetrahydrobiopterin + O(2) =

"I - COPACTOR: Binds 1 ferrous ion (By similarity).

"I - PATHMAY: Catabolism of phenylalanine; first (rate-limiting) step.

"I - SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID

"C HYDROXYLASES FAMILY.
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Best Local S
Matches 61
                                                            Complete
METAL
                                                                                                                     EMBL, AL646074; CAD17143.1; --
InterPro; IPRO01273; Asa_hydroxylase.
Pfam; PF00351; biopterin H; 1.
TIGRPRAMs; TIGR01267; Phe4hydrox mono;
PROSITE; PS00367; BIOPTERIN HYDROXYL,
Oxidoreductase; Monooxygenase; Phenyle
                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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PHHA OR RSC3355 OR RS02630.
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IS-JUN-2002 (Rel. 41, Last sequence update)
IS-JUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=GMI1000;
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Ralstonia.
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                                                                                                                            Monooxygenase; Phenylalanine catabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LASLGAPDEYIEKLAT----
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29.9%; Pred. No. 1.7e-09;
tive 35; Mismatches 87
MW;
IRON (POTENTIAL).
IRON (POTENTIAL).
; 2EBA9E216476371B
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                                     8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- PATHWAY: Catabolism of phenylalanine; first (rate-limiting) step.
-i- SUBINIT: MONOMER.
-i- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Volner A., Nersissian A.M., Abu-Omar M.M.;
Volner A., Nersissian A.M., Abu-Omar M.M.;
Volner A., Nersissian A.M., Abu-Omar M.M.;
Volner A., Nersissian Chromobacterium violaceum ";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!-CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-!-CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-!- CATALYTIC BINDS 1 COOPER ION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92011593; PubMed=1655752; On1681 A., Lidotta L.J., Benkovic S.J.; Mondallanine L.J., Benkovic S.J.; Mondalanine and expression of Chromobacterium violaceum phenylalanine hydroxylase in Escherichia coli and comparison of amino acid sequence with mammalian arcomatic amino acid hydroxylases."; Biol. Chem. 266:18454-18459(1991).
                                                                                                                                           153 --THFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL 210
                                                                                                                                                                      105 RAIGWQIVAVPGLVPDEVFFEHLANRRFPASWWMRRPDQLDYLQEPDGFHDIFGHVPLLI 164
                                                                                                                                                                                                                                         108 YRLLSSRFSLWKSYCPR-----FFLDYLEAFGLLSDFLDHQAVIKFFELE---- 152
                                                                                                                                                                                                                  211 HPSFSEFF--INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENH 268
                                                                                                                                                                                                                                                                                       269 BGRKAYGAVLISSPQELGHAFIDNV--RVLPLELDQIIRLPFNTSTPQETLFSIRHFDEL 326
                                     Gaps
                                                                                                        50 HRYTAADHATWRTLYDRQEALLPGRACDEFLQGLSTLG-----MSREGVPSFDRLNETLM 104
                                     95; Indels 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 172.
10.6%; Score 201; DB 1; Length 313; 26.2%; Pred. No. 8.6e-09; ive 41; Mismatches 95; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; beta subdivision; Neisseriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 297 AA.
P30957; Q9XC88; Q9R634;
P30957; Q9XC88; Q9R634;
01-7UL-1993 (Rel. 26, Created)
15-7UN-2002 (Rel. 41, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND SEQUENCE OF 1-20 STRAIN=ATCC 12540;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromobacterium violaceum.
                  Local Similarity 26.23
les 64; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   monooxygenase).
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                                                                                                                                                                                                                                                                                                                                                              327 VELT 330
                                                                                                                                                                                                                                                                                                                                                                                                 267 FDAT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=ATCC
                                   Matches
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PH4H DROME STANDARD; PRT; 452 AA.
P17576; 027599; 0277600; 046110;
01-AUG-1990 (Rel. 15, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UND-2002 (Rel. 41, Last annotation update)
Protein henna [Includes: Phenylalanine-4-hydroxylase (EC 1.14.16.1)
(PAH) (Phe-4-monoxygenase); Tryptophan 5-monoxygenase (EC 1.14.16.4)
(TRH) (Tryptophan 5-hydroxylase)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo, and Head; 
BEDINES-2156168; PubMed=1371286; 
Neckameyer W.S., White K., 
"A single locus encodes both phenylalanine hydroxylase and tryptophan 
Hydroxylase activities in Drosophilla."; 
J. Biol. Chem. 267:4199-4206(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         245 LQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQE----LGHAFIDNVRVLPLEL 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 FLDYLEAFGLLSDFL-DHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : | : | : | | | | | | | : | | : | | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 FLEGLERLEVDADRVPDFNKLNEKLMAATGWKIVAVPGLIPDDVFFEHLANRRFPVTWWL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Busecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Sequence and expression of the Drosophila phenylalanine hydroxylase
EMBL; M55915; AAA23115.1; ALT_FRAME.

BIRBI, A40996; A40996.

HSSP; P00439; 4RAH.

InterPro; IRROUA273; Aaa hydroxylase.

Fram; PF00351; biopperin H; 1.

FRINTS, PR00352; FWHYDRXLASE.

TIGRIAM; PF00351; Phe4hydrox mono; 1.

PROSITE; P$00367; BIOPTERIN HYDROXYL; 1.

PROSITE; P$00367; BIOPTERIN HYDROXYL; 1.

ROALdoreductase; Monooxygenase; Phenylalanine catabolism; Copper. METAL

METAL

COPPER (POTENTIAL).

METAL

H3 143 COPPER (POTENTIAL).
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Morales G., Requena J.M., Jimenez-Ruiz A., Lopez M.C., Ugarte M.,
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Ruiz-Vazquez P., Moulard M., Silva F.J.;
"Structure of the phenylalanine hydroxylase gene in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
10.4%; Score 196.5; DB 1; Length 297;
Best Local Similarity 27.4%; Pred. No. 1.8e-08;
Matches 63; Conservative 40; Mismatches 94; Indels 33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 297 AA; 33594 MW; AAA67B6097171FB0 CRC64;
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Hich R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Hich R.A., Sahburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Barndon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pefeiffer B.D.,
RA Barndon R.C., Bascer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Feannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J. Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Bocchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hoetin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hoetin D., Houston K.A., Howland T.J., Wei M.H., Hang Y., Lin X.,
RA Hostin D., Hollshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mcimel B.E. Kodira C.D., Kraft C., Kravit Z.S., Kulp D.L., Lin X.,
RA Hoetin D., Hollshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshian N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Siden-Klamo G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Merkulov G., Siden-Klamo G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palas S., Teretor C. Turner R., Venter E., Wang A.H.,
RA Mang Z.-Y., Wa
MEDLINE=20196006; PubMed=10731132;
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Best Local S
Matches 73
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EMBL; AJ001718; CAB04950.1; -.
EMBL; AJ001719; CAB51601.1; -.
EMBL; AJ001720; CAB51601.1; JOINED.
EMBL; AJ001722; CAB51599.1; -.
EMBL; AJ001722; CAB51597.1; -.
EMBL; AJ001723; CAB51597.1; -.
EMBL; AJ001723; CAB51597.1; -.
EMBL; AJ001723; CAB51597.1; -.
EMBL; AJ001723; CAB51597.1; -.
EMBL; AJ001723; CAB51597.1; -.
F1yBase; FBgn0001208; Hn.
F1yBase; FBgn0001208; Hn.
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EMBL; M32802; AAA65913.1; -.
EMBL; X98116; CAA66797.1; -.
EMBL; X98116; CAA66798.1; -.
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InterPro; IPR002911; ACT.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; P900351; biopterin_H; 1.
Pfam; P900442; ACT; 1.
Pfam; P900451; PYWHYDRXLASE.
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                                          279 ISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD
                                                                                                     303
                                                                                                                                                                                                                                                                                                                               186
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                                                                                                 QEIG-----LASLGAPDDYIEKLST-----IFWFTVEYGVCRQEGELKAYGAGL
                                                                                                                                                                                                                                                                                                                            WGIIFRNLTKLYKTHACR---EYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR
                                                                                                                                                         INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                                                                                                                                        PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                PVAGLLSSRDFLAGLAFRVFHSTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPAFAQFS
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160 MW;
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OPTERIN_HYDROXYL; 1.
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FK -> LR (IN REF. 2).

VHIESRSEL -> CILSRILAPWF (IN REF. 2).

PGYEFFVEADGKSGALGKAIEDVKEQCSYFNIISRDYKDNA
-> SSCYWRMENRSLGKSHRGCEGAMLATLTSSCRELQGV
MP (IN REF. 2).
R -> A (IN REF. 2).
A -> G (IN REF. 2).
5 -> C (IN REF. 2).
5 -> C (IN REF. 2).
C -> Q (IN REF. 2).
C -> C (IN REF. 2).
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Pred. No. 4.9e-08;
9; Mismatches 111;
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302

338 346 278 242

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84 WTVVAVPGLVPDDVFFDHLANRRFPAGQFIRKPHELDYLQEPDIFHDVFGHVPMLTDPVF 143
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Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
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357 357 IRON (BY SIMILARITY).
397 397 IRON (BY SIMILARITY).
524 AA, 59593 MW, 328106950A629802 CRC64;
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                                                                                                                                                                                                                                                                                                                                                             249 FGAIYERLASVSDIGVAEIVP 269
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Matches 77; Conservative 4
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SEQUENCE FROM N.A.

SEQUENCE PROM N.A.

STRAIN=ATCC 19089 / CB15;

MEDLINE-21173698; PubMed=11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Risen J., Heidelberg J.F., Alley W.R.K., Ohta N., Maddock J.R.,

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A. Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

A. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulboacter crescentus";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-! CATAVITIC ACTIVITY. L-phenylalanine + tetrahydrobiopterin + O(2) =

-! CATAVISINE Sinds I ferous ion (By similarity).

-! CATABOXISE SELONGS TO THE BIOPTERIN-DEPENDENT AROWATIC AMINO ACID

HYDROXYLASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensegibs-sib.ch).
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347 LSSYGELEYCLTDKPQLKDFE-----PEVTGV---TKYPITQFQPLYYVADSFETAKE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 WKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFE----LETHFSYYP------ 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 ----VSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSF 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caulobacter crescentus.
Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00351; biopterin_H; 1.
PRINTS; RR00372; PYWHYDRXLASE.
TIGRPAMs; TIGRO1267; PH64Mydrx mono; 1.
PROSITE; PS00367; BIOPTERIN HYDROXYL; 1.
Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 10.0%; Score 189.5; DB 1; Length 294; I Similarity 24.1%; Pred. No. 6.4e-08; 63; Conservative 43; Mismatches 108; Indels 47;
                                                                                                                                                                                                                                                                                                                                   15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Phenylalanine-4-hydroxylase (EC 1.14.16.1) (PAH) (Phe-4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 134 IRON (POTENTIAL).
294 AA; 32761 MW; A623276FD0506720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON (POTENTIAL).
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                                                                                                                                                                                                                                                                                    294 AA.
                                                      339 QGL--LESIP----LYNQEKYLSGFEVL 360
                                                                                                                    397 KTIKFANSIPRPFGVRYN--AYTQSVEVL 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001273; Aaa_hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE005836; AAK23591.1; -.
HSSP; P04176; 1PHZ.
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                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monooxygenase).
PHHA OR CC1612.
                                                                                                                                                                                                                                                                             PH4H CAUCR
Q9A7V7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine 3-monooxygenase (EC 1.14.16.2) (Tyrosine 3-hydroxylase) (TH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-tyrosine + tetrahydropteridine + O(2) = 3,4-dihydroxy-L-phenylalanine + dihydropteridine + H(2)O.
-!- COFACTOR: FERROUS ION.
-!- PATHWAY: Catecholamine biosynthesis; first step.
-!- PATHWAY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID HYDROXYLASES FAMILY.
                                                  144 ADY--------MQAYGEGGRRALGL-GRLANLARLYWYTVEFGLMNTPAGLRIY 188
                                                                                                                                                        275 GAVLISSPQELGHAFID-NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELT--- 330
                                                                                                                                                                                                               9.4%; Score 178.5; DB 1; Length 524;
14.3%; Pred. No. 9.8e-07;
.ve 41; Mismatches 114; Indels 85; Gaps
215 SEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
Sukaryote, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQA-LARH-----KCISILE
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InterPro; IRRO01273; Asa hydroxylase.
Pfan; PF00351; biopterin H; 1.
PRINTS; PR00372; FYWHYDRXLASE.
PROSTE; PS00367; BIOPTERIN HYDROXYL; 1.
Catecholamine biosynthesis; Oxidoreductase; Monooxygenase; Iron;
Neurotransmitter biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smye R.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-:- CATALYTIC ACTIVITY: L-phenylalanine + tetrahydrobiopterin + O(2) =
-:- COFACTOR: FERROUS ION (BY SIMILARITY).
-:- COFACTOR: CATABOLISM of phenylalanine; first (rate-limiting) step.
-:- SIMILARITY: BELONGS TO THE BIOPTERIN-DEPENDENT AROMATIC AMINO ACID
HYDROXYLASES FAMILY.
   TIGRFAMS; TIGRO1268; Phe4hydrox tetr; 1.

PROSITE; PS00367; BIOPTERIN HYDROXYI; 1.

Hypothetical protein; Oxidoreductase; Monooxygenase; Phenylalanine catabolism; Iron.

METAL 28 28 IRON (BY SIMILARITY).

METAL 290 290 IRON (BY SIMILARITY).

METAL 330 330 IRON (BY SIMILARITY).

SEQUENCE 457 AA; 52129 MW; 68365836DFEC8D4F CRC6
                                                                                                                                                                                                                                                                        EMBL; Z66497; CAA91286.1; -.
HSSP; P04176; IPHZ.
Wormbep; K08F8.4; CE21050.
InterPro; IPR002912; ACT.
InterPro; IPR001273; Aaa hydroxylase.
Pfam; PF00351; biopterin H; 1.
Pfam; PF001842; ACT; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PH4H CAEEL STANDARD; PRT; 457 AA PO925; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 40, Last annotation update 16-OCT-2001 (Rel. 40, Last annotation update Putative phenylalanine-4-hydroxylase (EC 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAY 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEEEHATWKAVYEKLGDLHLSHTCAVYRQNLKILQEEKVLTADRIPQIRDVNKFLQKKTG
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                                                                                                                                                                                                                                                      PR00372;
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                                                                                                                                                                                                                                                      FYWHYDRXLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
       IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
; 68365836DFEC8D4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            n update)
(EC 1.14.16.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PAH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366
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EMBL; J03131; AAA28718.1; -.
EMBL; J03131; AAA28729.1; -.
EMBL; M20230; AAA28721.1; -.
EMBL; M20231; AAA28720.1; -.
PIR; A29813; A29813.
PIR; B29813; B29813.
PIR; B29813; B29813.
PIR; B29813; B29813.

FBgn0002938; ninaC. ; IPR000719; Euk_pkinase

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-88151067; PUNCTION, AND ALTERNATIVE SPLICING.
MEDLINE-88151067; PubMed=2449973;
Montell C., Rubin G.M.;
"The Drosophila ninaC locus encodes two photoreceptor cell specific proteins with domains homologous to protein kinases and the myosin heavy chain head.";
Cell 52:757-772(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NINC DROME STANDARD; PRT; 1501 AA.

P10676; P10677;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Neither inactivation nor afterpotential protein C (EC 2.7.1.37).
NINAC.
                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreemer (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                  -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228
                                                                                                                                                                                                                                                                                                                                                        ACTIVITIES:

CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

SUBCELULLAR LOCATION: CYTOSKELETON.

ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and short form; are produced by alternative splicing.

SHAULARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE SER/THR FAMILY OF PROTEIN KIRASES.
                                                                                                                                                                                                                                                                                                                                  SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS SUPERFAMILY.
                                                                                                                                                                                                                                                                                                              SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: REQUIRED FOR PHOTORECEPTOR CELL FUNCTION. THE NINAC PROTEINS JOIN PUTATIVE SERINE/THREONINE-PROTEIN KINASE AND MYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QDVSDFLKDCTGYTIRPVAGLLSSRDFLAGLAFRVFHSTQYIRHHSAPKYTPEPDICHEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGHVPWLLHPSFSEFFINMGRLF----TKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAESFASAKNKLKSWAATINRPFQIRYNAYTQRVEILDKV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIEFGICQQDGEKKAYGAGLLSSFGELQYALSDKPEVVDFDPAVCCVTKYPITEYQPKYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE--LDQIIRLPFNTSTPQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LGHVPLFADVEFAQFSQEIGLASLGAPDDVIEKLATL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 25.5 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---FSIRH--FDELVELTSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 175.5;
Pred. No. 1.4e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                  THE MYOSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----YWF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        287
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Schizosaccharomyces pombe (Fission yeast).
    (L protein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                               SMART; SMOULD; 149;
PROSITE; PSS0096; 109;
PROSITE; PSS00109; PROTEIN KINASE ATP; FALSE NEG.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
Cytoskeleton; Actin-binding; ATP-binding; Myosin; Transferase; Vision; Serine/threonine-protein kinase; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKS
IFQVLLHYRAARF -> GKKTQVDRLREYDEEHIDISETPS
EAEEMFLEARMDEALAAVRIAKIEQASAEE (IN SHORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1083 FRGFRDPVRLPPLVNEKSGQLNENTADFIRPFAKKWREKSIFQVLLHYRAARFQDFVNLS 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 5.6%; Score 106.5; DB 1; Length 1501;
Best Local Similarity 22.4%; Pred. No. 1.8;
Matches 85; Conservative 58; Mismatches 130; Indels 107; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       943 SFHSDVVQQQMKALGVLDTVIARQ---KGFS----SRLPFDEFLRRYQFLAFDFDE--P 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 ALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI-----ENHEGRKAYGAVLISSPQEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 GHAFIDNVRVLPLELDQIIRL-----PFNTSTPQETLFSI-----RHFDELVELT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   839 PEMIETFRSSLDESIMLMFTWQLTKAGNLTMP---FEAVQHKDESERKSYALNTLSAGCI 895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 SILEFFKULLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSS-RFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 FF----LDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 IASVMRTLDKDNFSLTPDLIHDL-----LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQ 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 PKYILKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK----CI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEE-1994 (Rel. 28, Last sequence update)
1-FEE-1994 (Rel. 28, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (Large structural protein)
                                                                                                                                                                                                                                                                                                                                                                                       253 253 K -> Q (IN REF. 1; AAA28720/AAA28721).
1089 1089 P -> R (IN REF. 1; AAA28721).
1501 AA; 174269 MW; D167EABC82A3933A CRC64;
                                                                                                                                                                                                                                                   NON ALPHA-HELICAL, C-TERMINAL DOMAIN.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       896 SOVN-----NLRTLAANFRFTCLTLLKMLSQ---NANLGVHFVRCIRADL--EYKPR
                                                                                                                                                                                                                                                                                                          ACTIN-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                             MISSING (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2331 AA.
                                                                                                                                                                                                                                                                                                BY SIMILARITY
InterPro; IPR000048; IQ_region.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR001509; myosin head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF000619; pkinase; 1.
Probom; PD000001; Euk pkinase; 1.
Probom; PD000001; Euk pkinase; 1.
SwART; SM00015; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1143 ------0QVHIYNO 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            331 SKLEWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               1501
253
1089
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P35262;
                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                   NP BIND
BINDING
                                                                                                                                                                                                                                         DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                              524 -LGQADFSL--NQILDFAEKLEYLA-PSYRNFSFSLKEKELNIGRTFGK-----LPYR 572
Marburg virus (strain Popp).
Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
Marburg-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 FCVFKFIVAKNHYHSQGSWYKTTMDLHLTPYLRQHIVSNSFPSQAEIYQHLWEWYFVEHE 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 TLDXDNFSLTPDLIHDLLGHVPWLLHPSFSEFF-----INMGRLFTKVIEKVQALPSK 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 KTIIQGKLTPQQYCELF----SLQKHWGHPVLYIDVALDKVKKHAQSVKILKPKVMFET 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 FKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 EAFGL----LSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMR 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: PRIMARILY WITH THE N-TERMINAL HALF OF THE L PROTEINS OF RHABDOVIRUSES AND PARAMYXOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 KYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEF 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       471 PLFSTKIISDLSIFIKDRATAVNQECWDSVFDRSVLGYNPPVRFQSKRVPEQF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 2331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
5.5%; Score 104.5; DB 1; Length
Best Local Similarity 23.4; Pred. No. 44.4;
Matches 59; Conservatio. 42; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; $32776; $32776.
PIR; $44054; $44054.
InterPro; 1PR001016; Viral RNA pol L.
Pfam; PP00946; Paramyx RNA pol; 1.
Pfam; PPNA-direcTed RNA polymerase.
Transferase: RNA-direcTed RNA polymerase.
Transferase: A1, 26665 MW; 7PD1061D0EEF9B8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative transcriptional regulatory protein C3H8.08c. SPAC3H8.08C.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      563 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X68494; CAA48508.1; -. EMBL; Z29337; CAA82542.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                  NCBI_TaxID=33728;
                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA (N)
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010144;
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YASB SCHPO
AC 010144
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DT 15-JUN
DE PUTALIO
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                                                                                                                                                                                                                                                                                                                                                            RA Wood V. Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Gentles S., Wolfie S., Jones M., Leather S., McDonald S., McLean J.,
RA Gentles S., Wolfie S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Goliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Gliver K., O'Neil S., Pearson D., Ouail M.A., Rabbinowitsch E.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkaert G., Aert R., Robben J., Grymonprez B.,
RA Wodward J., Volkaert G., Aert R., Robben J., Grymonprez B.,
RA Gable C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gable C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gable C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S. J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Chritti L., Lowe T., McCombie W.R., Pallsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
C. C. CLUSTER DOMAIN.
C. C. CLUSTER DOMAIN.
                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 80
                                                                                                                                                                                                                                                                                                                                                    EMBL; Z69086; CAA93165.1; -.
HSSP; P12351; 1PYC.
InterPro; IPR001138; Fungi_TrN.
Pfam; PF00172; Zn_clus; 1.
SMART; SM00066; GAL4; 1.
PROSITE; PS00463; ZN2_CY6_FUNGAL_1; 1.
PROSITE; PS00468; ZN2_CYY_FUNGAL_2; 1.
Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.
DNA BIND 19 45 ZN(2)-CYS(6), FUNGAL-TYPE.
DNA BIND 19 45 ZN(2)-CYS(6), FUNGAL-TYPE.
SEQUENCE 563 AA; 64690 MM; C32CDBEA4F84D358 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21848401; Wood V., Gwilliam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN=972;
                                                                                      240
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  298
                                         121
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                                         YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI
                                                                                      DKEIIQMLLLRAYATKFRTRIRGVNTDLCRSIHVSTLVTPLF--QVTEKIGKNTSDLWFA
                                                                                                                             ILEFFKNLLFVHLLSLSKNQREGCSTDM-----AVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                            TLLPIIAATIQLSDLPDVILNFYNSAGI-----TPLESSRLINLKLNEISEQEYKHLCLP 239
                                                                                                                                                                                                                         TLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCIS 66
                                                                                                                                                                                                                                                                     80;
                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                                     5.4%;
-ECVLKY---RPPFIQHDTYGRLKP
                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                          Score 102; DB 1;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                     142;
                                                                                                                                                                                                                                                                                                               Length 563;
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                                         180
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RESULT 31
N133_YEAST
ID N133_YE
AC P36161;
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     Query Match
Best Local
                                                                                                                       EMBL; X80066; CAA56372.1; -.
EMBL; Z27116; CAA81633.1; -.
EMBL; Z28307; CAA82161.1; -.
PIR; S38160; S38160.
PIR; S39123; S39123.
SGD; S0001790; NUP133.
                                                                         TRANSMEM
SIMILAR
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94262327; PubMed=8203164; Garcia-Cantalejo J., Baladron V., Esteban P.F., Santos M.A., Bou Garcia-Cantalejo J., Baladron V., Esteban P.F., Jimenez A., del Re Remacha M.A., Revuelta J.L., Ballesta J.P.G., Jimenez A., del Re "The complete sequence of an 18,002 bp segment of Saccharomyces cerevisiae chromosome XI contains the HBS1, MRP-L20 and PRP16 ge and six new open reading frames."

Yeast 10:231-245(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=JUXUR;
MEDLINE=95112817; PubMed=7813444;
MEDLINE=95112817; PubMed=7813444;
Doye V. Wepf R., Hurt E.C.;
"A novel nuclear pore protein Nup133p with distinct roles in poly(A)+
RNA transport and nuclear pore distribution.";
RNBO J. 13:6062-6075(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Nucleoporin NUP133 (Nuclear pore protein NUP133).
NUP133 OR YKR082W OR YKR402.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278
                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear pore complex.
                                                                                                                                                                                                                                                                                                                                                                                                     DISTRIBUTION.
                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: INVOLVED IN POLY(A) + RNA TRANSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LILVDIEAKFYDPSNEDIQFRYIFLKMVFWTARVNLYQCFITLDSGILEDEE-----T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---LRCFFNDDISYN---FHLLLGR---LLDCGVSIYKSVHSLTVSKFIDKLESYESQLS
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                                               protein; Transport; Transmembrane.

4 217 233 POTENTIAL.

98 420 TO NUPL20 (AA 434-763)

E 1157 AA; 133319 MW; CGBDBB7D709C5C08 C
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   5.3%;
Score 100.5; DB Pred. No. 3.7;
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                   DB 1;
                     Length 1157;
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                                                       CRC64;
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Similarity

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Matches
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 14;
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                                                                                                                                                                                                                                                   926
                                                 826 ---STIVSLYET-FFNE-----FPKEFSF-----TLFEYLIKHKKLNDLIFRFPQQH 868
                                                                                                                                                        143 QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
                                                                                                                                                                                     DVLIQFFQESA-----PKYGHVAWIQ--QILDGSYADAMNTLKNITVDDSKKGESL---- 917
                                                                                                                                                                                                                                                                                  263 GLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRH 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ebola virus (strain Zaire Mayinga) (Ebo).
Viruses; SRNA negative-strand viruses; Mononegavirales; Filoviridae;
Ebola-like viruses.
 83; Gaps
                                                                                           EGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFL-----DH 142
                                                                                                                                                                                                                                                                                                                957 E--KNISNKLKKGEVQICKRFKNGS------IREVFNILVEELKSTTVVN 998
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                               30 NSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNL--LFVHLLSLSKNQR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRPL_BBOZM STANDARD; PRT; 2212 AA.

005318; 039794;
01-FBB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (Large structural protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate + {RNA}(N).
                                                                                                                                                                                                                    203 LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVES
                                                                                                                                                                                                                                               918 -----SECELHLINVAKLSSLIVEK------DULDINTLRKIQYNLDTIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99171703; PubMed=10073695; Volchkov V.B., Volchkova V.B., Chepurnov A.A., Blinov V.M., Netesov S.V., Feldmann H.; "Characterization of the L gene and 5' trailer region of Ebola
52; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                     999 LSDLVELYSMLD--DEESLFIPLRLLSVDGNLLNFEV 1033
                                                                                                                                                                                                                                                                                                                                               323 FDELVELTSKLEWMLDQGLLESIPLYNQEKYLSGFEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gen. Virol. 80:355-362(1999).
72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fartichman J.L., Meddman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nuven D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Feterson S.N., Smith H.O., Hucchison C.A. III, Venter J.C., The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 FFLDYLEAFGL----LSDFLDHQAVI-----KFFELETHFSYYPVSGFVAPHQYLSL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 LQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWL--LHPSFSEFF-----INMGR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        515 RVPEQF------LEQENFS-----IENVLSYAQKLBYLLPQYRNFSFSLKEKELNVGR 561
                                                                                                                                                                                                                                                                                                                                                  35 LIRLEMTPQQLCELF----SIQKHWGHPVLHSETAIQKVKKHATVLKALRPIVIFETY- 408
                                                                                                                                                                                                                                                                                                                                                                                                    73 NLLFVHLLSLSKNQREGCSTDMAVVS----TP----FFNRNLWYRLLSSRFSLWKSYCPR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                               409 ---CVFKYSIAKHYFDSQGSWYSVTSDRNLTPGLNSYIKRNOFPPLPMIKELLWEFY--- 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 -HLDHPPLFSTKIISDLSIFIKDRATAVERTCWDAVFEPN-----VLGYNPPHKFSTK 514
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                 13 ILKIALKLROSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILBFFK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycoplasma genitalium.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                  DB 1; Length 2212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-156; 269-402; 643-736 AND 808-947 FROM N.A. STRAIN-ATCC 33530 / G-37; SERINELINE-94075230; PubMed-8253680; Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III; "A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                   Indels
EMBL; X67110; CAA47483.1; -.
EMBL, AP086833.4 AAD14899.1; -.
EMBL; L11365; AABHO07.1; -.
InterPro; IPR001016; Viral_RNA_pol_L.
Pfan; PP00946; Paramyx RNA_pol; 1.
Transferase; RNA-directed RNA polymerase.
SEQUENCE 2212 AA; 252722 MW; SB07EDDC370E2934 CRC64;
                                                                                                                                                                                            ch 5.3%; Score 100.5; DB 1; 1 Similarity 23.1%; Pred. No. 8.5; 62; Conservative 42; Mismatches 95;
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Last annotation update)
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    Bacteriol. 175:7918-7930(1993).

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STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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Best Local
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Q27712;
15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Hepatopancreas;
MEDLINE=96201120; PubMed=8619632;
MEDLINE=96201120; PubMed=8619632;
James M.O., Boyle S.M., Trapido-Rosenthal H.G., Smith W.C.,
Greenberg R.M., Shiverick K.T.;
"CDNA and protein sequence of a major form of P450, CVP2L, in
hepatopancreas of the spiny lobster. Panulirus argus.";
Arch. Biochem. Biophys. 329:31-38(1996)
-i- FUNCTION: EFFICIENT IN CATALYZING THE MONOOXYGENATION OF
BENZPHETAMINE, AMINOPYRINE, BENZO(A) PYRENE, PROGESTERONE,
TESTNOSTERONE.
 similarity).
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EMBL;
EMBL;
EMBL;
EMBL;
TIGR;
                                                                                                                                                                                                                                                                               Panulirus argus (Spiny lobster).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
Palinura; Palinuroidea; Palinuridae; Panulirus.
                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 2L1 (EC 1.14.14.1) (CYPIIL1)).
                                                                                                                                                                                                                                                                                                                                                                                                                                              PANAR
                                                                                                                                                                                                                                                               NCBI_TaxID=6737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 11 31 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
                                           TESTOSTERONE.
CATALYTIC ACTIVITY: RH + reduced flav
oxidized flavoprotein + H(2)O.
SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKKEYTÉKDNLKFFÞFKADGSSRLEFDLSKÞDQRVIPFAFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNVNFHIDARLLTAELQNTVFSNPK---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQTDSLKNLFSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL----- 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----HAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFD 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IK--FFELETH-----FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U39688; AAC71293.1; ALT_INIT U01715; AAC43189.1; ALT_INIT U02251; AAD12514.1; -. U01749; AAD10562.1; -. U01775; AAD10595.1; -. MG075; -. MG075; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      951 9
1024 AA;
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llarity 19.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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               TO THE CYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 98.5; DB 1; Length 1; Pred. No. 4.6; 41; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
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                                                                        flavoprotein + O(2)
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A
               P450
                                            Endoplasmic
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                 FAMILY.
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                                           reticulum
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                                           (B)
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EXSBCHLT 35
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DT 30-M2
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SEQUENCE FROM N.A. STRAIN=CWL029;

NCBI_TaxID=83558;

Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.

MEDLINE=99206606; PubMed=10192388; Ralman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).

EX5B_CHLPN STANDARD; PRT; 1050 AA. 0927G7; Q952B1; Q9K2F2; 30-MAY-2000 (Rel. 39, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) Exodeoxyribonuclease V beta chain (EC 3.1.11.5). RECB OR CEN073B OR CP0007.

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Best Local S
Matches 74
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Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450; 1.
PROSITE; PS00086; CYTOCHROME_P450; 1.
Oxidoreductase; Monooxygenase; Electron transport Microsome; Endoplasmic reticulum.
BINDING 436 436 HEME (BY SIMILARITY)
SEQUENCE 492 AA; 56767 MW; F27EE702DD09D5EE C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U44826; AABO3106.1; -. HSSP; P00179; 1DT6.
371
                                                                 313
                                                                                                                                                                   274
                                                                                                                                                                                                                                    214
                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                     114 -MWQTH-RRFILRQLRDLGMGKSRLEAAIQHEAACLVQELKKHTDQPMPLPKSINLAVLN 171
                                                                                                                                                                                                                                                                                                                                                                    116 SLWKSYCPRFFLDYLEAFGL----LSDFLDHQAVIKFFELETHFSY----YPVS-----
                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                   56 KQALARHKÇISILEFFKNILFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRF 115
INODTELACYRL 382
                               YNQEKYLSGFEV
                                                                                                                                                                                                                                                                    VIWKLVADHRY--SLODQEGQYFTQLLTTTDNMQGFAL----NLFNYLPWLLMITPD
                                                                                                                                                                                                                                                                                                                                                                                                      KTALSKFECSDRPDFYTFKLF-----GEGNDVGVV----FSNGV----
                                                                 YLMKYPEVQAKIQREIDAAVPRGTLPSLEHKDKLAYFEATIHEV--HRIVSLVPLGVSHY
                                                                                                                                  -ATLDPSNPKDLLDAYLIDLQERKEDPLSTMNIETVRAVIMDLFGAGTETTSTMIRWTIL
                                                                                                                                                                 YGAVLISSPQELGHAF-----IDNVRVLPL--
                                                                                                                                                                                                                                                                                                   ---GFVAPHQYLSLLQD----RYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLL--HPS
                                                                                                                                                                                                   FVKNWMGVRVLRDGVCE-----LKDYMKT------
                                                                                                                                                                                                                                PSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                              ELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLESIPL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 97;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
                                                                                                                                                                                                   ----FIKEHQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collaboration -
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                                                                                                                                                                                                                                                                                                                                                                    161
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pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE001609; AAD18391.1; -. EMBL; AAE002211; -. EMBL; AP002545; BAA98448.1; -. HSSP; PI411; 1DPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001282; GGPD.
Pfam; PF00479; GGPD; 1.
Pfam; PF02781; GGPD_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Bidonuclease; Helicase; ATP-binding;
BDNA repair; Complete proteome.
21 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 LLSDFLDHQAVIKFFELETH---FSYYPVS-GFVAPHQYLSLLQDRYFPIAS------ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 ILDDL--HHFVDLLYTSETHSSLFSFKIAETFNFKHRLA----RYKPCAAFTVLENMS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 -VMRTLDKDNF----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306 WVERTLEFCNLDRIFNTLLVDLQEYLKQNYTPW-LSPDESVF-----ALEKLLSS 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96 ----VVSTPFFNR-----FG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 RLIHKNPALTHSQLVLHHITNYLKQDLWKNVLFQEQFHLLAVRYNVTSKHTSSLVDKLLA 196
                          MEDLINE=20150255; PubMed=10684935; Gill S.R., Heidelberg J.F., Watead T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gainn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L. Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.1%; Score 97; DB 1; Length 1050;
22.1%; Pred. No. 6.2;
tive 51; Mismatches 117; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 RIILQKENKEKQALARHKCISIL--EFFKNLLF---VHLLSLSKNQREGCSTDMA---- 95
                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5- to 3'-or 3'- to 5'-direction to yield 5'- phosphooligomucleotides.
-i- SUBUNIT: CONSIST OF THREE SUBUNITS; RECE AND RECD (BY SIMILARITY: BELONGS TO THE HELICASE FAMILY: UVRD SUBFAMILY.
                                                                                                                                                                                                       MEDLINE=2030349; PubMed=10871362;
Shizal M., Hirekawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138
from Japan and CWL029 from USA.";
"Longrison of Ses. 281:231-2314(200).
"I. FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE
UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEARYAGE OF SINGHE-
STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.
ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 142 N -> K (IN REF. 2).
182 182 V -> I (IN REF. 1).
1050 AA; 121056 MW, 6E2CD03C2AEBB3B7 CRC64;
                                                                                                                                   pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001655; AAD18877.1; -. EMBL; AE002164; AAF37903.1; -. EMBL; AP002547; BAA98945.1; -.
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(BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDINE-20150255; PubMed=10684935; Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarry G., Salzberg S.L., Eisen J., Fraser C.M.;
236 PSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGH---AFIDN 292
                                                                       355 SEAQPVVQAL---------REQYQLVLIDEFQDTDKQOWSIFSN 389
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MBDINES9206666; PubMed=10192388;

MBDINES92066666; Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,

Olinger L., Grimwood J., Davis R.W., Stephens R.S.;

"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

Nat. Genet. 21:385-389(1999).
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                                                                                                                                                                                               :: | : | : | | : | | | : | : | 390 LFISPKFTGSL----PLIGDPKQSIYEWRSADLPTYLTAKSSFSEDKQL 434
                                                                                                                                                                                                                                                                                                                                                                                                            O9ZBUG; JANUARU); PRT; 512 AA.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
315-MAY-2002 (Rel. 41, Last annotation update)
Glucose-6-phosphate 1-dehydrogenase (BC 1.1.1.49) (G6PD).
ZWF OR CPNO238 OR CP0524 OR CPJ0238.
Chlanydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiales; Chlamydophila.
                                                                                                                                              293 VRVLPLELDQIIRLPRNTSTPQETLFSIRHFDELVELTSKLEWMLDQGL
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YABD_SCHPO
ID YABD_S
AC Q09812
AC Q09812
DT 01-NOV
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Best Local S
Matches 83
MEDLINE-21484401; PubMed=11859360;
MEDLINE-21484401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YABD_SCHPO STANDARD; PRT; 529 AA.

009812;
01-NOV-1995 (Rel. 32, Created)
11-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C2G11.13 in chromosome I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFKNLLFVHLLSLSKNQREGCSTDMAVVSTPF-----FNRNLWY----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGTNNIVRPVKMDFRYDSYFQTTTPEAYERLLCDCIIGDRTLFTGGDEVMASWKLFTPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FKKS-----PYNLFAAEECSRCPIENDLL------IIRIQPDE-GVALKFNCKV 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSVLGYREEENVDKDSRVETYVALKTVINNPRWLGVP----FYLRAGKRLAKKSTDISII
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18.8%; Pred. No. 2
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Mismatches 124; Indels 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 512;
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RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Moodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gorgym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Goffeau A., Cadieu E., Dreano S., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schizosaccharomyces pombe.";
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein;
TRANSMEM 25 45
TRANSMEM 72 92
TRANSMEM 130 150
TRANSMEM 241 261
TRANSMEM 269 289
TRANSMEM 365 385
TRANSMEM 365 385
TRANSMEM 397 417
TRANSMEM 429 449
TRANSMEM 467 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).-!- SIMILARITY: SOME, TO YEAST YCL38C AND B.SUBTILIS YXIO.
                                                                                                                                                                                                                                                                    190
                                                                                       303
                                                                                                                                                                                                                                                                                                                                                                                                  120 SYCPRFFLDYLEAFGLLSD--FLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRY 177
362 NFQLTLLGMGISSFALLGTVIIPYLTEYFQLNSLQVVMIISILLPMAPLYGLLGYIPGFE
                                                                                                                                                                                                                                                                    DDLDSYITNTTIDSSEEEPYLLEHSLILNESAPPADVEDEHKAKIAARLSSVGFGSFFGA
                                                                                                                                                                                                                                                                                                                                                         SWSPSSFLLGKIVFLILVDLNFIISOSCYDSF-LPIFLRFYPITR--GPITLESALODET 189
                                                                                                                                                                                                                                                                                                          FPIASVMRTLDKDNFSLTPDLI-HDLLGH-----
                                                                                                                                RKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFN----TSTPQETLFS-----
                                                                                                                                                                            AILFQIIFTPILYKTNNNP-----IILPITVTVCSCWWLILSTPLCTIVTLPVENHSS
                                                                                                                                                                                                                     -INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGL-----IENHEG
                                                                                       -DAILTLLYNSVKESYHSFKHAMSISSIRLFLFSRLFINCGIQTSLSSAVIFGKARLNLS
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                                         irhederverisktemwidogriesibrynoekyisgee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18E2B0F2AFF88D8F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                127;
                                                                                                                                                                                                                                                                                                             --VPWLLHPSFSEFF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                                               218
                                                                                                                                   319
  421
                                                                                                                                                                                                                        270
                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
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TEGU HSV7J P52362; 01-OCT-1996 01-OCT-1996 16-OCT-2001

STANDARD;

B

(Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation update)

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POLY-ASN.
POLY-ASN.
POLY-LYS.
                                                                                                                                                                                                                                                                                                                                                                               EMBL; X79345; -; NOT ANNOTATED CDS. HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD000616; DNA topoisoII; 1.
ProDom; PD000742; DNA topoisoIV; 1.
                                                                                                                                                                                      -!- SUBUNIT: HOMODIMER (BY SIMILAR
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00433; TOP2c; 1
SMART; SM00434; TOP4c; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
            NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bhoinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1615 FTQHSF-----ELPLEKFSLLIIANN----PEFLF-------GSLQCPVDLAINS 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                   1265 ILKWLIVPVKELNTFFVATMSEFGEVIPFDYKHFR-ALEYEINSKYIEIENKIICNEIIE 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1378 FD--LLDNIAHFRFAFDFNHQQNLİLKLKDKFKTLRTDTVFERFPNLDDTFVSSMNVENF 1435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 CPRFFLDYLEAFGLLSDFLDHQAVI-----KFFELETHFSYYP-----VSGF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 VAPHQYLS-----TP- 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 ------DLIHDLLGHVPWLLHPSFSEFFINMGRL-FTKVI--EKVQALPSKKQRI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 QTLQSNLIAIVRCFW-FTVESGLIENHEGR------KAYGAVLIS----SPQ 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 ELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLDQGLLE 343
                                                                                                                                                                                                                                                                                                                                                   5.1%; Score 96; DB 1; Length 2059;
20.6%; Pred. No. 18;
Live 62; Mismatches 164; Indels 120; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 FFKNL--LFVHLLSLSKNQREGCSTD----MAVVSTPFFNRNLWYRLLSSRF--SLWKSY 121
                                                                                                                                                                                                                                                                                                                                                                                                          13 ILKIALKLRQSLSLFFQNSQS-LQRAYSTPYSYYRIILQKENKEKQALARHK--CISILE 69
                                                                                                                              Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: TREGUMENT PROTORIN.
-!- SIMILARITY: BELONGS TO PAMILY THAT GROUPS TOGETHER HSV-1 UL36,
EHV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOP2.
Plasmodium falciparum (isolate K1 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                             EMBL; U43400; AAC54693.1; -.
SEQUENCE 2059 AA; 239476 WW; AAE6CA6DEDC5D316 CRC64;
                                  Human herpesvirus (type 7 / strain JI) (HHV7).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-FKS-2000 (Rel. 39, Last annotation update)
DNA topoisomerase II (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1398 AA.
                                             Viruses; dsDNA viruses, no RNA st
Alphaherpesvirinae; Simplexvirus.
NCBI_TaxID=57278;
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                                                                                                                                                                                                                                                                                                                                                              Local Similarity 20.6
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Large tegument protein.
U31.
                                                                                                      SEQUENCE FROM N.A.
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TOP2 PLAFK
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TO TOP2 PLAFK
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DT 01-FEB
DT 30-MAY.
DE DNA tOI
GN TOP2.
GN PLABSMOTO OC EUKARY.
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-i- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY TRANSIENT BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75 ---LFVHLLSLSKN-----QREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYC 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROALT; SUCULTY, TOPOISONERASE II; 1.
ISOMETABS, TOPOISOMERASE, DNA-bInding, ATP-binding; Nuclear protein.
NP BIND 144 149 ATP (POTENTIAL).
ACT SITE 830 830 DNA CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAN RELAX BOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -. "SCELLANDOS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOY NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

-!- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
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1398 AA; 161029 MW; BAAD7BEE88FE5BE9 CRC64;
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20.8%; Pred. No. 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of double-stranded DNA.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR003594; ATPbind ATPase.
InterPro: IPR003594; CBPA NFFB topis.
InterPro: IPR001241; DNA topoisoll.
InterPro: IPR001205; DNA topoisoll.
Pfan; PF00204; DNA QTASSB; 1.
Pfan; PF00519; DNA topoisolV.
Pfan; PF00519; HATPSSC C; 1.
PRINTS; PR00615; CCAATGUBUTA.
PRINTS; PR00418; TPIZFAMILY.
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21;

102 266

120

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RESULT 40
SRB8_YEAT
IDB_SRB8_YEAT
AC P25648
DT 01-MAY
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PIR; S19495; S19495.
PIR; S19495; S19495.
TRANSFAC; T02152; -
SGD; S0006677; SRBB.
InterPro; IPR000651; RasGEF
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30-MAY-2000 (Rel. 39, Last annotation update)
Suppressor of RNA polymerase B SRB8.
SRB8 OR YCR081W OR YCR81W/YCR80W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95293223; PubMed=7774808;
Hengartner C.J., Thompson C.M., Zhang J., Chao D.M.,
Koleske A.J., Okamura S., Young R.A.;
"Association of an activator with an RNA polymerase
Genes Dev. 9:897-910(1995).
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P25648; P2
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Feldmann H., Mannhaupt G., Vetter I.;
Submitted (MAR-1992) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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STRAIN=Bristol N2;
Bentley D., Favello A.;
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STRAINE-Bristol N.P.
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MEDLINE-92369913; PubMed=1498366;
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Kuwabara P.E., Okkema P.G., Kimble J.;
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Rhabditidae; Pelode
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ETSTON R.;

mitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

FUNCTION: PROMOTES FEMALE DEVELOPMENT IN XX ANIMALS WHERE IT EVENTION: PROMOTE SEGMENT OF THE FEM PROTEINS TO THE MEMBRANE THEREBY SEQUESTERS ONE OR MORE OF THE FEM PROTEINS TO THE MEMBRANE THEREBY FREEING THE TRA-1 PROTEIN (A PUTATIVE TRANSCRIPTION FACTOR) TO ENTER THE MUCLEUS AND PROMOTE FEMALE DEVELOPMENT. IN XO ANIMALS IT ACTS AS A RECEPTOR FOR HER-1 WHICH PREVENTS IT FROM BINDING TO FEM PROTEINS THEREBY REPRESSING THE ACTIVITY OF TRA-1. SUBCELIULAR LOCATION: Integral membrane protein.

TISSUE SPECIFICITY: SOMATIC AND GERM LINE TISSUES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAKNFSAQKRVVSYMMPSLYRLLNILITYGIIKVPTYIRKLISSGLLYLQDSNDKFVHVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
ring transformer protein 2 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nematoda; Chromadorea; Rhabditida; rinae; Caenorhabditis.
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664

333 604 291 207

544 263 496 166 386

437

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NCBI_TaxID=2097;
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SEQUENCE 65
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRTLDK------DNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVI 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                254 ------RCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDN-----VRVLPLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           379 QHSDFVNGFESIW-TIEKAEELIHEFRLAL-----KEETEKFKENRMSKMIRVTSRV 429
                                                                                                                                                                                                                                                                                                                                                                                                   49 LQKENKEKQALARHKCISILEFFKNLLFVH--LLSLSKNQREGCSTDMAVVSTPFFNRNL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 WYRLLSSRFSLWKSYCPRFFLDYLEAFG---------LLSDFLDHQAVIKFFEL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 ETHFSYYPVSGF------VAPHQY-----LSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 -----PSKSFTNSTKDALFQKIKLWLLSIEPRQKTCAASIHSCDTPLDSEHYFNICTD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 MQSVDNFAEKKTKFKLEDVDEEFAMNLDCVDDQEQFIEWMQE-----LEIRKMYSHVT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EX------253
                                                                                                                                                                                                                                                                                                                                              5.0%; Score 95; DB 1; Length 1475;
16.7%; Pred. No. 14; No. 14;
tive 65; Mismatches 120; Indels 188; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 L----EMORLSPCLIVTPLNCFYDIYRIHGEISNWNKN-------TOFLNR-- 174
                                                                                                                                                                                                                                                                                                                                                                                         1 VHYCERTLDPKYILKIALKLRQS-----LSLFFQNSQSLQRAYSTPYSYRII 48
                                                                                                                                                                             SEX-DETERMINING TRANSFORMER PROTEIN 2.
SIMILARITY: TO MEMBRANE PROTEIN PATCHED OF D.MELANOGASTER.
                                                                                                                                                                                                                                                                                                                           1475 AA; 170352 MW; F8C6456B3D3654BE CRC64;
                                                                                                                                                         Transmembrane; Receptor; Signal.
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POTENTIAL.
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                                                                                                     EMBL; M91371; AAA28150.1; -.
EMBL; S42187; AAB22845.1; -.
                                                                                                              . 542187; AAB22845.1; -.; AC006608; AAF39755.1; A60026; A60026.
                                                                                                                                               CE23546
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les 75; Conservative
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1080
1475
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

METALNA-RACC 33536 / G-37;

MEDLINES-96056346; PubMed=7569993;

MEDLINES-96056346; PubMed=7569993;

MINTE O. Adams M.D., Clayton R.A.,

Fleischmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,

Fritchman J.L., Weidman J.F., Sandek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

"The minimal gene complement of Mycoplasma genitalium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fristschmann R.D. Bult C.J., Kerlavage A.R., Sutron G., Kelley J.M., Frlichmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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4.9%; Score 93.5; DB 1; Length 650;
Best Local Similarity 18.6%; Pred. No. 6.4%
Matches 59; Conservative 53; Mismatches 128; Indels 77; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 ILEFFKNLLFVHLLSLSKNQREGCSTDMAVVS--------TPFFNRNLWY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 LEKETDYDQNFKSFTEKFKDEKITNNQLGIVDIYNLFSGF--HKSVKSTVDLMNQLQKQV 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequencing.";
J. Bacteriol. 175:7918-7930(1993).
J. Bacteriol. BLONGS TO THE MG032 / MG096 / MG288 FAMILY.
-1- SIMILARITY.
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650 AA; 74802 MW; 30539DDC6F69DDC3 CRC64;
P47342; Q49188;
01-FEB-1996 (Rel. 33, Created)
30-MAX-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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InterPro; IPR004306; MG032/096/288_1.
InterPro; IPR004319; MG032/096/288_2.
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                                                                                                                                                                                   Hypothetical protein MG096.
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Pfam; PF03086; DUF240; 1.
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13;

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   Query Match
Best Local Similarity
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MEDIJINE=96026346; PubMed=7569993;

Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,

Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,

Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Puhrmann J.L.,

Mguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

"The minimal gene complement of Mycoplasma genitalium.";

Science 270:397-403 (1995).
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P473II; 049281;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein
                                                                                                                                   SMART; SM00382; AAA; I.

PROSITE; PS00211; ABC_TRANSPORTER; 1.

PROSITE; PS00211; ATP-binding; Transport; Complete Hypothetical protein; ATP (POTENTIAL).

NP_BIND 269 276 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U39686; AAC71283.1; -.
EMBL; U02154; AAD12436.1; -.
TIGR; MG065; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-i- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                       InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; BBC_transportr; 1.
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Peterson S.N., Hu P.-C., Bott K.F., Hutchison
"A survey of the Mycoplasma genitalium genome
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                                                                                             394
466 AA;
                                                                                          399 G
54009 MW;
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      4.9%;
                                                                                             GDEPTG -> WWWTYW (IN REF. 
, A585044B8A90391C CRC64;
      Score 92.5;
Pred. No. 5
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by using random
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Best Local S
Matches 54
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P13783;
01-JAN-1990
01-JAN-1990
16-OCT-2001
                                                                                                                                                                                                                                                                                                             SEQUENCE
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      72
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                                                                                                                         13
                                                                                                                         ILKIALKLROSLSLFFQNSOSLORAYSTPYSYYRIILOK-ENKEKQALARHKCISILEFF 71
          K-----PILFVHLLSLSKN-----QREGCSTDMAVVSTPFFNRNLWYRLL--
                                                                     IIKFTVRLRK-----TESLOKDIESALPSYKVVVSPFKNQEVSLFDRYE----
                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                             447
                                                                                                                                                                                          Conservative
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AA;

51110 MW;

89D08AB52718A104 CRC64;

4.9%;

37;

Score 92; DB Pred. No. 5.2; 37; Mismatches

DB 1; 5.2;

Length 447

82;

Indels

Gaps

12;

ETH 127 -SS 113

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Matches
                                                    EMBL; X03961; CAA27591.1; -. PIR; S28086; S28086. DNA recombination; DNA integration and an area are series and are series are series.
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Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
NCBI_TaxID=28985;
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-66232585; PubMed=3520486;

Chen X.J., Saliola M., Falcone C., Bianchi M.M., Fukuhara H.;

Chen X.J., Saliola M., Falcone C., Bianchi M.M., Fukuhara H.;

"Sequence organization of the circular plasmid pKD1 from the yeast

Kluyvercomyces drosophilarum.";

Nucleic Acids Res. 14:4471-4481(1986).

-i- FUNCTION: FLP CATALYSES RECOMBINATION BETWEEN THE LARGE INVERTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 GITTNAVLKGVDLAIKSHDFIVILGPSGSGKTTLLNI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                              REPETITIONS OF THE PLASMID. SIMILARITY: BELONGS TO THE "PHAGE" INTEGRASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKKQEILLNNWFNSNERLFLKNEVKKVNWLNSPRQKQQAAQIDDQNIIELKNVYKY-ITN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LQDRYFPIASVMRTLDKDNFSLTPDL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 13, Created)
(Rel. 13, Last sequence update)
(Rel. 40, Last annotation updat
FLP protein.
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                        DNA integration; Plasmid.
336 TRANSIENT COVALENT LINKAGE TO STRAND CLEAVAGE AND REJOINING
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STRAND CLEA
SIMILARITY)
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                                                              DURING
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us-09-438-185a-1047.rsp

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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Probable intron maturase (Maturase K).
                                                                                                                                                                         544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000442; Intron_maturse2.
InterPro; IPR002865; MatK N.
Pfam; PF01348; Intron_maturas2; 1.
Pfam; PF01824; MatK N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X86563; CAA60266.1; -.
MaizeDB; 118213; -.
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Matches 73; Conservative
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transcript editing.
J. Mol. Biol. 251:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chloroplast; mRNA I
SEQUENCE 544 AA;
                                                                                                                                                                                                                                                                               Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
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P48190;
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                                                                114 RFSLWKSYCPRPFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSG----FVAPHQY 169
                                                                                                                                                                                                                                                                                                                                         Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 QCYFSVWFQSQKVNINQLSKDNLEFLGYLSSLRLNPLVVRSQMLE-----NSFLIDN 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 HKCISILEFFKNLL--FVHLLSLSKNQ-----REGCSTDMAVVSTP-----FFNRNLW 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 ----IHHFFKVFVNNFPAILGLLKDPFIHYVRYHGRCILATKDTPLLMNKWKYYFVNLW 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPH 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 HVCE------YESIFFFLRKRSSHLRSTSYEVLFERIVFYGK------ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 HYCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALAR 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: WITH CORRESPONDING ORF IN OTHER PLANT CHLOROPLASTS, AND REGIONS OF SIMILARITY TO MATURASE-LIKE POLYPEPTIDES ENCODED BY MITOCHONDRIAL INTRONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana.";
DNA Res. 6:283-290(1999).
-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=cv. Columbia;
MEDLINE=20039611; PubMed=10574454;
Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
"Complete structure of the chloroplast genome of Arabidopsis
                                                                                                                            243 | : | | : | | : | | 243 L-----RVCSPIEKTVSSNRPTNQTHQFL---PESLARTFSRF 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.9%; Score 92; DB 1; Length 526; Best Local Similarity 22.1%; Pred. No. 6.4; Matches 65; Conservative 35; Mismatches 118; Indels
                                                                                                        170 LSLLQDRYFPIASVMRTLDKDNFSLTP-DLIHDLLGHVPWLLHPSFSEF 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast, mRNA processing.
SEQUENCE 526 AA, 63038 MW, 4798486C56ACC011 CRC64;
                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                    526 AA.
                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Chloroplast.
                                                                                                                                                                                                                                                                                            Probable intron maturase (Maturase K). MATK OR YCF14.
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InterPro; IPR000443; Intron maturse2.
InterPro; IPR002866; MatK.N.
Pfam; PF01348; Intron maturas2; 1.
Pfam; PF01824; MatK.N.
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                    STANDARD;
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STRAIN=cv. Columbia;
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MATK ARATH
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                            379 VRIKL--DSKIPISSIIGSLAKDKFC-----NVLGHPISKATW-TDSSDSDILNRFVR 428
168 QYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGH----VPWLLHPSFSEFFINMGR 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               199 LEYRSQDVPSLHLLRFFLYYYSNWNSFITSMKSI------FLLKKENKRLFRFL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RHKCISILEFFKNLLFVHLLS-----LSKNQREGCSTDMAVVSTPFFNRNLWY- 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 YNSYVSEYEFF--LLFLHKOSSCLRLTSSGTFLERIIFSGKMEHFGVMYPGFFRKTIWFF 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE-95395841; Pubmed=7666415;
Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
Maier equence of the maize chloroplast genome: gene content, hotspots of divergence and fine tuning of genetic information by
                                                                                                                                                                     224 LFTKVIEKVOALPSKKOR-----IQTLQSNLIAIVRCFWFTVESGLIE 266
                                                                                                                                                                                                                                                               429 ICRNISHYYSGSSKKKNLYRIKYILRLCCVKTLARKHKSTVRTFLKRLGSGLLE 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Mol. Biol. 251:614-628(1995).-!- FUNCTION: PROBABLY ASSISTS IN SPLICING CHLOROPLAST GROUP II
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18.6%; Pred. No. 6.7;
ive 64; Mismatches 140; Indels 116;
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44 AA; 64800 MW; 95D6C38D39EC84D0 CRC64;
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7 A A B B C A A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C A B B C 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen S.-H., Yang C.-Y., Chen P.-P., Setzer Gotto A.M. Jr., Chan L.; "The complete cDNA and amino acid sequence B-100.";
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Elackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein
B-100.";
Nucleic Acids Res. 14:7501-7503(1986).
SEQUENCE OF 709-9
MEDLINE=85270450;
Deeb S.S., Motuls
                                                                                                                                                                                Cladaras C., Hadzopoulou-Cladaras Zannis V.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., For Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy "DNA sequence of the human apolipoprotein B gene.";
DNA 6:363-372 (1987).
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=87161758;
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=87041416; PubMa
Law S.W., Grant S.M., I
Lee N., Brewer H.B. Jr
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Mammalia; Eutheria;
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[3]
SEQUENCE FROM N.A.
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                                                                                                                  4211 YTREELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L 4257
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                                                                                                                                                                                                                                                                                               4313 NIKOLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4370
                                                                                                                                                                                                                                                                                                                                                                                                         4371 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 4430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

Bult C.J. White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., Mahte O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake O., Pitzderald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidem J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberte K.M., Hurst M.A., Kaine B.P., Borrdowsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: S-adenosylmethioninamine + putrescine = 5'-methylthiodenosine + spermidine.
-!- PATHWAY: FIETH (LAST) STEP IN THE BIOSYNTHESIS OF SPERMIDINE FROM ARCHINE AND METHIONINE.
-!- SIMILARITY: BELONGS TO THE SPERMIDINE/SPERMINE SYNTHASES FAMILY.
                                                                                                                                                                    60 ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                         68; Gaps
                                                                        3 YCERTLDPKYILKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL 59
                                                                                                                                                                                                                                                                   114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4431 NPTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI--IKSQAIA 4483
                                                                                                                                                                                                                                                                                                                                                               167 -----HQYLSLLQDRYFPIASVMRT----LDKDNFSLTPDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
20.7%; Pred. No. 99;
ive 48; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-UTN-2002 (Rel. 41, Last annotation update)
Probable spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanococcus jannaschii.
Archaea; Euryarchaedcus; Methanococci; Methanococcales;
Methanocaldococcaeae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000051; SAM_bind.
InterPro; IPR001045; Sprmine synthase.
Pfam; PF01564; Spermine_synth; 1.
TIGRPAMB; TIGR00417; speE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U67486; AAB98300.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 273:1058-1073(1996)
  l Similarity 20.7%
61; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2190;
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Q57761:
     Local
                         Matches
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RESULT REPLIED ON A CONTROL OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF
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Best Local S
Matches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RRPL MEASA
P35975;
01-JUN-1994
01-JUN-1994
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Spermidine |
DOMAIN
                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=93227570; PubMed=8470368;

MOTI T. Sasaki K., Hashimoto H., Makino S.;

MOTI T. Sasaki K., Hashimoto H., Makino S.;

"Molecular cloning and complete nucleotide sequence of genomic RNA
the AIK-C strain of attenuated measles virus.";

Virus Genes 7:67-81(1993).

-i- FUNCTION: PROBABLE COMPONENT OF THE ACTIVE POLYMERASE. IT MAY
FUNCTION IN MRNA SYNTHESIS, CAPPING, METHYLATION AND POLY(A)
SYNTHESIS OF NEWLY SYNTHESIZED VIRAL MRNAS, RNA EDITING OF THE
GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.

-i- CAPALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
EMBL, S58435, AAB26147.1; -.
PIR; G48556; G48556.
InterPro; IPR0011016; Viral RNA pol L.
Pfam; PF00946; Paramyx_RNA_pol; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Morbillivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Measles virus (strain AIK-C) (Subacute sclerose panencephalitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEASA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=36408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 STPQETLFSIRHFDELVELTSKLEWMLDQGLL---ESIPLYNQE------KYL--SGFEV 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
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                                                                                                                                                                                                                                                                                              SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYPVSGFVAPHQYLSLLQDRYFPIASVM----RTLDKDNFSLTPDLIHDLLGHVPWLLHP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NPRNVLVIGGGDGGTVREVVKHKSVETVDFVELDEKVIEACKKYMPKLSCEIDNEKVNLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YREKSGF----QEIEIIDTYDFGKALILDNTFQTTERDEF----IYHELISHIPLFTHP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.8%;
l Similarity 19.1%;
46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS01330;
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biosynthesis; Transferase; Complete proteome
BS 126 BINDING TO DECARBOXYLATED
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          293 AA; 33899 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
ase beta subunit (EC 2.7.7.48) (Large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITDGIKYVAETEKKYDVIIVDCPDPVG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 91.5;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87;
                                                                                                                                                                                                                              a collaboration - MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P12576;
01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA polymerase beta subunit (EC 2.7.7.48) (Large
Cattaneo R., Schmid A., Spielhofér P., Kaelin K., Baczko K., Meulen V., Pardowitz J., Flanagan S., Rima B.K., Udem S.A.; "Mutated and hypermutated genes of persistent measles viruses whice caused lethal human brain diseases."; Virology 173.415-425(1989).

-i- FUNCTION: PROBABLE COMPOUNT OF THE ACTIVE POLYMERASE. IT MAY FUNCTION IN MRNA SYNTHESIS, CAPPING, METHVLATION AND POLY (A) SYNTHESIS OF WEALY SYNTHESIS VIRAL MRNAS, RNA EDITING OF THE SYNTHESIS OF WEALY SYNTHESIS OF VIRAL MRNAS, RNA EDITING OF THE GENE TRANSCRIPT, AND PROTEIN KINASE ACTIVITY.

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate {RNA}(N).
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SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                 "Measles virus L protein evidences elements of ancestral polymerase.";
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88219537; PubMed=2835864;
Blumberg B.M., Crowley J.C., Silverman J.I., Menonna J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Paramyxovirinae; Morbillivirus.
                                                                                                                                                                                                                                                                                                                                                                                              Dowling P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Measles virus (strain Edmonston) (Subacute sclerose panencephalitis
                                                                                                                                                                                                                                                  MEDLINE=90085790; PubMed=2596022;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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-!- SIMILARITY: WITH L PROTEIN OF OTHER PARAMYXOVIRUSES.

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                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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4.8%; Score 91; DB 1; Length 2183;
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Pfan; PF00946; Paramyx, RNA_pol; 1.
Pransferase; RNA-directed RNA_polymerase.
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Novel Chlamydia pneumoniae protein useful in the manufacture of a medicament for treatment or prevention of infection due to Chlamydia, preferably Chlamydia pneumoniae, and for diagnostic purposes

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Claim 1; Page 134; 364pp; English.

Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia Cpneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding them. The proteins are predicted to be immunogenic and may therefore be useful in vaccine production and for diagnostic purposes. Chlamydia pneumoniae is a common cause of respiratory disease in humans, and is also involved in the development of cardiovascular diseases such as composed in farction, cerebrovascular disease, aortic aneurysm, and stycke. The proteins and nucleic acids of the invention may be used in vaccines and pharmaceutical compositions for the pneumoniae infections. The proteins may also be used in the detection of Chlamydia pneumoniae, and the nucleic acids may be used in pcR, branched DNA probe assay or blotting techniques for determining Chlamydia pneumoniae gene expression. The present sequence represents a composition.

Sequence 362 AA;

밁 Ś Query Match Best Local S Matches 362 tch 100.0%; Score 1889; DB 23; Length al Similarity 100.0%; Pered. No. 8 (6e-182; 362; Conservative 0; Mismatches 0; Indels ٥, Gaps 60 60

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                                                                                                                                                                                         4 MVSTPFLTVFSMEKLLS------KIFLDYLEAFGLLSDFLDHQAVIKFFELETHF
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Query Match 66.2%; Score 1250.5; DB 20; Length 259; Best Local Similarity 91.8%; Pred. No. 1.3e-117; Matches 245; Conservative 3; Mismatches 8; Indels 11;
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Chimeric - Unidentified.
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61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFPRNRLMYRLLSSRFSLWKS 120
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97FR-0014673,
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21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                      Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; ph aromatic aminotransferase; phhC; milk protein; animal protein; casein; proteinaceous food product; globulin; whey protein; phenylketonuria; PKU; inherited metabolic disorder; impaired brain function; nootropic; cell therapy; phhAB fusion protein.
                        Unidentified
                                                                                                                                                                                                                                                                                                                          AAE11161 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product having phenylalanine hydroxylase activity, that is derived a prokaryotic organism, is useful for treating phenylketonuria in
                                                                                                                                                                                           phhAB fusion protein fragment
                                                                                                                                                                                                                                       18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 2; Fig 5; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 SILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRF 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                PLE---AMRTPYRIDILQPLYFVLPDLKRLFQLAQE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSK 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ER---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID---NVRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VATFIRTPEELDYLOEPDIFHEIFGHCPLLTNPWFAEFTHTYGKLGLKA-----SKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLDGIEQLG-----LPHERIPQLDEINRVLQATTGWRVARVPALIPFQTFFELLASQQFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLDYLEAFGLLSDFLDHQAVIKFFELE-----THFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLEFGFKLKTTQYVARQPD------DNGFIHYPETEHQVWNTLITRQLKVIEGRACQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VFLARLYWMTIEFGLVETDOGKRIYGGGILSSPKETVYSLSDEPLHQAFN 231
                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.5%;
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                                                                                                                                                                                                                                                                                                                          415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 237; DB 22;
Pred. No. 4.4e-15;
6; Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
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Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived a prokaryotic organism, is useful for treating phenylketonuria in
                                                                                                                                                                                                             14-MAR-2000; 2000US-0525116.
                                                                                                                                                                                                                        14-MAR-2001; 2001WO-DK00172
                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                            Example 8; Fig 18; 91pp; English.
                                                                                                                                                                     WPI; 2001-590055/66.
                                                                                                                                                                                                  (NILA-) NILAB APS.
                                                                                                                                                                                                                                                WO200168822-A2
                                                                                                                                                                                                                                                                            Region
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                                                                                                                                                                                M, Ravn P,
Jensen SH,
                                                                                                                                                                                     Ravn
                                                                                                                                                                                                                                                           396..415
                                                                                                                                                                                                                                                                                        /note= "I
295..336
                                                                                                                                                                                                                                                                           /note= "phhAB
353..380
                                                                                                                                                                                                                                                                                                   /note=
228..2
                                                                                                                                                                                                                                                                                                                         /note= "phhAB fusion 94..157
                                                                                                                                                                                                                                                                                                                                    /note= "phhAB
55..90
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 21..46
                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                 "phhAB
                                                                                                                                                                                                                                                                                                               . . 223
                                                                                                                                                                                Madsen SM,
Gjetting '
                                                                                                                                                                                                                                                                                                                    "phhAB
                                                                                                                                                                                                                                                                                             "phhAB
                                                                                                                                                                                                                                                                      fusion peptide #7"
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                                                                                                                                                                               Vrang A,
f, Nielsen
                                                                                                                                                                                                                                                          peptide
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E;
                                                                                                                                                                                                                                                                                  #6"
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                                                                                                                                                                                                                                                                                                                     #3=
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                                                                                                                                                                                      Bredmose L;
                                                                                                                                                    from
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The patent discloses novel cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase (PAH) activity such as phenylalanine hydroxylase (phhA), 4a-carbinolanine dehydratase (phhA) as phenylalanine hydroxylase (phhA), 4a-carbinolanine dehydratase (phhA) approximate an approximate an approximate an approximate an approximate an approximate an approximate an approximate an approximate an approximate an approximate an approximate app

Sequence 415 AA;

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Query Match
Best Local S
Matches 61
  61;
Similarity 24.9
51; Conservative
          12.5%;
 52;
Score 235.5; DB 22;
Pred. No. 5.9e-15;
2; Mismatches 103;
 Indels
                 Length 415;
 33;
Gaps
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8 맑 Ş 153 81 26 93 RVLQATTGWRVARVPALIPFQTFFELLASQQFPVATFIRTPEELDYLQEPDIFHEIFGHC 140 DMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHQAVIKFFELE 152 DNGFIHYPETEHQVWNTLITRQLKVIEGRACQEYLDGIEQLG-----LPHERIPQLDEIN ----THESYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNESLTPDLIHDLLGHV 206 80

4,

Gaps

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Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                         107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                174 WGTVPQELNKLYPTHACR----EYLKNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                     159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                      219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRÇFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
Yang Y, Wejhrman T, Goodrich R;
                                                                                                27;
                                                           Query Match 12.3%; Score 231.5; DB 22; Length 444; Best Local Similarity 27.8%; Pred. No. 1.6e-14; Matches 64; Conservative 43; Mismatches 96; Indels 27;
                                                                                                                                                                                                                                                                                                                                         279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                         335 LSSISELKHALSGHAKVKPFDPKITCKQECLITTFQDVYFVSESFEDAKE 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 20; Page 4255-4256; 6221pp; English.
were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM79208 standard; Protein; 444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
20-UJN-2000; 2000US-0598075.
19-UJL-2000; 2000US-062325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-065351.
20-OCT-2000; 2000US-063325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein SEQ ID NO 1870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2001; 2001WO-US04098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-476283/51.
                                 444 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157190-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
                                 Sequence
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Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM79208;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polymeroleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissum growth factor activity, immunomodilatory activity and activity, tissum growth factor activity, immunomodilatory activity and activity, the useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis, tissue growth factor; immunomodulatory, cancer, leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ma Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing
               PWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIE 266
                                     267 NHEGRKAYGAVLISSPQELGHAFID---NVRVLPLELDQIIRLPFNTSTPQETLFSIRHF 323
                                                                                                    : | : : | : : | | : | | : | | : | | 106GKIYGGGILSSPKETVYSLSDEPLHQAFNPLE---AMRTPYRIDILQPLYFVLPDL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cao Y,
ng ZW;
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Wang D, Wang J, Zhang J, Ren F, Chen R, Wang
Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 446-447; 6221pp; English.
                                                                                                                                                                                                                                                                      AAM80192 standard; Protein; 444 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000; 2000US-0496914.
27-AFR-2000; 2000US-0560875.
20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-062325.
01-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0653325.
30-NOV-2000; 2000US-0693325.
                                                                                                                                                                                                                                                                                                                                                                           Human protein SEQ ID NO 3838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-2001; 2001WO-US04098.
                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-476283/51.
                                                                                                                                                  324 DELVELTSK 332
                                                                                                                                                                                 242 KRLFOLAGE 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200157190-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                        AAM80192;
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AAM80192
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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Ma Y;

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PRODUCTION OF STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET STREET ST
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Best Local S
Matches 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuronal tryptophane hydroxylase; nTPH; neuronal disease; primary haemostasis deficiency; allergy; transplantation; serotonin; antiarteriosclerosis; thrombolytic; anticoagulant; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurone specific tryptophane hydroxylase.
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                                    Claim 21; Fig 9; 21pp; German
                                                                                     and treating primary hemostatic de
activity of tryptophan hydroxylase
                                                                                                                                      Regulating levels of serotonin, useful for diagnosing neuronal disease and treating primary hemostatic deficiency, comprises controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-AUG-2000; 2000DE-1043124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2001; 2001WO-DE03178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiallergic; gynaecological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO17329 standard; Protein; 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200217891-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                               (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSSISELKHVLSGHAKVKPFDPKITCKQECLITTFQDVYFVSESFEDAKE 384
                                                                                                                                                                                                                                                    2002-281015/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEIG-----LASLGASEEAVQKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPFYTPEPDTCHELLGHVPLLAEPSFAQFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WGTVFQELNKLYPTHACR---EYLKNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity
63; Conser
                                                                                                                                                                                                                                                                                                                         'n
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                                                                                                                                                                                                                                                                                                                     Bader M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 227.5; DB 22; pred. No. 4.2e-14; 3; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2581), 2111 (AAK pages from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AAK52582) and 3666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334
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Best Local (
                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a method of influencing the level of serotonin, which involves the specific regularion of TPH (tryptophan hydroxylase) and/or neuronne-specific TPH (nTPH) activity. The method is used for the diagnosis of neuronal diseases and for treating deficient primary haemostasis. Also reducing production of serotonin is used to treat arteriosclerosis and thrombosis, particularly where associated with diabetes mellitus, and to treat excessive (or normal but unwanted) immune system responses, e.g. allergy, (auto) immune diseases, risks associated with pregnancy, particularly pre-eclampsia, and transplant rejection. The present sequence is a neurone-specific TPH protein.
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                               219
325
                                   279
                                                                           281
                                                                                                                                                     221
                                                                                                                                                                                                                              164 WGTIFRELNKLYPTHACR---EYLRNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR 220
                                                                                                                                                                                           159
                                                                                                                                                                                                                                                                    107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                          Local
LSSISELKHALSGHAKVKPFDPKIACKQECLITSFQDVYFVSESFEDAKE
                                                                                                             INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL
                                                                                                                                                     PVAGYLSPRDFLSGLAFRVFHCTQYVRHSSDPLYTPEPDTCHELLGHVPLLAEPSFAQFS
                                                                                                                                                                                      PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                   ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE
                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                      434 AA;
                                                                                                                                                                                                                                                                                                            Conservative
                                                                              -LASIGASEETVOKLAT-----CYFFTVEFGLCKQDGQLRVFGAGL
                                                                                                                                                                                                                                                                                                                              12.0%;
                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                          Score 226.5;
Pred. No. 5.1e
43; Mismatches
                                                                                                                                                                                                                                                                                                                              le-14;
                                                                                                                                                                                                                                                                                                                                            DB 23; Length
                                                                                                                                                                                                                                                                                                            97;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                434;
                                                                                                                                                                                                                                                                                                            27;
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                 278
                                                                                                                                                       280
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4.

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RESULT 8
AAR50185
                                                                                                                                                                   Human; rat; tyrosine hydroxylase; TH; substitution; N-termina enhanced enzymatic activity; wild-type; transformation; dopam Parkinsons disease, Alzheimers disease; brain; encapsulation; selectively permeable; polymer capsule; antibody.
                                                                                                                                                                                                                                                                                                                              04-NOV-1994
                                             05-APR-1994.
                                                                                       US5300436-A.
                                                                                                                               Rattus rattus.
                                                                                                                                                                                                                                                                                 Rat tyrosine hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                         AAR50185;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAR50185 standard; Protein;
13-MAR-1991;
                                                                                                                                                                                                                                                                                                                            (first entry)
  91US-0669446
                                                                                                                                                                                                                                                                                                                                                                                                                      498
                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                      N-terminal;
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dopamine;

13-MAR-1991; 26-JAN-1993;

91US-0669446 93US-0009075

Modified DNA encoding variant tyrosine hydroxylase with N-terminal amino acid substn. and cells contg. it - can to treat diseases associated with defective function of enzyme, e.g. Parkinson's disease or Alzheimer's disease

used

WPI; 1994-125849/15.

Filer D,

Friedhoff AJ,

Goldstein

`3 ĕ

ū,

(UYNY) UNIV NEW YORK STATE.

Disclosure; Fiig 5; 27pp;

English

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353 G-----LASLGASDEEIEKLST-----VYWFTVEFGLCKQNGELKAYGAGLLSS 396
                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAR36740-41 represent the human and rat tyrosine hydroxylase protien respectively. These sequences may be used in the construction of a varient tyrosine hydroxylase which contains at least one amino acid substitution in the N-terminal 55 mino acids. The substitution ocrresponds to an amino acid selected from SerB, SerB1, Arg37, Arg38 (Gln39, Ser40, Leu42, Ile42, Glu43, Asg44, Ala45, Arg46 or Lys47. The enzymatic activity of the varient protein: as at least 3-fold greater than that for the wild type protein. Cells transfected with the DNA encoding these proteins may be used for treating neurological disorders associated with a deficiency in tyrosine hydroxylase or dopamine. These proteins may be used to generate antibodies specific for the varient tyrosine hydroxylases to monitor the enzyme during a treatment regimen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 WKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHFSYYPVS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 GLLSAKDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFSQDI 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   233 WKEVYVTLKGLYATHACREHLEGFOLLERYCGYREDSIPOLEDVSRFLKERTGFOLRPVA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222 GRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 GFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 POELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTSKLE 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         397 YGELLHSLSEEPEVRAFDPDTAAVQPYQDQTYQPVYFVSESFNDAKDKLRNYASRIQ 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; rat; tyrosine hydroxylase; TH; substitution; N-terminal; enhanced enzymatic activity; wild-type; transformation; dopamine; Parkinsons disease; Alzheimers disease; brain; encapsulation; selectively permeable; polymer capsule; antibody.
                                                                                                                                                                                                                Genetically modified tyrosine hydroxylase having increased activity - used for treating neurological disorders e.g. parkinson's and Alzheimer's diseases and affective disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 221; DB 14; Length 498;
larity 27.4%; Pred. No. 22e-13; Conservative 37; Mismatches 99; Indels 36
                                                                                                                           Wu J;
                                                                                                                           Filer D, Friedhoff AJ, Goldstein M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR50184 standard; Protein; 497 AA.
                                                                                                                                                                                                                                                                                                              Disclosure; Fig 5; 20pp; English.
                                  13-MAR-1991; 91US-0669446.
                                                                             (UYNY ) UNIV NEW YORK STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human tyrosine hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 65; Conserva
                                                                                                                                                                        WPI; 1993-175456/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5300436-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
This sequence represents rat tyrosine hydroxylase (TH) and may be used in the production of the varient TH molecules of the invention. These varients contain amino acid substitutions in the N-terminal portion of the molecule, and in the rat molecule these substitutions.

These varients contain amino acid substitutions in the N-terminal portion of the molecule, and in the rat molecule these substitutions.

Arg46. Varients containing one or more of these amino acid substitutions have substantially enhanced enzymatic activity compared to the wild-type enzyme. The most pref. substitution being Ser40 for Tyr or Leu. DNA encoding the TH varients, and cells card for Tyr or Leu. DNA may be used for treating diseases associated with defective function of TH, or dopamine, eg. Parkinsons disease and Alzheimers disease, and effective disorders. The cells can then compared into the brain or encapsulated in a selectively permeable polymer capsule which allows release of the cells products but protects them from attack by the hosts antibodies or cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            287 QLRPVAGLLSAKDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 QFSQDIG------LASLGASDESIEKLST-----VYWFTVEFGLCKQNGELKAYG 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 SSRFSLWKS------YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, rat, tyrosine hydroxylase, substitution, N-terminal, dopamine,
neurological disorder, antibody, varient.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.7%; Pred. No. 1.8e-13;
Matches 65; Conservative 39; Mismatches 103; Indels 36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AEELATWKEVYVTLKGLYATHACREHLEGFQLLERYCGYREDSIPQLEDVSRFLKERTGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR36741 standard; protein; 498 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0669446.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat tyrosine hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                 498 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC used in the production of the varient TH molecules of the invention. CC These varients contain amino acid substitutions in the N-terminal CC portion of the molecule, and in the human molecule these substitutions are pref. at positions Ser19, Ser31, Arg37, Arg38, CC ser40, Leu41, Glu43, Asp44, Al445, Arg46 or Lya47. Varients CC substantially enhanced enzymatic activity compared to the wild-type CC substantially enhanced enzymatic activity compared to the wild-type CC substantially enhanced enzymatic activity compared to the wild-type CC substantially enhanced enzymatic activity compared to the wild-type CC substantially enhanced enzymatic activity compared to the wild-type CC substantially enhanced enzymatic activity compared to the wild-type CC substantially enhanced enzymatic activity compared with this DNA CC may be used for treating diseases associated with defective function CC of TH, or dopamine, eg. Parkinsons disease and Alzheimers disease, and effective disorders. The cells can then be implanted into the brain or encapsulated in a selectively permeable polymer capsule which allows release of the cells products but protects them from CC attack by the hosts antibodies or cells.
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified DNA encoding variant tyrosine hydroxylase with N-terminal amino acid substh. and cells contg. it - can to treat diseases associated with defective function of enzyme, e.g. Parkinson's disease or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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26-JAN-1993;
                  Human tyrosine hydroxylase
                                                                                       AAR36740;
                                                                                                                       AAR36740 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Filer D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-MAR-1991;
                                                  20-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                        216
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                                                                                                                                                                                                                                                                                                                                                        346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 SSRFSLWKS-----YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155
                                                                                                                                                                                                                                                                                                                                                                                                                          286 QLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 AEEIATWKEVYTTLKGLÝATHACGEHLÉÁFALLERFSGYREDNIPQLEDVSRFLKERTGF 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1994-125849/15.
                                                                                                                                                                                                              RIQ 452
                                                                                                                                                                                                                                                                                                                                                                            EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                                                                                              KLE 334
                                                                                                                                                                                                                                                                                   AGLLSSYGELLHCLSEEPEIRAFDPEAAAVQPYQDQTYQSVYFVSESFSDAKDKLRSYAS
                                                                                                                                                                                                                                                                                                                   AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRHF----DELVELTS
                                                                                                                                                                                                                                                                                                                                                      QFSQDIG-----LASLGASDEEIEKLSTLS--
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65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Friedhoff AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497
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                                                    (first entry)
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93US-0009075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                           497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 220; DB 15;
Pred. No. 2.8e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wu J;
                                                                                                                                                                                                                                                                                                                                                        -WFTVEFGLCKONGEVKAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 497;
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Modified-site
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                                                                                                                                                                                                                Human; rat; tyrosine hydroxylase; substitution; N-terminal; dopamine; neurological disorder; antibody; varient.
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                                                                                                                                                                                  Modified-site
                                                                                                                                                                                           Modified-site
                                                                                                                                                                  /note=
222
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152
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                       note=
                                                                                                                                                                      "Phosphorylation site"
                                                                                                                                                                              "Phosphorylation site"
                                                                                                                                                                                       "Phosphorylation site"
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US5212082-A.

/note= "Phosphorylation site"

18-MAY-1993.

13-MAR-1991; 13-MAR-1991; 91US-0669446

91US-0669446

(UYNY) UNIV NEW YORK STATE

Filer D, Friedhoff AJ, Goldstein ζ ž

N-PSDB; AAQ41886

Genetically modified tyrosine hydroxylase having increased activity - used for treating neurological disorders e .g. parkinson's and Allheimer's diseases and affective disorder s e.g. disorders

Disclosure; Fig 6; 20pp; English.

tyrosine hydroxylase protien respectively. These sequences may be used in the construction of a varient tyrosine hydroxylase which contains at least one amino acid substitution in the N-terminal 55 amino acids. The substitution corresponds to an amino acid selected from Ser8 Ser31, Arg37, Arg37, The enzymatic activity of the varient proteins is at least 3-fold greater than that for the wild type protein. Cells transfected with the DNA encoding these protein may be used for treating neurological disorders associated with a deficiency in tyrosine hydroxylase or dopamine. These proteins may be used to generate antibodies specific for the varient tyrosine hydroxylases to monitor the enzyme during a treatment regimen. The sequences given in AAR36740-41 represent the human and rat

Sequence 497 AA;

Length 497;

밁 á В S 밁 S 밁 8 8 Matches Query Match Best Local 332 390 346 276 156 226 112 SSRFSLWKS------YCPRFFLDYLEAFGLLSDFLDH------QAVIKFFELETHF 155 QFSQDIG----QLRPVAGLLSAKDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFA AEEIATWKEVYTTLKGLYATHACGEHLEAFALLERFSGYREDNIPQLEDVSRFLKERTGF KLE 334 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHF----DELVELTS EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG SYYPVSGEVAPHQYLSLLQDRYFPIASVMRTLDKDNESLTPDLIHDLLGHVPWLLHPSFS AGLLSSYGELLHCLSEEPEIRAFDPEAAAVQPYQDQTYQSVYFVSESFSDAKDKLRSYAS Similarity Conservative -LASIGASDEEIEKLSTLS---11.6%; Score 219; DB 14; 26.7%; Pred. No. 3.5e-13; tive 38; Mismatches 104; 104; WFTVEFGLCKQNGEVKAYG Indels 36; Gaps 345 331 275 215 285 389 ა •

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493 PASTAVQPYQDQEYQPIYYVAESFEDAKDKFRRWVSTMSRPFEVRFN-PHTERVEVLDSV 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hybrid molecules are produced by covalently linking (1) a portion (A) of the binding domain of a cell-binding ligand, allowing binding of the mol. to an animal cell; a portion (B) of a translocation domain of a protein able to translocate (C) across the cell cytoplamic membrane, and and (3) a portion (C) which is to be introduced into the cell. (A) is derived from a steroid or polypeptide hormone, a single-chair analogue of a monoclonal antibody able to bind an antigen expressed on the cell surface, or a polypeptide toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybrid, fusion, membrane translocation, binding region; HIV; infection; toxin; steroid; hormone; monoclonal antibody; antigen; diphtheria; exctoxin; phenylketonuria; cholera; interleukin; IL-2; protease; epidermal growth factor; ricin; tetanus; hexosaminidase; Shiga-like toxin A; SLT-A; PH; ligand; insulin; nuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hybrid molecules for targetting chemical entity to cell - have membrane trans-locating and cell binding-regions and used to treat HIV infection, genetic enzyme-deficiency disorders etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 213.5; DB 12; Length 452; Pred. No. 1.1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Fig 13(1-3); 59pp; English
                                                                                                                                                                                                                                                                            AAR13119 standard; Protein; 452 AA.
                                                             331 SKLEWMLDQGLLESIPLYN 349
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26.6%;
                                                                                              552 DKLETLVHQMNTEILHLTN 570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phenylalanine hydroxylase.
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N-PSDB; AAQ12712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                          AAR13119;
                                                                                                                                                                                                                  RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLI6176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       389 STQYVRHVNSPYHTPEPDSIHELLGHMPLLADPSFAQFSQEIG------LASLGASD 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 DYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        329 EYRAAFQKLQDEQIFVETRLPQLQEMSDFLRKNTGFSLRPAAGLLTARDFLASLAFRIFQ 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292 --NVRVLPLE----------LDQIIRLPFNTSTPQFTLFSIRHFD--FLVELT 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFID-----
                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 21438; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster polypeptide SEQ ID NO 21438.
                                                                                                                                                                          ABB64882 standard; Protein; 579 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li PWD,
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC, Adams M,
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(ABB57737-ABB72072)
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450 RIQ 452
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AAW25788 standard;

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This protein comprises for human phenylalanine hydroxylase (PH). A DNA molecule (see AAT91638) encoding PH was used to construct a PH-diphtheria toxin B' gene that was expressed in E. coli. The resulting hybrid protein can be used in the treatment of phenylketonuria. The active PH enzyme is targeted to, and incorporated into, the broad range of cells which native diphtheria normally attacks, achieving the widespread therapy that is needed for this inherited disorder. Claimed hybrid proteins comprise a translocation domain and a cell binding domain. They can be used for the delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation
                                                                                                                                                                                                                                                                                                                                                                     New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a translocation domain of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phenylalanine hydroxylase; human; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B';
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human phenylalanine
                                                                                                                                                                                                                                                                                                                       Example 5; Fig 13A-C; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1997-470103/43.
DB; AAT91639.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGLLSSFGELOYCLSEKPKLLPLELEKTAIONYTVTEFOPLYYVAESFNDAKE 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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84US-0618199.

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89US-0456095.

90US-0538276.

93US-0102387.
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Best Local :
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25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shiga-like toxin; p
cytosol; therapy; q
adipocyte; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poiso; adipocyte; cancer; virus; infection; antibody.
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                                                            Recombinant DNA molecule encoding a three part hybrid protein used the treatment of Aids and genetic deficiency diseases - \,
                                                                                                                                              WPI; 1999-632431/54.
N-PSDB; AAZ30664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-AUG-1993;
07-JUN-1984;
            Example 5; Fig 13; 31pp; English
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                                                                                                                                                                                                                      Murphy
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85US-0742554.
89US-0456095.
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Pred. No. 1.1e-12;
4; Mismatches 100;
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RESULT 1

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AX AAW

XX AX

AX AAW

XX Cell

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KW Phe

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Murphy

(SERA-)

SERAGEN

27-JUN-1991; 07-JUN-1984; 07-JUN-1984;

25-APR-1985; 07-JUN-1985;

US5668255-A.

Homo sapiens phenylketonuria;

16-SEP-1997

The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of a ranalocation domain of a naturally cocurring protein of the binding domain of a naturally cocurring protein of a ranalocation domain of a naturally cocurring protein comprises a portion of a translocation domain of a naturally cocurring protein coxin, which translocation domain of a naturally cocurring protein coxin, which translocate the third both in part of the across the cytoplaemic coxin, which translocate the third both of the call, and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the human phenylalanine hydroxylase for use in generating the hybrid molecule enables the direction of appropriate invention. The hybrid molecule enables the direction of appropriate cortexage or affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is especially used in treating energing the missing function, to supplying the missing function, to supplying cellular levels of a particular enayme or a scarce precursor or cofactor, to direction of a praticular enayme or cortex precursor or cofactor, to direction such as particular enayme or a scarce precursor or cofactor, to direction such as (involved in the process of getting non-therapeutic substances such as contractable labels into cells.

452 AA; Sequence

Query Match

4 104 RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155 156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215 241 RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 300 216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275 301 QFSQEIG-----LASLGAPDEYIEKLAT-----IYWFTVEFGLCKQGDSIKAYG 344 / Match 11.3%; Score 213.5; DB 20; Length 452; Local Similarity 26.6%; Pred, No. 1.1e-12; Ordels 27; Gaps e8 62; Conservative 44; Mismatches 100; Indels 27; Gaps 276 AVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRHFDELVE 328 Matches ò qq à g ò

AAY78593 standard; Protein; 452 AA

345 AGLLSSFGELOYCLSEKPKLLPLELEKTAIONYTVTEFOPLYYVAESFNDAKE 397

Human phenylalanine hydroxylase protein sequence. 05-MAY-2000 (first entry)

Phenylalanine hydroxylase; translocation domain; cell destruction; cell binding domain; genetic deficiency disease; cell targetting; cancer; adipocyte; enzyme delivery; anti-viral; HIV.

US6022950-A

07-JUN-1995;

84US-0618199. 91US-0722484. 85US-0726808. 95US-0479510. 07-JUN-1984; 27-JUN-1991; 25-APR-1985;

85US-0742554. 89US-0456095. 90US-0538276. 93US-0102387. WPI; 2000-160390/14. (SERA-) SERAGEN INC N-PSDB; AAZ90020. 04-AUG-1993; 22-DEC-1989; Murphy JR;

New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and HIV infections -Example 5; Fig 13; 32pp; English.

This sequence represents the phenylalanine hydroxylase protein sequence.

The encoded protein can be included in the hybrid protein of the included in the hybrid protein of the consequence. The encoded protein can be included in the hybrid protein of the consequence is targeted to. The hybrid protein comprises a first part which is a portion of the binding domain of a call-binding ligand, effective to cause the hybrid molecule to bind to a call binding ligand, effective to part comprises a portion of a translocation domain of anturally occurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates the third part comprises a chemical and into the cytosol of the call, where each of the first and third entity to be introduced into the call, where each of the first and third entity to be introduced into the second and third part comprises a chemical covalent bond attaching the second and third part is cleavable. The phenylalanine hydroxylase protein can form part of the third portion of the translocation domain transfers the hybrid molecule across the call and the translocation domain through a cleavable bond, can then carry out its cleavable. The function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to affected calls an enzyme supplying the missing function, to supplement callained revels of a particular enzyme or a scarce precursor or cofactor, to direct toxins or other poisons to destroy particular calls (auto as adipocytes, cancer calls, or a trunslation of the complexed calls an enzyme such as a trunslations and a particular enzyme or a calls calls antibodies to viral infections.

452 AA; Sequence

104 RNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155 184 KKTWGTVFKTLKSLYKTHA---CYBYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQTCTGF 240 156 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215 241 RLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 300 216 EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG 275 301 QFSQEIG-----LASLGAPDEYIEKLAT-----IYWFTVEFGLCKQGDSIKAYG 344 27; Gaps 11.3%; Score 213.5; DB 21; Length 452; 26.6%; Pred. No. 1.1e-12; ive 44; Mismatches 100; Indels 27; 276 AVLISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVE 328 Similarity 26.6 62; Conservative Query Match Local Matches

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AAB13327;

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                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is Cod-5 from Caenorhabditis elegans. Cod-5 is the aromatic amino acid hydroxylase that synthesises serotonin from CC precursor L tryptophan. The cod-5 gene was knocked out to produce mutants completely lacking in serotonin. These mutants were found to have defects CC in metabolic control. A number of C. elegans proteins that have mammalian homologues acting in the insulin signalling pathway were also identified. The C. elegans age-1 gene encodes a homologue of the mammalian PI 3-kinase whilst daf-2 encodes a homologue of the mammalian cC insulin receptor. The C. elegans AKT kinase and PKB kinase act downstream CC insulin receptor. The C. elegans PTEN lipid phosphatase homologue, CC insulin signalling. The C. elegans PTEN lipid phosphatase homologue, CC DAF-18, has been found to act upstream of AKT in the pathway. This CC discovery has enabled mammalian PTEN action to be mapped to the insulin CC signalling pathway. Conserved DAF motifs can be used to design probes to conclude the conserved DAF motifs can be used to design probes to predisposition towards the development of glucose intolerance conditions, and chestry and disherers.
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Best Local S
Matches 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing and treating obesity and impaired glucose tolerance using modulators of daf-18 expression and/or activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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472
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                                                                                                                                                                                                                                                                                                                 104 RNLW---YRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH-----QAVIKFFELETHF 155
                                                                                                                                                                                                              SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215
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DB; AAA91624.
                                                                    ENGSNHERFKVYGAGLLSSAGELQHAVEGSATIIRFDPDRVVEQECLITTFQSAYFYTRN
                                                                                                     ---ENHEGRKAYGAVLISSPOELGHAFIDNVRVLPLELDQIIRLPFNTSTPOETLFSIRH 322
                                                                                                                                        QFSQEIG-----LASLGASEEDLKKLATL-----YFFSIEFGLSSDDAADSPVK 411
                                                                                                                                                                         EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLI------
                                                                                                                                                                                                                                                                                    RKTWGIIYRKLR---ELHKKHACKQFLDNFELLERHCGYSENNIPQLEDICKFLKAKTGF 307
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                                                                                                                                                                                                                                                                                                                                                    10.9%; Score 206.5; DB 21; 25.2%; Pred. No. 7.1e-12; tive 47; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                        Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                         Length 532;
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104 RNIWYRLLSSRESIWKSYCPREFIDYLEAFGLISDF-LDH------QAVIKFFELETHF 155

Indels 27;

Gaps

RIRPVAGLISSRDFIGDLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFA 334 SYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFS 215 KKTWGTVFKTLKSLYKTHA---CYEYNHIFPLLEKYCASHEDNIPQLEDVSQFLQTCTGF 274

EFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYG

----LASLGAPDESIEKL-----

-APIYWFTVEFGLCKQGDSIKAYG

275

Local

Similarity 28., 58; Conservative

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ANUSULT 18
ANUSO703
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ACC AAUSO
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                                                                                                                                                                                                            The invention relates to novel human secreted polypeptides. The polypeptides and antibodies to the polypeptides are useful for certaining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for cidentifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to abscrant expression or physiological interactions of the polypeptide. Vectors comprising the nucleic acids encoding the polypeptides and cells genetically engineered to express them are also useful for producing the proteins. CC The proteins are useful in genetic vaccination, testing and concerning the used as mutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in come, cartilage, tendon and/or nerve tissue growth or regeneration; to mean of leukaemias. ANU29510-ANU31304 represent the amino acid cc sequences of novel human secreted proteins of the invention.
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                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding a range of human polypeptides, useful in genetic vaccination, testing and therapy - \,
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26-JAN-2001; 2001US-0770160.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; Page 332; 765pp; English.
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                                                                                                                                                      491 AA;
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10.6%; Score 199.5; DB 22; 28.4%; Pred. No. 3.2e-11; tive 36; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491
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279 ISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
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                                                       339 QGL--LESIP----LYNQEKYLSGFEVL 360
                                                                              397 KTIKFANSIPRPFGVRYN--AYTQSVEVL 423
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                                                                                                                                                    ABB71186 standard; Protein; 555 AA.
                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231.
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11-JUL-2000; 2000US-0614150.
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Best Local Similarity 32.0%
Matches 47; Conservative
                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                          Drosophila melanogaster.
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                                                                                                                                                                                                                                                                              pharmaceutical
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                                                                                                                                                                                                           26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 PVAGLLSSRDFLAGLAFRVFHSTQYIRHPSKPMYTPEPDVCHELMGHVPLFADPAFAQFS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 WYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSD---FLDH-----QAVIKFFELETHFSYY 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159 PVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFF 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 INMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  303 QEIG-----LASLGAPDDYIEKLST-----IFWFTVEYGVCRQEGELKAYGAGL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 10.3%; Score 194; DB 22; Length 452; Local Similarity 27.1%; Pred. No. 1e-10; es 73; Conservative 39; Mismatches 111; Indels 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 WGIIFRNLTKLYKTHACR---EYNHVFPLLVDNCGFREDNIPQLEDVSNFLRDCTGFTLR 242
                                                                                                                                                                                                                        Drosophila, developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 10623; 21pp + Sequence Listing; English.
                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 10623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myers EW;
                                                                                                          ABB61277 standard; Protein; 452 AA
             276 AVLISSPQELGHAFIDNVRVLPLE 299
                             379 AGLLSSFGEFQYCLSEKPKLLPLE 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Li PWD,
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                                                                                                                                                                                                                                       pharmaceutical.
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interactions -
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347 LSSYGELEYCLTDKPQLKDFE-----PEVTGV---TKYPITQFQPLYYVADSFETAKE 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 QAVIKEPELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLIHDL 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 QDVSVYLKRKTGFQLRPVAGYLSPRDFLSGLAFRVFHCTQYIRHSSDPFYTPEPDCCHEL 343
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32.0%; Pred. NO. Se-0.95; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                               Query Match
Best Local S
Matches 37
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26-JAN-2001; 2001US-0770160
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59
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                                                                                                                           Local Similarity les 37; Conserv
                        WFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLELDQ 302
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WFTVEFGLCKQGDSIKAYGAGLLSSFGELQYCLSEKPKLLPLELEK 104
                                                               DICHELLGHVPLFSDRSFAQFSQEIG---
                                                                                           DLIHDLIGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCF 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                            200 AA;
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                                                                                                                           8.1%; Score 153; DB 22;
34.9%; Pred. No. 4.3e-07;
tive 21; Mismatches 32;
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                                                                 -LASIGAPDEYIEKLAT----
                                                                                                                               32;
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RESULT 22
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                                                                                                                                                                                                                           The patent discloses novel cells comprising a nucleic acid encoding cas gene product having phenylalanine hydroxylase (phA) activity such cas phenylalanine hydroxylase (phA), 4a-carbinolamine dehydratase (phB) and aromatic aminotransferase (phC), which are derived from a prokaryotic organism. The patent also relates to fusion proteins comprising a protein enhancing and/or stabilising the patent also relates to fusion the patent also relates to fusion the patent also relates to fusion the patent also relates to fusion the patent also relates to fusion the patent also relates and useful for producing PAH. The sequences of the invention are also useful for producing PAH. The sequences of the invention are also useful for producing PAH. The sequences of the invention are also useful for producing PAH. The sequences of the invention are also useful for producing PAH. The sequence food product (animal protein such as a milk protein derived from casein, globulin or a whey protein the food product starting material with the cells or fusion proteins cannot found that do not cause phenylketonuria material is converted into compounds that do not cause phenylketonuria (PKU) by the enzymatically active product. PAH enzyme is useful for menufacturing a medicament for treating PAH, which is an inherited menufacturing and metabolites that can cause impaired brain function. The present sequence is a peptide sequence of phhAB custom protein.
                             Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel recombinant cells comprising a nucleic acid encoding a gene product having phenylalanine hydroxylase activity, that is derived a prokaryotic organism, is useful for treating phenylketonuria in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phenylalanine hydroxylase; PAH; phhA; 4a-carbinolamine dehydratase; phl aromatic aminotransferase; phhC; milk protein; animal protein; casein; proteinaceous food product; globulin; whey protein; phenylketonuria; PKU; inherited metabolic disorder; impaired brain function; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE11092 standard; peptide; 64 AA.
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Arnau J, Jensen SH,
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                                                                                                                                        Sequence
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                                                                                                                                                                                                               fusion protein.
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                                                                                                                                        64 AA;
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5.8%; Score 109.5;
35.6%; Pred. No. 0.0;
tive 15; Mismatches
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Gjetting T,
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, Nielsen
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E;
                                                              DB 22;
                                                                  Length
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Matches

al Similarity 21; Conserv

Conservative

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Indels

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29-MAY-2001; 2001WO-US10836.
                                                                                             30-MAY-2000; 2000US-206132P.
29-AUG-2000; 2000US-228716P.
                                                                                                                                                                                                                                 systemic cytokine damage.
                                                                                                               Shimkets RA, Leach MD;
                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                      WPI; 2002-106308/14.
                                                          myasthenia gravis.
                                                                                                                         N-PSDB; ABN21920
                                                                       WO200192523-A2.
                                                                Homo sapiens.
                  24-JUN-2002
                                                                               06-DEC-2001
                                                                                                                                                                                                                                                    Sequence
           ABP06168;
ABP06168
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.7%; Score 108.5; DB 22; Length 1501;
22.4%; Pred. No. 0.24
ive 58; Mismarches 130; Indels 107; Gaps
       126 FLDYLEAFGLLSDFLDH-QAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPIASVM 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 SILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSS-RFSLWKSYCPR 124
                                                    10 PKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHK----CI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 10374; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 10374.
                                                                                                                                  185 RTLDXDNFSLTPDLIHDLLGHVPWLLHPSFS 215
                                                                                                                                                                               74 RRPDQIDYIAEPDLFHDLFGHVPVLMNPLFA 104
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                                                                                                                                                                                                                                                                                                                                                              ABB61194 standard; Protein; 1501 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL05297.
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Matches 85;
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                                                                                                                                                                                                                                                                                       hyperproliferative disorder, psoriasis; benign tumour; haemorrhage, degenerative disorder, osteoarthritis; neurodegenerative disorder, cardiovascular disease, diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiendy; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders
                                                                                                                                                                                                                                                      Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
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5.8%; Score 109.5; DB 2
Best Local Similarity 28.6%; Pred. No. 0.0041;
Matches 26; Conservative 20; Mismatches 44
                                                                                                                                                                                              Human ORFX protein sequence SEQ ID NO:12318.
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ABP06168 standard; Protein; 104 AA
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                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176) and the encoded proteins
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 Sequence
                           sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                             Disclosure; SEQ ID NO 23847; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                   New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                               WPI; 2001-656860/75.
N-PSDB; ABL09788.
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                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRGFRORVRLPPLVNEKSGQLNENTADFIRPFAKKWREKSIFQVLLHYRAARFQDFVNLS
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                                                                                                                                                                                                                                                                                                                     Adams M,
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2000US-0614150
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and c
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                                           WIPO
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Query Match

58

Score 103.5;

BB 22;

Length 1782;

The invention relates to improving the production of a secondary metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A), an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment;
                                                                                                                                                                                                                                                                                                                                 New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP35686 standard; Protein;
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as ovalicin), a glucan synthase inhibitor, gliotoxin family of compounds, a fungal toxin, a modulator of cell surface receptor signalling; a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biomass required for the production, which translates into decrease in the waste that must be handled in downstream processing. The sequences given in records ABP3575-ABP3572 represent ZBC proteins.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                 325
                                                                                                                                                                                                                              Query Match 5.4%; Score 102; DB 23; Length 563; Best Local Similarity 21.1%; Pred. No. 0.27; Matches 80; Conservative 56; Mismatches 142; Indels 102; Gaps
                                                                                                                                                                                                                                                                                                                       185 TLLPIIAATIQLSDLPDVILNFYNSAGI-----TPLESSRLINLKLNEISEQEYKHLCLP 239
                                                                                                                                                                                                                                                                                                                                                     67 ILEFFKNILLFVHLLSLSKNQREGCSTDM-----AVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                121 YCPRFFLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFPI 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 ---LRCFFNDDISYN---FHLLLGR---LLDCGVSIYKSVHSLTVSKFIDKLESYESQLS 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377 LILVDIEAKFYDPSNEDIQFRYIFLKMVFWTARVNLYQCFITLDSGILEDBE-----T 429
                                                                                                                                                                                                                                                                                                                                                                                240 DKEIIQMLLLRAYATKFRTRIRGVNTDLCRSIHVSTLVTPLF--QVTEKIGKNTSDLWFA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 RI------QTLQSNLIAIVRCFW------FTVESGLIENHEGRKAYGAV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 LISSPQELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWML 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430 IIGN---LGESCIQCVRLL---ISQITIL-----EKRGWLLVALLEIIHALMLAAFCR 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; primer; detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                         7 TLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCIS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                               298 LC-----EIDGL-----ECVLKY---RPPFIQHDTYGRLKP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:14279.
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11-JAN-2000; 2000JP-0118776.
02-MAX-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                    563 AA;
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The present invention describes primer sets for synthesising 5602
[11] Length cDNAs defined in the specification. Where a primer set
[22] Comprises: (a) an oligo-dT primer and an oligomucleotide complementary
[23] Comprises: (a) an oligo-dT primer and an oligomucleotide complementary
[24] Comprises one of
[25] Complementary strand of a polynucleotide which comprises one of
[26] Complementary strand of a polynucleotide which specification, where the
[27] Complementary strand of a polynucleotide which comprises a 5'-end
[28] Sequence and an oligomucleotide comprises a 5'-end
[27] Sequence and an oligomucleotide comprises a 5'-end
[28] Sequence complementary to a
[28] Sequence complementary to a
[28] Sequence complementary to a
[28] Sequence complementary to a
[29] Sequence of a polynucleotide which comprises a 5'-end
[29] Sequence and an oligomucleotide sequence, where the
[28] Sequence of a polynucleotide sequence of sequence
[29] Sequence of a polynucleotide sequence
[20] Sequence of a polynucleotide sequence
[20] Sequence of a polynucleotide sequence
[20] Sequence of sequence
[21] Sequence
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                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 lill-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.3%; Score 101; DB 22; Length 456;
23.3%; Pred. No. 0.28; Indels 128; Gaps
ive 41; Mismatches 98; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ----VLLDVAYAYĞKLSFHQTQVSQRLATDLLSLMPSLTSGEVAHCAKSFALLKWLSL--- 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 QRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPLE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 KCISILEFF-KNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSY 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 ----PLFGAFAQH-VLNRAQDITLPHLCSVLLAFARLNFH--PDQEDQFFSLVHEKLGSE 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 226 LPGLEPALQVDLVWALCVLQQAREAELQAVLHPEF--------HIQFLGGKS 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 QKDQNTFQKLLHI-----NATALLEYPE---YSGPLLPASAVAPGPSALDR-KVTPLQ 318
                                                                                                           Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 FSYYPVSGFVAPHQYLSLLQDRYFP-IASVMRTLDKDNFSLTPD-----LIHDLLG--
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                                                                                                Saito K, Y.
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID 14279; 2537pp + CD ROM; English.
                                                                                                Isogai T, Nishikawa T, Hayashi K, S
Sugiyama T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB59689 standard; Protein; 2042 AA
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                                                                                     Ota T, Is
Ishii S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventueseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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11-JUL-2000; 2000US-0614150.
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                                                                                                1047
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                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form specification, but was obtained in electronic i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 5859; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-celinteractions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001;
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SPQELGHAFID--NVRVLPLELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD 338
                                          IIHAF--IILLTYSNSNMPESIPILD-----YWFP------PGRPAPVAFLPS
                                                                                                                                                                                                          LSGLKIIFRHSGDF--ENEW--LLKSLQQIPHFYEVKPFIIPQLRAACQVENCPELIMAY 986
                                                                                                                                                                                                                                   STDMAVV---STPFFNRNLWYRLLSS------
                                                                                                                                                                                                                                                                IINEENSRDAEL-----VNFLRNLIFDGNLSHQIVCELLDYIFRRLSSTVKQSRVAA 930
                                                                                                                                                                                                                                                                                          2001-656860/75.
                                                                   MGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLIS
                                                                                                                        VAPHQYLSLLQDRYFPIASVMRTLDKDNFSLTPDLI---HDLLGHVPWLLHPSFSEFFIN
                                                                                                                                                                               LE---AFGL---LSDFLDH-----QAVIKFFELETH-----FSYYPVSG-----F
                                                                                                 VMFNNYIIKLREYHEPY-----EWTEYPDLLMVQFDDGVQLP--LH-----IN
                                                                                                                                                    IQFITAHTLNDPVNEMLDHVIDMAQLIVERSTMFQHIIISQEDYDYVPDENRIQTLKCLF
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                Score 101;
Pred. No. 2
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format directly from
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19 KLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKNLLFVH 78

Query Match Best Local : Matches 9

1 Similarity 19.9

5.2%; S 19.9%; P Live 77;

Score 99; DB Pred. No. 1.1; 7; Mismatches

DB 19; ; 1.1; hes 122;

Length 924;
; Indels 164;

Gaps

27;

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                                                      The present sequence represents a p102 protein. This protein is present CC the secretion associated 175 (SA-175) complex. Bight proteins form the CSA-175 complex, which binds a syntaxin-containing (SC) complex. The CSA-175 polypeptides and nucleotide sequences encoding them can be used CC for screening for compounds which modulate vesicular release involved in CC enhance binding between the SA-175 and SC complexes may be used to treat CC an affective disorder such as depression, manic-depressive disorders and CC disease or Huntington's disease. Compounds which inhibit binding between the treat CC disease or Huntington's disease. Compounds which inhibit binding between the SA-175 and SC complexes may be used to treat a disorder of thought, CC such as schizophrenia, or for anaesthesia. The compounds can also be used to inhervent in the endocrine system for treatment of hormonal CC imbalances, the immune system for intervention in antigen processing, as ererted immunomodulators, and viral processing, as well as sell-as applications, such as regulation of membrane trafficking CC during rapid cell division.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1128 MPQEQVQLLPDWLKLKMIRSSVDRLIEAALNDLTPDQIVLFVQNFGTPVNSMSKLLAMLD 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated vesicule secretion associated poly:peptide(s) - develop products for treating e.g. effective disorder, neurodegenerative disease, hormone imbalances, immune system
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    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disorders or tumours
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N-PSDB; AAV42653.
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    924 AA;
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Arnau J, Jensen SH,
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                                                     1024 AA;
                                                                                        Local Similarity
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                                     79 LLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRF----SLWKSYCPRFFLDYLEAF 133
                                                              287 PLNIKRNIQKG---DYDVVIND-----YEKAKSLFGKTEVQVFKKY-----YAËVE 329
                                                                                                              330 AGIEDL--RELLIKKL-LETPSTLHDOKRYIRYLSDLHAPGDPAWQCIGAQHKWTLKLMQ 386
                                                                                                                                                                   DCKEGHMKSLKGNPGPHSPM----LDLDN-----DARPSVLGHLSQTASLKRGSSFQS 435
                                                                                                                                                                                              ------PSFSEFFINM--GRLFTKVIEK---VQALPSK 238
                                                                                                                                                                                                                   436 GRDDTWRYKTPHRVAFVEKLTKLVLSQLPNFWKLWISYVNGSLFSETAEKSGQIERSKNV 495
                                                                                                                                                                                                                                               KQR-----IQTLQSNLIAIVR--CFWFTVESGLIENHEGRKAYGAVLIS---SPQELG 286
                                                                                                                                                                                                                                                                      496 RQRQNDFKKMIQEVMHSLVKLIRGALLPFSLREG-----DGRQ-YGGWEVQAELSGQWLA 549
                                                                                                                                                                                                                                                                                                 HAFIDNVRV------HPLELDQIIRLPFNTSTPQETLFSIR-------HFDELV 327
                                                                                                                                                                                                                                                                                                                         550 HV-İQTIRLTYESLTALEIPNDMLÖİİ------ÖDLILDLRIHCIMVTLQHTAEEIK 599
                                                                                        -----APHQY-LSLLQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated or recombinant immunogenic polypeptides from Mycoplasma genitalium have mol.wt. of 16 kba (AAM19603) (WGO74) and 116 kba (AAM19604) (WGO75). They are homologues of 16 and 116 kba proteins (see also AAW19601-02) obtd. from Mycoplasma pneumoniae. A genomic DNA sequence of M. genitalium contains contiguous open reading frames that code for the 2 polypeptides. Mycoplasma 16 or 116 kba proteins, or immunogenic fragments that include a T or B cell epitope, can be used in vaccines for prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycoplasma; immunogen; vaccine; diagnosis; pneumonia; inflammation.
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                                                                                                                                           D-----RYFFIASVMRTLDKDNFSLTPDLIHDLLGHV------
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                                                                                        134 GLLSDFLDHQAVIKFFELETHFSYYPVSGFV-----
                                                                                                                                                                                                                                                                                                                                                  328 ELTSKLEWMLDQGLLESIPLYNQEKYLSGFEVL 360
                                                                                                                                                                                                                                                                                                                                                                    600 RLAEKEDWIVDNEGLTSLPCQFEQSIVHSLQSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW19604 standard; Protein; 1024 AA
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                                                                                                                                                                                            207 ----PWLLH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         758 VNVNFHIDARLLTAELQNTVFSNPK-----PVIKSPVELSKSLFEVWKTIFENSVNQI 810
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        564 QQTDSLKNLFSV----IGDILSETNVNKITLHAVKNNELLSLVETASTLKIKHL----- 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 OREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDHOAV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 -----ELLNFFPDTKDITPT 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 IK--FFELETH-----FSYYPVSGFVAPHQYLSLLQDRYFPIASVMRTLDKDNF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 IKKVLFESENYKTLRKKYENEGFPGYHWAKFIVPGTFNSAENTFYSAI------DKT 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         699 KSIRDLFADML-FGKSLESVNDSDSFIKINGSFTLITKNDNLNLLPNYHSLITKNVGYQI 757
                                                                                                                                                                                                                                                                                                                                                                                                                             29 QNSQSLQRAYSTPYSYYRIILQKENKEK---QALARHKCISILEFFKNLLFVHLLSLSKN 85
Mycoplasma infections, partic, in humans. They can also be used diagnostically to detect Mycoplasma, or to raise antibodies useful in immunoasanys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               193 SLTPDLIHDLLGHVPWLLHPSFSEFFINMGRLFT-----KVIEKVQALPSKKQRIQT
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Gjetting T, Nielsen E;
                                                                                                                                                                                                                                               5.2%; Score 98.5; DB 18; Length 1024; illarity 19.9%; Pred. No. 1.4; Conservative 41; Mismatches 134; Indels 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 LQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   811 LKKEYTFKDNLKFFFFKADGSSRLEFDLSKPDQRVIPFAFVD 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses novel cells comprising a nucleic acid encoding car gene product having phenylalanine hydroxylase (PAH) activity such car sphenylalanine hydroxylase (phhA), 4-carbinolamine dehydratese (CC as phenylalanine hydroxylase (phhA), 4-carbinolamine dehydratese (CC (phhB) and aromatic aminotransferase (phhC), which are derived for producing proteins comprising a protein enhancing and/or stabilising the proteins comprising a protein enhancing and/or stabilising the for producing pAH. The sequences of the invention are also useful CC for preparing a proteinaceous food product (animal protein such car a milk protein derived from casein, globulin or a whey protein case a milk protein derived from casein, globulin or a whey protein case the food product starting material which the cells or fusion proteins contacting case that at least part of the phenylalanine content of the starting material is converted into compounds that do not cause phenylatoruria (PKU) by the enzymatically active product. PAH enzyme is useful for manufacturing a medicament for treating PKU, which is an inherited cate of the content of the phenylalanine on the body of the content. The present sequence is a peptide sequence of phhAB crustinn protein.
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Matches 15
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   The present invention provides the protein and coding sequences of
                                                            Example 2; SEQ ID NO 474; 509pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-SEP-2001; 2001WO-US26015
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                                                                                                                 An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC.
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DB; ABN32392.
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Yang Y,
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Wehrman
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T, Drmanac
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Pred. No.
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RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            novel human proteins. These were isolated from expressed sequences tags (ESTS). They can be used to stimulate cell growth, to regulate haematopoisesis e.g. to treat aplastic anaemia, to help tissue regrowth e.g. in burn treatment, to regulate the immune system e.g. to treat multiple sclerosis, to regulate activin or inhibin e.g. to treat inferrility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                           Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis; sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine; neutralising epitope.
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                                                                                                                                                                                                                                                                                                                                                                                                   C. pneumoniae protein involved in metabolism of nucleic acids.
                                                                                                                                       04-NOV-1998;
21-NOV-1997;
                                                                                                                                                                                                                           03-JUN-1999.
                                                                                                                                                                                                                                                                                               Chlamydia pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY35368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY35368 standard; Protein;
Genome sequence of Chlamydia pneumoniae
                                   WPI; 1999-357842/30
                                                                     Griffais R;
                                                                                                                                                                                           20-NOV-1998;
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                                                                                                       (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 KLROSLSLFFONS-----OSLORAYSTPYSYYRIILOKENKEKOALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 L-LFVHLLSLSKNQREGCSTDM-AVVSTPFFNRNLWYRLLSSRFSLW-------KSY 121
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97FR-0014673.
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
                                             AMY34584-Y35879 represent the proteins encoded by all the open reading frames in the complete genome (see AMX91990) of Chlamydia pneumoniae.

C. pneumoniae causes respiratory disease such as pneumonia and bronchius and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent citis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see AMY3484-Y3589) can be used in immunogenic compositions as vaccines. Vectors containing C. pneumoniae especially where the vector directs the expression of a neutralising epitope of C. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                   5.1%; Score 97; DB 20; Length 419;
22.1%; Pred. No. 0.59;
tive 51; Mismatches 117; Indels 104; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 -VMRTLDKDNF----SLTPDLIHDL-LGHVPWLLHPSFSEFFINMGRLFTKVIEKVQAL 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 LLSDFLDHQAVIKFFELETH---FSYYPVS-GFVAPHQYLSLLQDRYFPIAS----- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 WVERTLEFCNLDRIFNTLLVDLQEYLKQNYTPW-LSPDESVF-----ALEKLLSS 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 PSKKORIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGH---AFIDN 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 SEAQPVVQAL----------REQYQLVLIDEFQDTDKQQWSIFSN 390
                                                                                                                                                                                                                                                                                                                                                                                                                         96 ----VVSTPFFNR------NLMY-RLLSSRFSLWKSYCPRFFLDYLEA-----FG 134
                                                                                                                                                                                                                                                                                                                                                      46 RIILOKENKEKQALARHKCISIL--EFFKNLLF---VHLLSLSKNOREGCSTDMA---- 95
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               Page 1164; Disclosure; 1912pp; English.
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99US-0123180.
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05-MAR-1999;
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25-MAR-1999;
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19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

99US-0144325. 99US-0144331. 99US-0144332. 99US-0144333.

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n fragment SEQ ID NO: 38083.	nal transduction pathway; metabolic pathway; c mapping; gene expression control; promoter;						•	•		٠						•	•									_		-																			
17-OCT-2000 (first entry) Arabidopsis thaliana protein fragment	ification; signal assay; genetic ma	equence.	haliana.			2000EP-0301439		99US-0121825. 99US-0123180.	99US-0123548	99US-0125788	99US-0126785	99US-0127462	99US-UIZ8234 99US-0128714	99US-0129845	99US-0130077	99US-0130510	99US-0130891	99US-0132048	99US-0132407	99US-0132485	99US-0132486	99US-0132487 99US-0132863	99US-0134256	99US-0134218	99US-0134221	99US-0134370	99US-0134941	99US-0135124	99US-0135353	99US-0136021	99US-0136392 99US-0136782	99US-0137222	99US-U13/528 99US-0137502	99US-0137724	99US-0138094 99US-0138540	99US-0138847	99US-0139119	99US-0139453	99US-0139492	99US-0139454	99US-0139456	99US-0139457	99US-0139455	99US-0139460	99US-0139461 99US-0139462	99US-0139463	99US-0139750
17-OCT-2000 Arabidopsis tl	Protein identification; hybridisation assay; ger	termination s	Arabidopsis thaliana	EP1033405-A2.	06-SEP-2000.	25-FEB-2000:		25-FEB-1999; 05-MAR-1999;	09-MAR-1999;	23-MAR-1999;	29-MAR-1999;	01-APR-1999;	08-APR-1999;	16-APR-1999;	19-APR-1999; 21-APR-1999;	23-APR-1999;	23-APR-1999;	30-APR-1999;	30-APR-1999;	05-MAY-1999;	06-MAY-1999;	07-MAY-1999;	11-MAY-1999;	14-MAY-1999; 14-MAY-1999;	14-MAY-1999;	14-MAY-1999;	19-MAY-1999;	20-MAY-1999;	21-MAY-1999; 24-MAY-1999.	25-MAY-1999;	28-MAY-1999;	01-JUN-1999;	04-JUN-1999;	07-JUN-1999;	10-JUN-1999;	10-JUN-1999;	14-JUN-1999; 16-JUN-1999;	16-JUN-1999;	17-JUN-1999;	18-00N-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;	18-JUN-1999;
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27-AUG-1999; 27-AUG-1999; 30-AUG-1999;

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99US-0154779 99US-0155139 99US-0155486

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166 P-HQ---YLSL-LQDRYFPIASVMRTLDKDNFSLTPDLIHDLLGH-------VPWLLH
                                                                                                                                                                                                                                                                                                    ----TIQEWVQSAPDVHLHLPAPNVFIPTDLSL-KDADDKETVPVLLRKTPF--SRLWYK 496
                                                                                                                                                                                                                                                        HKCISILEFFKNILFVHL------LSLSKNQREGCSTDMAVVSTPFFNRNLWYR
                                                          LSDNGFELTLLGYNHKLRILLETVVGKIANFEVKPDRFAVIK----ETVTKEYQNYKFRQ
                                                                                                                                                                                 - PDTMFSKPKAYVKMDFNCPLAVSSPDAAVLTDIFTRLLMDYLNEYAYYAQVAGLYYGVS
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pred. No. 2.8;
18; Mismatches 128; Indels 1
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06-MAY-1999;
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11-MAY-1999;
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21-APR-1999;
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09-MAR-1999;
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25-MAY-1999;
27-MAY-1999;
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Query Match Best Local S Matches 97

Similarity

5.0%;

Conservative

48;

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Fri Jan 10 10:56:10 2003

5.0%; Score 95; DB 21; Length 970;

US-0147260 US-0147310 US-0147310 US-0147310 US-0147310 US-0148319 US-01488319 US-01488319 US-0148868 US-0148686 US-0148686 US-0148686 US-0148686 US-0148686		UNS - UL55689 UNS - UL55689 UNS - UL55689 UNS - UL5783 UNS - UL5783 UNS - UL5783 UNS - UL5929 UNS - UL5929 UNS - UL5929 UNS - UL5938 UNS - UL5938 UNS - UL5938 UNS - UL5938 UNS - UL5938	2 0.160741 2 0.160741 2 0.160811 3 0.160811 3 0.16081 3 0.16081 3 0.16081 3 0.16181
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29-MAR-1996;
02-APR-1996;
25-OCT-1996;
Helicobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori
                                                                                                                                                                                                                                                                                                      27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                        09-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H. pylori ORF hp5p15641_5211687_c2_29 cellular protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW55671 standard; Protein; 293 AA.
                                                                                                               Alm RA,
                                                                                                                                                                                        28-OCT-1996;
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                                                                                                                                                    (ASTR )
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                                                          1997-503122/46.
DB; AAV25080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYHQAMYYCSLILQDQTWP------WTEEL--DVLSHLEAEDVAKFVPMLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSDNGFELTLLGYNHKLRILLETVVGKIANFEVKPDRFÄVIK----ETVTKEYQNYKFRQ 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - PDTMFSKPKAYVKMDFNCPLAVSSPDAAVLTDIFTRLLMDYLNEYAYYAQVAGLYYGVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HKCISILEFFKNLLFVHL------LSLSKNQREGCSTDMAVVSTPFFNRNLWYR 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPAIVOKVVDELSPSNERIFWESOKFEGOTDKAEPWYNTAYSLEKITSS------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----GEGMKYFYHQDGSNPSDENSÅLVHYIQVHRDDFSMNIKLQLFGLVAKQ
                                                                                                                                                    ASTRA AB.
                                                                                                                 Smith D;
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96US-0625811.
96US-0758731.
96US-0736905.
96US-0738859.
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8; Mismatches 128; Indels 174; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is the sequence of a Helicobacter pylori cellular protein.

CC The protein may be used in a vaccine to prevent or treat H. pylori

CC useful as potential H. pylori polypeptide binding compounds,

CC useful as potential H. pylori life cycle activators or inhibitors. The

CN H. pylori in a sample and the diagnosis of H. pylori infection of

CC acid sequences complementary to the DNA act as antisense sequences and

CC acid sequences complementary to the DNA act as antisense sequences and

CC against the protein can be used in immunoassays to evaluate the abundance

CC and distribution of H. pylori mRNA. Antibodies

CC H. pylori (ATCC 55679) was determined from overlapping contigs generated

CC by mechanically shearing the bacterial DNA. The sequences were analysed

CC offined by computer evaluation. To identify likely H. pylori artigens for

CC vaccine development, the amino acid sequences predicted coding regions

CC membrane proteins. Having identified and determined the sequences of

CC interest, particular regions can be isolated from H. pylori by ECR

CC more amplification for recombinant polypeptide production, e.g. in E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 38
                                                                                                                                                                                                                                              Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis.
                                                                                                                                                                                                          Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                    S. epidermidis open reading frame protein sequence SEQ ID NO:1930.
                                                                                                                                                                                                                                                                                                                                           03-SEP-2001
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                                                            09-NOV-1999;
                                                                                              09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                                                                                                                                                                                                                                  AAG82418 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection and for diagnosis of H. pylori infection
                                                                                                                                     17-MAY-2001.
                                                                                                                                                                         WO200134809-A2
                       (GLAX ) GLAXO GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 PIASVMRTLDKDNFSLTPDLIHDLLGHVP-----W-----W-----LLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 E 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 NSFGFV---SPRDIGQMWIDQFDWVYREMDYAVFSMTIHPDVSARPQVLLMHEKIIEHIN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 KAYGAVLISSPQELGHAFIDNVRVLPLELDQIIRL----PFNTSTPQETLFS---IRHFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                212 PSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIAIVRCFWFTVESGLIENHEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 NDFTPYFVRVGDSWSKIDYSLEAKDWMKPLIRGVETNLVEIPANWYLDDLPPMMFIKKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 PIAMTAKQ-EEDVLLKSVELIKDLTGKAPTGYVAPWWEFSNITNELLLKHGFKYDHSLMH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 5.0%; Score 94; DB 1 Similarity 21.0%; Pred. No. 0.67 38; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   293 AA;
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                            99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .67;
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WPI; 2001-316495/33.

Kimmerly WJ;

N-PSDB; AAH53268

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AAH53304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAGG1454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) wish the production of vectors containing them which are used to produce hosts cells which express the polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the actument of S. epidermidis infections, e.g. endocarditis. AAH5391 to AAH5509 represent specifically claimed S. epidermidis genomic DNA polymucleotide sequences from the present invention. AH55091 to AAH5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.

N. B. The present invention specifically claims all the polymucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, on sequences are given in the disclosure for SEQ ID NO:4455 to 4464.
                                                                                                           Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis
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                                                                                                                                                                                Claim 18; Page 528; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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ID AAW1
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23; 382 KDDILS---KIQLSVESNFKLNHSNHILPIFEKSKEILDYHHATLDGYIESAIDREKQSS 438 209 IKDNMNVHFSRTYLRIMSHVYLNNPLTSQIKRLYPFVFNTLYDSIRQLSQDTNIQLSBDE 268 252 IVRCFWFTVESGLIENHEGRKAYGAVLISSPQ--ELGHAFIDN------VRVL--PLE 299 325 DINNYHFEGIDLLITTHDFDTSQ---LLQIPKVIQVSPLFSDEDAKKIEFFVKAMQNPLS 381 300 LDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEWMLD-----QGLLES----- 344 ' Match
5.0%; Score 94; DB 22; Length 528;
Local Similarity 20.5%; Pred. No. 1.6;
les 91; Conservative 71; Mismatches 172; Indels 110; Gaps 94 ISKHIDNHQLSTSENKIQQLLVHLILLIKHSQPEEEDWSTDTESLTIAKKCIKDINETLG 153 108 YRLLSSRFSLWKSYCPRFFLDY-LEAFGL-----LSDFLDH------QAVI 146 154 YOLNNK----TSECFSFFISYHFNKFDLGIQQLFIQSYIDRLIELMEQHIGFPFSQDTI 208 147 KFFELETHFS--YYPVSGFVAPHQYLSLLQDRYFP----IASVMRTLDKD-NFSLTPDL 198 IHDLLGHVPWLLHPSFSEF-----FINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251 59 LARH---KCIŞILEFFKNLLFVHLLSLSKN---QREGCŞTD-----MAVVSTPFFNRNLW 107 11 KYILKIALKIRQSLSLFFQNSQSLQRAY-----STPYSYYRIILQK-----ENKEKQA 58 35 KFDIYLSIKKKÓGI-MIDASTTŚISNÁVLHINQLTDDDFKVENLÍLÓELPQAHTRKÍKÓI 93 -----IPLYNQEKYLSGFEVL 360 439 TYIGKGIALPHGNPEKVLKSHMII 462 237 DFQLTIVTCKQFPKLSCIQLNCIDTQFTKLLDDNPTELDWPTYVDQNPLTMHKIIQLILM 296

167 HQYLSLLQDRYFPIASVM-----RTLDKDNFSL-----TPDLIHDLLGHVPW 208

186 YKPLLFEIVSNADTNONSHMKKKLELISYRNESLKNNSSIR------NVIMSASNAN

66 EFINKMENFEFLPLSLHILMIFWNDICQIDTNAPVAATITSSQKEPFFLVTKITDMLLHK 125

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Novel yeast SRB (suppressor of RNA polymerase B) proteins SRB4, SRB5, SRB9, SRB9, SRB10 and SRB11 (AAW18321-28) are transcription regulatory factors that act as positive and negative regulators of RNA polymerase II activity, and are components of the RNA polymerase II holoenzyme. They were identified using methods designed to identify transcription factors involved in RNA polymerase II c-terminal domain (CTD) function. SRBs and SRB9 appear to repress CTD activity. Genomic clones (AAT59904-11) for the SRBs have been obtd. SRBs can be used to treat diseases resulting from alteration or deletion of the SRB gene, pref. by gene transfer technology. They can also be used in in vitro transcription of DNA and to identify endeds. that modify gene transcription.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .Match
Local Similarity 18.4%; Pred. No. 5.2;
es 96; Conservative 67; Mismatches 156; Indels 202; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purified RNA polymerase II holo:enzyme - comprises RNA polymerase II and one or more regulatory proteins, pref. suppressor of RNA polymerase B proteins or SWI/SNF proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 YILKIALKIRQSLSEFFQNSQSLQRAYSTPYSYYRII-----LQKENKEKQALARHKCI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 YILE---KLIFDMTNHYNDSQQL-RTWKRQISYFLKLLGNCYSLRLINKE---IFHHWLV
                                                                                                             Transcription regulatory factor; suppressor of RNA polymerase B; SRBB; RNA polymerase II; holoenzyme; SWI/SNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 SILEFFKNILF----VHLLSLSKNOREGCSTDMAVVST-----PFF-
                                                                                                                                                                                                                                                                                                                                                                                                                   Chao DM, Koleske AJ, Thompson CM, Young RA;
                                                                                 Yeast transcription regulatory factor SRB8
                                                                                                                                                                                                                                                                                                                                                                                (WHED ) WHITEHEAD INST BIOMEDICAL RES
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                                                                                                                                                                                                                                                                                                                             95US-0521872.
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                                                (first entry)
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                                                                                                                                                                    Saccharomyces cerevisiae
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N-PSDB; AAT59908.
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11-OCT-1995;
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                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                  The present invention is related to a Lactococcus lactis nucleotide sequence (ABA90521) and related proteins (ABB3000-ABB55621). The nucleic acid sequence is useful in the detection and/or amplification of nucleic acid sequence, particularly to identify Lactococcus lactis or related species. The proteins of the invention are useful for the biosynthesis or biodegradation of a composition of interest. The invention helps research in lactic bacteria, particularly useful in the production of yogutt and cheese.

Note: The sequence data for this patent is based on equivalent patent wo200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; SEQ ID No 1759; 2504pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleotide sequence useful in the identification or Lactococcus lactis and related species - {\sf}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bolotine A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRG ) INRA INST NAT RECH AGRONOMIQUE.
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2002-043418/06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------EWMLD---QGLLESIPLYNQEKYLSGFEVLC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINLKISPLMKSQYNMVLRNVMEYDVKFYEIFNFDQVVEITEQIKMRILSNDITNLQLSK
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical insging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations

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Schall TJ, Penfold M;
                            WPI; 2002-351718/38.
N-PSDB; ABK68823.
                                                                                                                                                                                                                                                                                                                                                                                                                                             333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU33268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
 other traits to assess biodiversity
responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00100-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences.
                                                                                                                                                                                                                                                  | |: | | : | | | 391 ALHQA-DLIDIYRTLHPKSTAYTFFSAPHHTYSKIDHILGSKALLSKCKRTEIITNCLSD 449
                                                                                                                                                                                                                                                                                                                                                        551 -------KIDRPLARLIKKKEKNQIDAIKNDKGDITIDPIBIKIT 588
                                                                                                                                                                                                          335 YAPNTGAPRFIKQVLSDLQRDL----DSHTLIMGDFNTPLSTLDRSMRQKVNKDTQELNS 390
                                                                                                                                                                                                                                                                                     94 MAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAFGLLSDFLDH---QAVIK-FF 149
                                                                                                                                                                                                                                                                                                     150 ELE----THFSYYPVSGFVAPHQYLSL-----LQDRYFPIASVMRTLDKDNFSLTPD 197
                                                                                                                                                                                                                                                                                                                                                                                        198 LIHDLLGHVPWLLHPSFSEFFINMGRLFTKVIEK-----VQALPSKKQRIQTLQSNLIAI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                           253 VRCFWFTVESGLIENHE----S 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   589 IREYYKHLYANKLENLEEMDKFLDKYTLPRLNQEEVESLNRPITGAEIVAIINSLPTKKS 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282 P-----OELGHAFIDNVRVLPLELDQIIRLPFNTSTPQETL----FSIRHFDELVELTS 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 PGPDGFTAEFYQRYKEELLVCPTFLFE--KHPVNYDFEQETLHFSPISLRSSEELNLSTY 706
                                                                                                                                Query Match

4.9%; Score 93; DB 22; Length 744;
Best Local Similarity 19.2%; Pred. No. 3.2; 3.2;
Matches 87; Conservative 73; Mismatches 140; Indels 152; Gaps
                                                                                                                                                                                 3 YCERTLDPKYILKIALKIROSLSLFFQNSOSLORAYSTPYSYY-RIILOKENKEKQAL-- 59
                                                                                                                                                                                                                                   60 ARHKCISILEFFKNL-----EGCSTD 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CMV; US28; vaccine; virucide; neuroprotective; antiinflammatory; ophthalmological; retinitis; encephalitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---EWMLDQGLLESIPLYNQ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     707 RLYGWSEEQSLWVIRTWARVQKFRAAVPLVNE 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RhCMV unique short region US28.4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU96092 standard; Protein; 333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-AUG-2000; 2000US-229365P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-2001; 2001WO-US27392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHEM-) CHEMOCENTRYX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhesus cytomegalovirus.
                                                                                                      744 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 KL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200218954-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pneumocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-MAR-2002
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAU96092;
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The invention relates to an isolated or recombinant homologue of US28 protein which binds a chemokine (encoded by an open reading frame in the unique short (US) region in human cytomegalovirus (CWW) genome), having at least 75% identity to a rheasum monkey RhUS28.1-RhUS28.5, Rh78 and RhUS33 (encoded by an open reading frame 78 in the unique long (UI) and CRW sister of the comprising an immunogenic acids. Also included are a vector comprising the nucleic acids, a cell comprising the nucleic acids, a vaccine comprising an immunogenic CWV polypeptide encoded by at least a region of CWV genome in which the polypeptide encoded by at least a region of CWV genome in which the polypeptide encoded by at least a region of CWV genome in which the polypeptide encoded by at least a region of CWV genome in which the polymuclectide sequence encoding US28 or inactivated, identifying an agent that reduces CWV dissemination in an animal, by determining whether the agent inhibits the expression or us28 homologue and treating an animal infected with CWV or at risk of infection by CWV. by administering the agent to the animal. The vaccine is useful for treating an animal infected with cytomegalovirus or at a risk of infection by CWV. The vaccine is also useful for inducing a treating an animal infected with cytomegalovirus or at a creating diseases including retinitis, encephalitis and pneumocystis caused by CWV us or UL protein used to construct the vaccine of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and in methods for
Isolated or recombinant homologues of US28 proteins and nucleic acids encoding the proteins, for use in vaccine compositions for treating an animal infected with, or at risk of infection by, cytomegalovirus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 KQRIQTLQSNLIAIVRCFWFTVESGLIENHEGRKAYGAVLISSPQELGHAFIDNVRVLPL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 SSAVLNLEVHLCS----FWLPLIM-----SANCYYQAKRRASPDQLHELYRCSLLITII 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.9%; Score 92; DB 23; Length 333;
21.7%; Pred. No. 1.3;
.ive 44; Mismatches 101; Indels 72; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 YCPRF-FLDYLEAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAPHQYLSLLQDRYFP 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92 WCRSLTFVFYLTVFAR-----AFF-----AFF------YLLLIWDRYSV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, vaccination, gene therapy, nutritional supplement, stem cell proliferation, haematopoiesis, nerve tissue regeneration,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 IASVMRTLDKDNFSLTPDLIHDLLGHVPWLLHP-SFSEFFINMGRLFTKVIEKVQALPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 ELDQIIRLPFNTSTPQETLFSIRHFDELVELTSKLEW 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 TTYAİVWFPFHLALLIDALISISH----VEPSSALHW 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human secreted protein #3759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU33268 standard; Protein; 919 AA.
                                                                                                                                                                                          Claim 69; Page 67; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel human secreted polypeptides. The projectides and antibodies to the polypeptides are useful for determining the presence of or predisposition to a disease associated with altered levels of polypeptide. The polypeptides are also useful for identifying agents (agonists and antagonists) that bind to them. Cells expressing the proteins are useful for identifying a therapeutic agent for use in treatment of a pathology related to aberrant expression or physiological interactions of the polypeptide. Vectors comprising engineered to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as mutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; in treatment of leukaemias. AAU33510-AAU33304 represent the amino acid of sequences of novel human secreted proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                AAY31237 standard; Protein; 3923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 20; Page 750; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding a range of human vaccination, testing and therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-APR-2000; 2000US-0552929
26-JAN-2001; 2001US-0770160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-APR-2001; 2001WO-US08656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune suppression; immune stimulation; anti-inflammatory; leukaemia
                                                                                              787
                                                                                                                                                             727
                                                                                                                                                                                             167
                                                                                                                                                                                                                            669
                                                                                                                                                                                                                                                          114
                                                                                                                                                                                                                                                                                                                                                        567
                                                                                                                                                                                                                                                                                                                       60
                                                                                              NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI--IKSQAIA 839
                                                                                                                              ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                            NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA
                                                                                                                                                                                                                                                          RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP----
                                                                                                                                                                                                                                                                                         RKHKLIDVISMYREL----LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED
                                                                                                                                                                                                                                                                                                                           ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                                                                                                                                                                                                          YTREELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L
                                                                                                                                                                                                                                                                                                                                                                                        YCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                             SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS
                                                                                                                                                                                             -----HQYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI--------
                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT
                                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 92;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptides, useful in genetic
                                                                                                                                                                                                                                                                                                                                                                                                                       118;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       68;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                           899
                                                                                                                                                                                                                                                                                                                                                          613
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Query Match

Local

Similarity

4.9%; Score 92; DB 20.7%; Pred. No. 44; tive 48; Mismatches

DB 20; Length 3923; 44; 118;

Indels

68;

Gaps

12;

3617 59 61;

Conservative

3618

3571

3673 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 3730

114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166

60 ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113

LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED

3 YCERTLDPKYILKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL YTREELCTMFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L

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This invention describes a novel method for the genetic treatment of hyperlipidemia by altering genes, in hepatcoyres, for apoprotein (apo) B, E or Al. Low density lipoprotein (LDL) levels in the blood are reduced by altering an apo B gene (I) in a hepatcoyre. The invention describes a method for the therapeutic and/or prophylactic method involving altering an apo B gene in hepatcoytes by introducing the mutations Argilacys or Cys158Arg and a method for ameliorating atheroscis by altering the apo Al gene in a hepatcoyte so that the altered protein can dimerize. Altering expression of apo genes regulates levels of high and low density lipoprotein cholesterol. Altering expression of apo B, E and Al genes is used to treat or prevent atherosclerosis, coronary heart disease, Alzheimer's disease, hypobetalipoproteinemia, This sequence represents a fragment of the human Apo B protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo E; Apo B; hyperlipidemia; human; treatment; hepatocyte; apoprotein; Apo Ai; low density lipoprotein; blood; therapy; atherosclerosis; high density lipoprotein; HDL; cholesterol; coronary heart disease; Alzheimer's disease; hypobetalipoproteinemia; dysbetalipoproteinemia.
Sequence
                                                                                                                                                                                                                                                                                                            Mutating apolipoprotein genes in hepatocytes to control cholesterol levels, e.g. for treating or preventing hyperlipidemia, particularly atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-527333/44.
N-PSDB; AAZ09525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-1998;
12-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-1999
                                                                                                                                                                                                                                                                            Claim 4; Page 75-83; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         Bandyopadhyay PT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9940789-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human Apo B protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY31237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (YESH ) UNIV MINNESOTA.
3923 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0108006
98US-0074497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-US17908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Apo B
/note= "Partial sequence, no start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             Kren BT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Roy-Chowdhury J,
                                                                                                                                                                                                                                                                                                                                                                                                                             Steer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        given"
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This sequence represents the human apoliporptoein B-100 (apoB-100).

Fragments of this sequence can be used in the peptide of the invention, which has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100).

21 - than terminus of the peptide, or 1-47 amino acids (as);

22 = the C terminus of the peptide, are used for simultaneous, separate compositions containing the peptide, a terminal amide group or 1-77 as.

32 = the C terminus of the peptide, a terminal amide group or 1-77 as.

33 = the C terminus of the peptide, a terminal amide group or 1-77 as.

34 = the C terminus of the peptide, a terminal amide group or 1-77 as.

35 = the C terminus of the peptide, a terminal amide group or 1-77 as.

36 = the C terminus of the peptide, a terminal amide group or 1-77 as.

37 = the C terminus of the peptide, a terminal amide group or 1-77 as.

38 = the C terminus of the peptide, a terminal amide group or 1-77 as.

39 = the C terminus of the peptide, a terminal amide perior or signification (e.g. during or after spread; the peptide are used for simultaneous, separate or spread to inhibit thromboplastin and peptide, inhibits activation of the surface of thromboplastin and of platelete by thrombin. It binds to the treating of the peptide are applied to the much smaller than the treating than the treatine than the treatine treating the treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine treatine tr
                                    3731 SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS 3790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thrombopbastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14; prothrombinase complex.
167 -----HQYLSLLQDRYFPIASVMRT----LDKDNFSLTPDLI------ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity - used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis
                                                                                                                                                                  3791 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI--IKSQAIA 3843
                                                                                                             200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9%; Score 92; DB 19; Length 4536; 20.7%; Pred. No. 55; Live 48; Mismatches 118; Indels 6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 42-47; 60pp; English
                                                                                                                                                                                                                                                                                                         AAW41262 standard; peptide; 4536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruckdorfer KR, Ettelaie C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-GB01255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96GB-0009702.
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4536 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9743311-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1998
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Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density density lipoproteins (VLDL), intermediate density lipoprotein (IDL), low density lipoproteins (VLDL), and lipoprotein a. The specification density lipoproteins (LDL) and lipoprotein a. The specification binding and in vivo transport of nucleic acids. Binding domains (see AAW96827-77) and nuclear localisation sequences (see AAW96878-97) for use in the composition can be derived from the present sequence. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis.
                          4184 YTREELCTWFIREVGTVLSQVYSKVHNGSEIL-----FSYFQDLVITLPFE-----L 4230
                                                                                                                                                                                          4286 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4343
                                                                                                                   4231 RKHKLIDVISMYREL----LKDLSKEAQEVFKAIQSLKTTEVL-RNLQDLLQFIFQLIED 4285
                                                                                                                                                                                                                                                                                60 ARHKCISILEFFKNLLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                               114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
                                                                                                                                                                                                                                                  167 -----HOYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI------ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and
YCERTLDPKYILKIALKIRQSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL
                                                                                                                                                                                                                                                                                                                                                                   4404 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKËKIAELSATAQEI--IKSQALA 4456
                                                                                                                                                                                                                                                                                                                                      200 ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of human apolipoprotein B-100 (apoB-100).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1A-C; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW96826 standard; protein; 4536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Query Match
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Matches 61
This polypeptide comprises a novel thermostable DNA polymerase of the thermophilic anaerobe Thermoanaerobacter thermophicous Its amino acid sequence was deduced from an isolated genomic DNA sequence (see AAT90447). Recombinant DNA polymerase can be produced in host cells. The enzyme can be used in claimed methods: (a) for strand displacement amplification (SDA) when used with a thermostable restriction enzyme; (b) for production of cDNA when used in conjunction with polymerase and deoxyribonucleotides; and (c) to provide reverse transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                    Example 1; Page 49-52; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  New DNA polymerase from Thermoanaerobacter thermohydrosulfuricus - useful for strand displacement amplification, reverse transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9721821-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoanaerobacter thermohydrosulfuricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA polymerase; exonuclease; strand displacement amplification; Thermoanaerobacter thermohydrosulfuricans; reverse transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoanaerobacter thermohydrosulfuricus DNA polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW26605 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4404 NFTSQLSSQVEQFLHRNIQEYLSILTDPDGKGKEKIAELSATAQEI -- IKSQAIA 4456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4286 NIKQLKEMKFTYLINYIQDEINTIFNDYIPY--VFKLLKENLCLNLHKFNEFIQNELQEA 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4231 RKHKLÍDVISMYRBÍ----ÍKDÍSKEAQEVFKAIQSIKTTEVL-KNÍQDLLQFIFQÍIED 4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMSH ) AMERSHAM LIFE SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 RFSLWKSYCPRFFLDYL--EAFGLLSDFLDHQAVIKFFELETHFSYYPVSGFVAP---- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 YCERTLDPKYILKIALKLROSLSLFFQNSQSLQRAYSTPYSYYR---IILQKENKEKQAL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-332792/30
DB; AAT90447.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---HDLLGHVPWLLHPSFSEFFINMGRLFTKVIEKVQALPSKKQRIQTLQSNLIA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQELQQIHQYIMALREEYFDPSIVGWTVKYYELEEKIVSLIKNLLVALKDFHSEYIVSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----HQYLSLLQDRYFPIASVMRT-----LDKDNFSLTPDLI--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARHKCISILEFFKNILFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLW-----YRLLSS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61;
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Similarity 20.7%;
61; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mamone JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4536
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%; Pred. No. 55;
48; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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          Mamone JA, Davis M,
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                                                                                                                                                                                        17-MAR-1999;
                                                                                                                                                                                                                                                   23-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thermoanaerobacter thermohydrosulfuricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA polymerase; thermostable enzyme; amplification;
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                                                                                                                                18-MAR-1998;
                                                                  (AMSH ) AMERSHAM PHARMACIA BIOTECH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reverse transcription; exonuclease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDGF 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                    98US-0044106.
                                                                                                                                                                                        99WO-US05612
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Mismatches 141;
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RESULT 47
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WPI; 1999-562049/47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                              This sequence represents the DNA polymerase of Thermoanaerobacter thermohydrosulturious (TE), deduced from PCR amplified genomic DNA (see AAZ19659). Claimed DNA polymerases (see AAX18131. AAX1815 and AAX31816) have the exonuclease activity of this enzyme removed by having 540-582 amino acids removed from the N-terminus or having an amino acid substitution at position 8 or 706 of the sequence. A novel method for PCR uses an enzymatically active DNA polymerase that has at least 80% identity in its amino acid sequence to the Ttb DNA polymerase and has an exonuclease activity removed. Kits for and reverse transcription-PCR are claimed that utilise such Exonant everse. The Tt DNA polymerase is stable at elevated bNA polymerases. The Tt DNA polymerase is stable at elevated temperatures, e.g. 70+ deg C. Removal of its exonuclease activity does not affect its ability to replicate DNA or its thermostability.
                                                        polymerase from Thermoanaerobacter thermohydrosulfuricus, used amplification, sequencing, polymerase chain reaction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               352 KEIFEKEDFEFTTHEIKDFLVRLSYKGIECKSKYIDTAVMAYLLNPSESNY--DLDRVLK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : || : || : || 410 KYL-KVD-VPSYEGIFGKGRDKKKIEEIDENILADYICSRCVYLFDLKEKLMNFIEEMDM 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVIEKVQALPS------ZKKQRIQTLQSNLIA---IVRCFW------ 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR---LPFN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | | : | : | | : | | 468 KKLLLEIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKIYKEAGYQFN 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 4.8%; Score 91.5; DB 20; Length 872; Local Similarity 17.5%; Pred. No. 5.7; Conservative 70; Mismatches 141; Indels 139; Gaps es 74; Conservative 70; Mismatches 141; Indels 139; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 TLLQD------DRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQTE-----DL 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 TSTPQE-TLFSIRHFDELVELTSKLEWMLDQGLLESIPLYN--------QEKY 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter thermohydrosulfuricus DNA polymerase D8A mutant.
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                                                                                                                       Example 6; Fig 2; 71pp; English.
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                                                                                        reverse transcription
            WPI; 1999-562049/47.
N-PSDB; AAZ19859.
                                                                                                                                                                                                                                                                                                                                                                                        872 AA;
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This sequence represents a claimed mutant DNA polymerase of Thermoanderobacter thermohydrosulfuricus (Tt) in which the Asp-8 residue of the native enzyme is replaced by Ala. This amino acid substitution removes the acondidease activity of the DNA polymerase. Claimed DNA polymerases have their exonuclease activity removed by N-terminal deletion or amino acid substitution. A novel method for PCR uses an enzymatically active DNA polymerase and has an exonuclease activity removed. Kits for that has at least 80% identity in its amino acid sequence to the Tt DNA polymerase and has an exonuclease activity removed. Kits for PCR, strand displacement amplification of DNA, DNA sequencing, and reverse transcription-PCR are claimed that utilise such Exo-DNA polymerases. The Tt DNA polymerase is stable at elevated temperatures, e.g. 70+ deg C. Removal of its exonuclease activity choses not affect the ability to replicate DNA or its thermostability. Note: the present sequence is not shown in the specification but is derived from the Tt DNA polymerase seugnece given in figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA polymerase from Thermoanaerobacter thermohydrosulfuricus, used for DNA amplification, sequencing, polymerase chain reaction and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 LLFVHLLSLSKNOREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 GLLSDFLDHQAVIKFFELETHFSYYPV-----SGFVAPHQYLSLLQDRYFPIASV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 KVIEKVQALPS------KKQRIQTLQSNLIA---IVRCFW------------257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 TLLQD------NRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQTE-----DL 351
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DNA polymerase; thermostable enzyme; amplification; sequencing;
                                                                                                                                                                                                                                                                                                                                                                 /note= "wild-type Asp is substituted by Ala"
                                          PCR; reverse transcription; exonuclease; mutant.
                                                                                                                                     Thermoanaerobacter thermohydrosulfuricus
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                                                 This sequence represents a claimed mutant DNA polymerase of Thermoanaerobacter thermohydrosulfurious (Tt) in which the Phe-706 residue of the native enzyme is replaced by Tyr. This amino acid substitution removes the exonuclease activity of the DNA polymerase. Claimed DNA polymerases have their exonuclease activity removed by N-terminal deletion or amino acid substitution. A novel method for PCR uses an enzymatically active DNA polymerase that has at least 80% identity in its amino acid sequence to the Tt CDNA polymerase and has an exonuclease activity removed. Kits for PCR, strand displacement amplification of DNA, DNA sequencing, and reverse transcription-PCR are claimed that utilise such Exo-CDNA polymerases. The Tt DNA polymerase is stable at elevated temperatures, e.g. 70+ deg C. Removal of its exonuclease activity Note: the present sequence is not shown in the specification but is concerned from the Tt DNA polymerase sequence given in figure 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New DNA polymerase from Thermoanaerobacter thermohydrosulfuricus, used for DNA amplification, sequencing, polymerase chain reaction and reverse transcription -
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   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 23; Page -; 71pp; English.
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Query Match
34.8%; Score 91.5; DB 20; Length 872;
Best Local Similarity 17.5%; Bred, No.5.7;
Matches 74; Conservative 70; Mismatches 141; Indels 139;
585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 LKIALKLRQSLSLFFQNSQSLQRAYSTPYSYYRIILQKENKEKQALARHKCISILEFFKN 73
IDGF 588
                                  LSGF 357
                                                                        VNSPKQLSEFLFEKLNLPVIKKTKTGYSTDSEVLEQLVPYNDIVSDIIEYRQLTKLKSTY
                                                                                                           TSTPQE-TLFSIRHFDELVELTSKLEWMLDQGLLESIPLYN------QEKY
                                                                                                                                                KKLLLEIEMPLVEVLKSMEVSGFTLDKEVLKELSQKIDDRIGEI---LDKIYKEAGYQFN
                                                                                                                                                                                     ----FTVESGLIENHEGRKAYGAVLISSP-QELGHAFIDNVRVLPLELDQIIR----LPFN
                                                                                                                                                                                                                          KYL-KVD-VPSYEGIFGKGRDKKKIEEIDENILADYICSRCVYLFDLKEKLMNFIEEMDM 467
                                                                                                                                                                                                                                                                                                                                       MRTLDKDNFSLTPDLIHDLL-------GHVPWLLHPSFSEFFINMGRLFT 226
                                                                                                                                                                                                                                                                                                                                                                            TLLQD------NRNIAFYPLIYEGEIKKIAFSFGKDTVYIDVFQTE-----DL 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLFVHLLSLSKNQREGCSTDMAVVSTPFFNRNLWYRLLSSRFSLWKSYCPRFFLDYLEAF 133
                                                                                                                                                                                                                                                             KVIEKVQALPS-----KKQRIQTLQSNLIA---IVRCFW---------
                                                                                                                                                                                                                                                                                                    KEIFEKEDFEFTTHEIKDFLVRLSYKGIECKSKYIDTAVMAYLLNPSESNY--DLDRVLK 409
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